Editor Note

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Functionality and Clinical Effects of Anti-Cov2 Vaccines (Aka Mrna) And Integration on Mitochondrial DNA

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Abstract

1. This issue would require many pages, but it is briefly described here for easier understanding

2. The writer refers to the Molecular Biology Experts and to reading the copious literature on the proteins/enzymes found in mRNA vaccines using the BLASTP approach (Appendix 1)

3. The reference literature, apart from being written in English, is also worded in an extremely technical style

4. They are given a specific functional sequence, aimed at the incorporation and expression of vaccine mRNA into the genome of the mitochondria (mtDNA)

5. The vaccine mRNA does not refer to the segment relating to the Spike protein, but to the entire viral genome

6. Therefore, the Ribosomes are not the final destination of the vaccine mRNA; instead, the Mitochondria are actually the seat of a DNA, accommodating the SARS-Cov2 genome in the same way as it does in the nuclear genome.

7. Both the Mitochondria and Ribosomes are located in the Ergastoplasm and are separated from the cytosol by an oxidation/reduction barrier 'in mV' (= one thousand times) three times higher than that of the cytosol.

8. Article from Science: Oxidized Redox State of Glutothiane in the Endoplasmic reticulum - 11 September 1992 volume 257, page 1496:15026

9. Thus only an mRNA that exits from both the nuclear and mitochondrial genomes has the enzyme support that allows it to reach the ribosomes, overcoming the resistance of the oxidation/reduction barrier

10. If this were not the case, RNA viruses would not lengthen the pathway, integrating before the genome and then reaching the ribosomes again as mRNA (it must be said that, in an RNA virus, the genomic RNA is the same as the RNA coming out of the nucleus), but would immediately aim to reach the ribosomes, as RNA vaccines are said to do.

11. Nano technologies are said to be the architects of this miraculous and rapid rush to the ribosomes of vaccine mRNA

12. These nano-technologies are nothing more than a sequence of proteins/enzymes - undeclared - which are now described here in their function in the main patterns

13. a) ryanodine receptor-
by managing the Ca++ ion flux channels, it first depolarises the mitochondrial membrane, which is the first step for mRNA entry and then it lowers the oxidative/reductive level of the ergastoplasm, activating an osmotic "Δ" (= delta-difference) around the mitochondria, releasing the protonated ions (=H +) present in the virtual space of the two sheets forming the mitochondrial membrane into the area.

14. b) ABC transporter - ATP - binding protein
By binding to ATP, it allows vaccine RNA to enter the mitochondria

15. c) Epical complex lysine methyltran spherase
By providing mobility for the entering mRNA, it allows to reach the stretch of mitochondrial DNA most suitable for integration

16. d) DDLS - Typ - integrase/transpasase
It simultaneously does the work performed before by reverse transcriptase and integrase, and then inserts a viral genome RNA, similar to the genomic RNA in RNA viruses, into the mitochondrial genome.

17. e) Pullulanase
The hydrolysis of the (1 → 6) X - D glucoside bonds of mitochondrial DNA paves the way for the action of the

18. f) DNA Helicase
which by copying the inserted DNA - DNA from the mRNA vaccine - makes it more permanently stored in the mitochondrial genome
19. - Note -
The presence of DNA Helicase in mRNA vaccines is further proof that integration does not take place in the core genome. It is impossible for the nuclear genome to simultaneously absorb and copy a viral genome when, due to the 'restitutio ad integrum' acquired during evolutionary times, it tends to shed the viral genome after the infection is past. If this were not the case, the 'Spanish flu' contracted by our grandparents could reappear today through genetics.
20. g) DNA J homolog subfamily B
completes the job, aiding the release of the new mRNA and providing it with support to reach ribosomes as is the case for all mRNAs of both nuclear and mitochondrial origin.
21. A larval infection of low-intensity SARS Cov2 has thus occurred at the mitochondrial site
22. This infection is evidenced by the presence of biochemical patterns associated with the existence of a viral cycle in the blood of multi-vaccinated with SARS vaccine- Cov2
They are:
1. Fatty acid synthase
2. Interlenkui 17 F
3. ATP defendent RNA Helicase DH X 58
4. TIR domain containing aslapter Molecule 1
5. Vam 6/Vps39-litie protein
6. NACHT, LRR aust PY D damains containing protein 1
7. Replicase paly protein 1a
8. Basigm
9. Spike glycoprotein
and the list goes on.
23. The picture described is not devoid of secondary clinical events, commonly referred to as 'adverse events'.
(a) Weakness asthenia. Mitochondria are the seat of ATP production - the human energy source. The new role given by vaccines to mitochondria reduces their ATP production ability.
(b) Cardiac arrhythmias and arrests due to the action of the ryanodine receptor, which eliminates Ca++ ions not only in skeletal muscles, but also in the myocardium, resulting in altered and impaired ventricular contractility
(c) 5-7 months following the third dose of the mRNA vaccine, a loss of CD+19 can be observed. A new form of immunodeficiency is arising that has yet to be fully understood.

24. To date, no serious effects from SARS-Cov2 on a massive scale are recorded, not because the vaccines under consideration have promoted an effective immune action, with a corresponding memory for future defence, but because a fact has occurred that in nature is a real stretch: the larval SARS-Cov2 infection at the mitochondrial site is opposed by another infection at the nuclear site, thus creating an opposition similar to that which occurs between two algebraic numbers of opposite sign. They decrease in value.
25. Antic-Covid19 mRNA vaccines are dangerous.

Side note

Considering that, at the onset of Covid 19 infection, a marked asthenia with abnormal and paradoxical albumin consumption was observed in infected patients, whereas fat reserves were not mobilised via the usual beta-oxidation of fatty acids, it can therefore be assumed, unlikely as it may sound, that SARS-Cov2, after manipulation, from its reductive oxide, may have a dual integration site - the nuclear genome and the mitochondrial genome. This results in the disruption of ATP production and the organic energy disorders noted and, possibly, even the most severe forms of the disease. Hence the need for mitochondrial integration that antagonises the virus embedded in the nucleus by the vaccine mRNA, as described in the previous pages.

PRIMARY SOURCES

1. Ansovini Technology Patent US8852582B2.
2. Ansovini R. Determination of an Antiviral Activity of a Composition Comprising Glutathione Reductase (GSSG-R) and Oxidized Glutathione (GSSG) for Pharmaceutical use: Experiments In vitro and In vivo. J Biomed Res Environ Sci. 2020 Jun 17; 1(2): 029-038. doi: 10.37871/jels1117, Article ID: jels1117.
3. Ansovini R, Compagnucci L. The Hypothetical Role of Erythrocytes in COVID-19: Immediate Clinical Therapy. J Biomed Res Environ Sci. 2020 Jul 02; 1(3): 048-050. doi: 10.37871/jels1119, Article ID: JELS1119.
4. Ansovini R, Compagnucci L. Use of Polio Vaccine Salk vs SARS- CoV-2E and HIV-1E 2, both as Therapeutic Drug and Effective Vaccine to Make Memory-Cells Able to Stop Reinfections. J Biomed Res Environ Sci. 2020 Nov 18; 1(7): 311-312. doi: 10.37871/jbres1160, Article ID: JBRES1160.
5. Ansovini R. The Truth about mRNA Vaccines. J Biomed Res Environ Sci. 2022 Jan 29; 3(1): 094-095. doi: 10.37871/jbres1406, Article ID: jbres1406.
6. Hwang C, Sinskey AJ, Lodish HF. Oxidized redox state of glutathione in the endoplasmic reticulum. Science. 1992 Sep 11;257 (5076):1496-502. doi: 10.1126/science.1523409. PMID: 1523409.

Appendix 1

BLASTP search results

BLASTP 2.0MP-WashU [04-May-2006] [linux26-x64-I32LPF64 2006-05-10T17:22:28]

Suplimentary code is mentioned in below of the reference section

References

1. Gish, W. (1996-2006) http://blast.wustl.edu
2. Shevchenko, A., Sunyaev, S., Loboda, A., Shevchenko, A., Bork, P., Ens, W., & Standing, K. G. (2001). Charting the proteomes of organisms with unsequenced genomes by MALDI-quadrupole time-of-flight mass spectrometry and BLAST homology searching. Analytical chemistry, 73(9), 1917-1926. Abstract

Query= query_sequence
(203 letters)

Echofilter:

>Unfiltered+0
PTGGHDRNSGNYLRGLSSWARGATAYSREHTRPTRGFTVTHRTSASAYRHPSNTHRGAGA
VRRSDGDNMRSAPLTHRHVFDDRRVYDQYYRVFSDVMREGLHMSKLTHSPGRVDLAMMRD
GVDVHRLSGLAMRAHSHHTRVGPDHTRMASECHRDTGLLERSAWWELRSSRLYCKLANLL LRLMALRRRDDGNYLRASQLLLR

Database: NCBI nr95 (MS-BLAST) 144,844,843 sequences; 49,010,334,033 total letters.

Searching....10....20....30....40....50....60....70....80....90....100% done

Color Key: red = positive hit; green = borderline hit; black = negative result

High Total
Sequences producing High-scoring Segment Pairs: Score Score
/:CUE79935.1 inositol 1,4,5-trisphosphate/ryanodine recep... 64 189
/:WP_151079925.1 MULTISPECIES: hypothetical protein [uncl... 40 183
/:XP_029901852.1 F-box DNA helicase 1 [Myripristis murdjan]/ 56 180
/:ADG75409.1 alpha-1,6-glucosidase, pullulanase-type [Cel... 57 179
/:XP_019169829.1 PREDICTED: probable serine/threonine-pro... 53 173
/:XP_029218919.1 apical complex lysine methyltransferase ... 52 168
/:QAA76796.1 Transketolase [Candidatus Bipolaricaulis sib... 60 168
/:XP_025997073.1 dnaJ homolog subfamily B member 6-B-like... 59 168
/:WP_068254241.1 hypothetical protein [Janibacter coralli... 53 167
/:XP_011265016.1 dnaJ homolog subfamily B member 6-B isof... 59 164
/:WP_084032530.1 DDE-type integrase/transposase/recombina... 51 163
/:WP_019146189.1 deoxyguanosinetriphosphate triphosphohyd... 49 161
/:WP_003931701.1 hypothetical protein [Mycolicibacterium ... 47 159
/:XP_023095958.1 basic proline-rich protein-like [Felis c... 46 159
/:XP_001707494.1 Hypothetical protein GL50803_32673 [Giar... 46 154
/:NBB68986.1 phosphoenolpyruvate carboxylase [Alphaproteo... 59 145
/:HFE44551.1 hypothetical protein [Nannocystis exedens]/ 53 144 /:WP_153398479.1 penicillin-binding protein 2 [Ornithinic... 51 143
/:WP_102647918.1 alpha,alpha-trehalose-phosphate synthase... 74 142
/:TAM50426.1 alpha,alpha-trehalose-phosphate synthase (UD... 74 142
/:WP_074578074.1 DUF2169 domain-containing protein [Polar... 53 141
/:XP_011702985.1 PREDICTED: dnaJ homolog subfamily B memb... 59 141
/:RLS30951.1 hypothetical protein DWH78_13845 [Planctomyc... 51 140
/:KZS03838.1 Uncharacterized protein APZ42_033339 [Daphni... 61 139
/:WP_057246641.1 hypothetical protein [Duganella sp. Root... 49 139
/:WP_113617232.1 hypothetical protein [Chitinophaga flava... 64 139
/:WP_102069824.1 alpha,alpha-trehalose-phosphate synthase... 68 138
/:XP_012255663.1 dnaJ homolog subfamily B member 6-like i... 59 138
/:WP_094301623.1 cobalamin biosynthesis protein [Azospiri... 48 137
/:WP_131518914.1 glycerophosphodiester phosphodiesterase ... 49 137
/:NDC61331.1 bifunctional diaminohydroxyphosphoribosylami... 55 136
/:TMF77358.1 hypothetical protein E6I15_04945 [Chloroflex... 49 136
/:WP_115533291.1 alpha,alpha-trehalose-phosphate synthase... 68 136
/:XP_012135622.1 PREDICTED: dnaJ homolog subfamily B memb... 59 136
/:XP_012522221.1 dnaJ homolog subfamily B member 6 isofor... 59 135
/:HEG86595.1 murein biosynthesis integral membrane protei... 55 134
/:WP_069321809.1 CatB-related O-acetyltransferase [Sphing... 47 134
/:WP_156384232.1 hypothetical protein [Marmoricola sp. Le... 53 134
/:WP_051399855.1 ABC transporter ATP-binding protein [Amy... 63 134

/:AHB48716.1 succinate-semialdehyde dehydrogenase [Hyphom... 68 133
/:WP_156876682.1 ABC transporter permease subunit [Microb... 61 133
/:WP_119999131.1 bifunctional diaminohydroxyphosphoribosy... 49 133
/:WP_147454093.1 hypothetical protein [Tessaracoccus anta... 51 133
/:WP_125052186.1 ABC transporter permease [Streptomyces r... 52 133
/:WP_087292204.1 hypothetical protein [Pseudoflavonifract... 55 132
/:OHC49295.1 choline ABC transporter ATP-binding protein ... 53 132
/:WP_147027147.1 helix-turn-helix domain-containing prote... 50 132
/:ERS86211.1 hypothetical protein Q672_15090 [Marinobacte... 57 132
/:MAF67130.1 hypothetical protein [Planctomycetes bacteri... 61 132 /:VEI03626.1 Galactokinase [Acidipropionibacterium jensen... 51 132
limiting value of parameter V = 50.

>/:CUE79935.1 inositol 1,4,5-trisphosphate/ryanodine receptor, putative [Bodo saltans]/ Length = 2655
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Score = 64 (33.9 bits)
Identities = 9/12 (75%), Positives = 9/12 (75%)
Query: 118 MRDGVDVHRLSG 129
MRDG VHRL G
Sbjct: 372 MRDGLQVHRLPG 383
Score = 49 (26.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 161 RSAWWELRS 169
R A WELRS
Sbjct: 985 RTASWELRS 993
Score = 39 (21.4 bits)
Identities = 5/7 (71%), Positives = 6/7 (85%)
Query: 154 RDTGLLE 160
RDT +LE
Sbjct: 607 RDTSILE 613
Score = 37 (20.4 bits)
Identities = 5/8 (62%), Positives = 6/8 (75%)
Query: 171 RLYCKLAN 178
RL+C L N
Sbjct: 997 RLFCRLTN 1004
>/:WP_151079925.1 MULTISPECIES: hypothetical protein [unclassified
Hymenobacter]//:KAA9327478.1 hypothetical protein F0P96_15970
[Hymenobacter sp. MA3]//:QHJ06184.1 hypothetical protein
GUY19_02265 [Hymenobacter sp. BT182]/
Length = 306
Total Score: 183
Score = 40 (21.9 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 187 RRRDD 191
RRRDD
Sbjct: 275 RRRDD 279
Score = 37 (20.4 bits)
Identities = 5/6 (83%), Positives = 5/6 (83%)
Query: 25 AYSREH 30
AY REH
Sbjct: 156 AYEREH 161
Score = 37 (20.4 bits)
Identities = 5/7 (71%), Positives = 6/7 (85%)
Query: 62 RRSDGDN 68
RRSD D+
Sbjct: 182 RRSDNDD 188
Score = 37 (20.4 bits)
Identities = 6/9 (66%), Positives = 7/9 (77%)
Query: 81 DDRRVYDQY 89
DDRR +QY
Sbjct: 263 DDRRGRNQY 271
Score = 32 (17.9 bits)
Identities = 5/7 (71%), Positives = 5/7 (71%)
Query: 6 DRNSGNY 12
DR GNY
Sbjct: 138 DRRGGNY 144
>/:XP_029901852.1 F-box DNA helicase 1 [Myripristis murdjan]/
Length = 1043
Total Score: 180
Score = 56 (29.9 bits)
Identities = 7/8 (87%), Positives = 8/8 (100%)
Query: 115 LAMMRDGV 122
LAMMR+GV
Sbjct: 387 LAMMRNGV 394
Score = 54 (28.9 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 27 SREHTRP 33
SREHTRP
Sbjct: 166 SREHTRP 172
Score = 37 (20.4 bits)
Identities = 5/7 (71%), Positives = 5/7 (71%)
Query: 123 DVHRLSG 129
D HR SG
Sbjct: 900 DLHRVSG 906
Score = 33 (18.4 bits)
Identities = 4/7 (57%), Positives = 5/7 (71%)
Query: 165 WELRSSR 171
W+LR R
Sbjct: 619 WQLRTPR 625
>/:ADG75409.1 alpha-1,6-glucosidase, pullulanase-type [Cellulomonas flavigena
DSM 20109]/
Length = 1975
Total Score: 179
Score = 57 (30.4 bits)
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Query: 17 SSWARGATA 25
SSWARGA A
Sbjct: 497 SSWARGASA 505
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Identities = 9/10 (90%), Positives = 9/10 (90%)
Query: 57 GAGAVRRSDG 66
GA AVRRSDG
Sbjct: 1345 GAFAVRRSDG 1354

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 Identities = 5/8 (62%), Positives = 6/8 (75%)
Query: 41 HRTSASAY 48
 HRT AS +
Sbjct: 823 HRTAASTF 830
 Score = 33 (18.4 bits)
 Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 166 ELRSS 170
 ELRSS
Sbjct: 1827 ELRSS 1831
>/:XP_019169829.1 PREDICTED: probable serine/threonine-protein kinase WNK10
 isoform X1 [Ipomoea nil]/
 Length = 638
Total Score: 173
 Score = 53 (28.4 bits)
 Identities = 8/12 (66%), Positives = 8/12 (66%)
Query: 94 SDVMREGLHMSK 105
 SDVM HMSK
Sbjct: 302 SDVMQNSNHMSK 313
 Score = 50 (26.9 bits)
 Identities = 7/11 (63%), Positives = 8/11 (72%)
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M         SEC RD G+
Sbjct: 540 MMSECTRDSGI 550
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 Identities = 4/9 (44%), Positives = 6/9 (66%)
Query: 13 LRGLSSWAR 21
 + + SWAR
Sbjct: 135 IKAIKSWAR 143
 Score = 33 (18.4 bits)
 Identities = 5/9 (55%), Positives = 6/9 (66%)
Query: 11 NYLRGLSSW 19
N         +R L SW
Sbjct: 95 NIIRSLDSW 103
>/:XP_029218919.1 apical complex lysine methyltransferase [Besnoitia besnoiti]//:PFH34910.1 apical complex lysine methyltransferase
 [Besnoitia besnoiti]/
 Length = 677
Total Score: 168
 Score = 52 (27.9 bits)
 Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 18 SWARGAT 24
 SWARGAT
Sbjct: 55 SWARGAT 61
 Score = 44 (23.9 bits)
 Identities = 5/6 (83%), Positives = 5/6 (83%)
Query: 86 YDQYYR 91
 YD YYR
Sbjct: 115 YDDYYR 120
 Score = 39 (21.4 bits)
 Identities = 5/9 (55%), Positives = 6/9 (66%)
Query: 117 MMRDGVDVH 125
 M R G D+H
Sbjct: 371 MKRAGLDIH 379
 Score = 33 (18.4 bits)
 Identities = 4/7 (57%), Positives = 5/7 (71%)
Query: 130 LAMRAHS 136
 + M AHS
Sbjct: 410 ISMMAHS 416
>/:QAA76796.1 Transketolase [Candidatus Bipolaricaulis sibiricus]/
 Length = 699
Total Score: 168
 Score = 60 (31.9 bits)
 Identities = 11/19 (57%), Positives = 12/19 (63%)
Query: 92 VFSDVMREGLHMSKLTHSP 110
 VFSD MR + MS L H P
Sbjct: 452 VFSDYMRPSIRMSALMHVP 470
 Score = 43 (23.4 bits)
 Identities = 6/6 (100%), Positives = 6/6 (100%)
Query: 185 ALRRRD 190
 ALRRRD
Sbjct: 522 ALRRRD 527
 Score = 33 (18.4 bits)
 Identities = 5/6 (83%), Positives = 5/6 (83%)
Query: 64 SDGDNM 69
 SDGD M
Sbjct: 157 SDGDLM 162
 Score = 32 (17.9 bits)
 Identities = 6/8 (75%), Positives = 6/8 (75%)
Query: 56 RGAGAVRR 63
 RGA A RR
Sbjct: 304 RGAEAERR 311
>/:XP_025997073.1 dnaJ homolog subfamily B member 6-B-like isoform X1 [Solenopsis invicta]//:XP_025997074.1 dnaJ homolog subfamily B
 member 6-B-like isoform X1 [Solenopsis invicta]/
 Length = 325
Total Score: 168
 Score = 59 (31.4 bits)
 Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 83 RRVYDQY 89
 RRVYDQY
Sbjct: 99 RRVYDQY 105
 Score = 44 (23.9 bits)
 Identities = 8/13 (61%), Positives = 8/13 (61%)
Query: 26 YSREHTRPTRGFT 38
 Y R RP RGFT
Sbjct: 70 YQRAASRPGRGFT 82
 Score = 33 (18.4 bits)
 Identities = 4/4 (100%), Positives = 4/4 (100%)
Query: 102 HMSK 105
 HMSK
Sbjct: 314 HMSK 317
 Score = 32 (17.9 bits)
 Identities = 4/8 (50%), Positives = 6/8 (75%)
Query: 193 NYLRASQL 200
 +YL AS +
Sbjct: 300 DYLKASRI 307
>/:WP_068254241.1 hypothetical protein [Janibacter corallicola]/
 Length = 350
Total Score: 167
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 RGA Y EHTR
Sbjct: 31 RGASGYRPEHTR 42
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Score = 48 (25.9 bits)
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DL M RDGV V R
Sbjct: 59 DLVMTRDGVLVDR 71
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Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 166 ELRSS 170
ELRSS
Sbjct: 126 ELRSS 130
Score = 33 (18.4 bits)
Identities = 4/7 (57%), Positives = 6/7 (85%)
Query: 186 LRRRDDG 192
+ RR+DG
Sbjct: 268 IPRREDG 274
>/:XP_011265016.1 dnaJ homolog subfamily B member 6-B isoform X1 [Camponotus floridanus]//:XP_011265018.1 dnaJ homolog subfamily B member 6-B isoform X1 [Camponotus floridanus]//:XP_011265019.1 dnaJ homolog subfamily B member 6-B isoform X1 [Camponotus
floridanus]//:XP_011265020.1 dnaJ homolog subfamily B member 6-B isoform X1 [Camponotus floridanus]//:XP_011265021.1 dnaJ homolog subfamily B member 6-B isoform X1 [Camponotus
floridanus]//:XP_011265022.1 dnaJ homolog subfamily B member 6-B
isoform X1 [Camponotus floridanus]/
Length = 326
Total Score: 164
Score = 59 (31.4 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 83 RRVYDQY 89
RRVYDQY
Sbjct: 99 RRVYDQY 105
Score = 40 (21.9 bits)
Identities = 6/7 (85%), Positives = 6/7 (85%)
Query: 32 RPTRGFT 38
RP RGFT
Sbjct: 76 RPGRGFT 82
Score = 33 (18.4 bits)
Identities = 4/4 (100%), Positives = 4/4 (100%)
Query: 102 HMSK 105
HMSK
Sbjct: 315 HMSK 318
Score = 32 (17.9 bits)
Identities = 4/8 (50%), Positives = 6/8 (75%)
Query: 193 NYLRASQL 200
+YL AS +
Sbjct: 301 DYLKASRI 308
>/:WP_084032530.1 DDE-type integrase/transposase/recombinase, partial
[Mycobacterium avium]/
Length = 564
Total Score: 163
Score = 51 (27.4 bits)
Identities = 7/10 (70%), Positives = 8/10 (80%)
Query: 32 RPTRGFTVTH 41
RPTRG+ V H
Sbjct: 53 RPTRGYVVAH 62
Score = 41 (22.4 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 82 DRRVY 86
DRRVY
Sbjct: 387 DRRVY 391
Score = 39 (21.4 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)
Query: 57 GAGAVR 62
GAGAVR
Sbjct: 72 GAGAVR 77
Score = 32 (17.9 bits)
Identities = 4/4 (100%), Positives = 4/4 (100%)
Query: 28 REHT 31
REHT
Sbjct: 46 REHT 49
>/:WP_019146189.1 deoxyguanosinetriphosphate triphosphohydrolase [Aeromicrobium massiliense]/ Length = 408
Total Score: 161
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DDRRV+D
Sbjct: 177 DDRRVFD 183
Score = 43 (23.4 bits)
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 119 RDGVDVHR 126
R+GVD HR
Sbjct: 186 REGVDGHR 193
Score = 36 (19.9 bits)
Identities = 5/7 (71%), Positives = 6/7 (85%)
Query: 141 VGPDHTR 147
V P+HTR
Sbjct: 315 VVPEHTR 321
Score = 33 (18.4 bits)
Identities = 4/4 (100%), Positives = 4/4 (100%)
Query: 19 WARG 22
WARG
Sbjct: 159 WARG 162
>/:WP_003931701.1 hypothetical protein [Mycolicibacterium vaccae]//:ANI42376.1 hypothetical protein MYVA_5330 [Mycolicibacterium vaccae
95051]//:EJZ10366.1 hypothetical protein MVAC_09332
[Mycolicibacterium vaccae ATCC 25954]/
Length = 261
Total Score: 159
Score = 47 (25.4 bits)
Identities = 6/7 (85%), Positives = 7/7 (100%)
Query: 189 RDDGNYL 195
RDDG+YL
Sbjct: 227 RDDGDYL 233
Score = 44 (23.9 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)
Query: 119 RDGVDV 124
RDGVDV
Sbjct: 117 RDGVDV 122
Score = 36 (19.9 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 63 RSDGD 67
RSDGD

Sbjct: 103 RSDGD 107
Score = 32 (17.9 bits)
Identities = 4/7 (57%), Positives = 5/7 (71%)
Query: 13 LRGLSSW 19
LRG+ W
Sbjct: 66 LRGIRPW 72
>/:XP_023095958.1 basic proline-rich protein-like [Felis catus]/
Length = 399
Total Score: 159
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Identities = 8/14 (57%), Positives = 8/14 (57%)
Query: 49 RHPSNTHRGAGAVR 62
R P THRG A R
Sbjct: 114 RPPPGTHRGTAAAR 127
Score = 40 (21.9 bits)
Identities = 8/12 (66%), Positives = 8/12 (66%)
Query: 126 RLSGLAMRAHSH 137
RLSG A R H H
Sbjct: 276 RLSGAARRRHAH 287
Score = 38 (20.9 bits)
Identities = 5/6 (83%), Positives = 5/6 (83%)
Query: 115 LAMMRD 120
LA MRD
Sbjct: 209 LALMRD 214
Score = 35 (19.4 bits)
Identities = 5/7 (71%), Positives = 5/7 (71%)
Query: 15 GLSSWAR 21
GLS W R
Sbjct: 27 GLSAWDR 33
>/:XP_001707494.1 Hypothetical protein GL50803_32673 [Giardia lamblia ATCC
50803]/
Length = 261
Total Score: 154
Score = 46 (24.9 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)
Query: 187 RRRDDG 192
RRRDDG
Sbjct: 200 RRRDDG 205
Score = 38 (20.9 bits)
Identities = 5/6 (83%), Positives = 6/6 (100%)
Query: 122 VDVHRL 127
V+VHRL
Sbjct: 74 VEVHRL 79
Score = 37 (20.4 bits)
Identities = 8/11 (72%), Positives = 8/11 (72%)
Query: 106 LTHSPGRVDLA 116
LTH P RV LA
Sbjct: 21 LTHDPERVLLA 31
Score = 33 (18.4 bits)
Identities = 4/5 (80%), Positives = 5/5 (100%)
Query: 81 DDRRV 85
+DRRV
Sbjct: 5 EDRRV 9
>/:NBB68986.1 phosphoenolpyruvate carboxylase [Alphaproteobacteria bacterium]/ Length = 904
Total Score: 145
Score = 59 (31.4 bits)
Identities = 9/10 (90%), Positives = 9/10 (90%)
Query: 154 RDTGLLERSA 163
RD GLLERSA
Sbjct: 487 RDAGLLERSA 496
Score = 47 (25.4 bits)
Identities = 6/7 (85%), Positives = 6/7 (85%)
Query: 45 ASAYRHP 51
A AYRHP
Sbjct: 332 ATAYRHP 338
Score = 39 (21.4 bits)
Identities = 6/9 (66%), Positives = 7/9 (77%)
Query: 119 RDGVDVHRL 127
R+ DVHRL
Sbjct: 444 REMLDVHRL 452
>/:HFE44551.1 hypothetical protein [Nannocystis exedens]/
Length = 909
Total Score: 144
Score = 53 (28.4 bits)
Identities = 8/13 (61%), Positives = 9/13 (69%)
Query: 14 RGLSSWARGATAY 26
RGLS W R TA+
Sbjct: 82 RGLSGWERSGTAF 94
Score = 46 (24.9 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)
Query: 49 RHPSNT 54
RHPSNT
Sbjct: 144 RHPSNT 149
Score = 45 (24.4 bits)
Identities = 5/9 (55%), Positives = 6/9 (66%)
Query: 161 RSAWWELRS 169
R WW+ RS
Sbjct: 231 RREWWDVRS 239
>/:WP_153398479.1 penicillin-binding protein 2 [Ornithinicoccus halotolerans]/
Length = 776
Total Score: 143
Score = 51 (27.4 bits)
Identities = 6/7 (85%), Positives = 7/7 (100%)
Query: 92 VFSDVMR 98
VFSD+MR
Sbjct: 721 VFSDIMR 727
Score = 49 (26.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 55 HRGAGAVRR 63
HRGA A RR
Sbjct: 71 HRGAAALRR 79
Score = 43 (23.4 bits)
Identities = 5/6 (83%), Positives = 6/6 (100%)
Query: 83 RRVYDQ 88
RRVY+Q
Sbjct: 363 RRVYEQ 368
>/:WP_102647918.1 alpha,alpha-trehalose-phosphate synthase (UDP-forming)
[Burkholderia dabaoshanensis]//:PMS16331.1
alpha,alpha-trehalose-phosphate synthase (UDP-forming)
[Burkholderia dabaoshanensis]/
Length = 458
Total Score: 142
Score = 74 (38.9 bits)
Identities = 10/13 (76%), Positives = 11/13 (84%)

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Query: 83 RRVYDQYYRVFSD 95
 RR YDQYYR FS+
Sbjct: 73 RRDYDQYYRGFSN 85
 Score = 36 (19.9 bits)
 Identities = 5/8 (62%), Positives = 6/8 (75%)
Query: 184 MALRRRDD 191
 MA RR+D
Sbjct: 436 MAVLRRND 443
 Score = 32 (17.9 bits)
 Identities = 4/5 (80%), Positives = 5/5 (100%)
Query: 157 GLLER 161
 GL+ER
Sbjct: 273 GLIER 277
>/:TAM50426.1 alpha,alpha-trehalose-phosphate synthase (UDP-forming)
 [Paraburkholderia sp.]/
 Length = 458
Total Score: 142
 Score = 74 (38.9 bits)
 Identities = 10/13 (76%), Positives = 11/13 (84%)
Query: 83 RRVYDQYYRVFSD 95
 RR YDQYYR FS+
Sbjct: 73 RRDYDQYYRGFSN 85
 Score = 36 (19.9 bits)
 Identities = 5/8 (62%), Positives = 6/8 (75%)
Query: 184 MALRRRDD 191
 MA RR+D
Sbjct: 436 MAVLRRND 443
 Score = 32 (17.9 bits)
 Identities = 4/5 (80%), Positives = 5/5 (100%)
Query: 157 GLLER 161
 GL+ER
Sbjct: 273 GLIER 277
>/:WP_074578074.1 DUF2169 domain-containing protein [Polaromonas sp. JS666]//:SDN52763.1 Uncharacterized protein YjbI, contains pentapeptide repeats [Polaromonas sp. JS666]/
 Length = 895
Total Score: 141
 Score = 53 (28.4 bits)
 Identities = 6/7 (85%), Positives = 7/7 (100%)
Query: 87 DQYYRVF 93
 D+YYRVF
Sbjct: 331 DHYYRVF 337
 Score = 48 (25.9 bits)
 Identities = 6/8 (75%), Positives = 8/8 (100%)
Query: 67 DNMRSAPL 74
 ++MRSAPL
Sbjct: 321 EDMRSAPL 328
 Score = 40 (21.9 bits)
 Identities = 5/6 (83%), Positives = 5/6 (83%)
Query: 159 LERSAW 164
 LER AW
Sbjct: 783 LERAAW 788
>/:XP_011702985.1 PREDICTED: dnaJ homolog subfamily B member 6 isoform X1 [Wasmannia auropunctata]//:XP_011702986.1 PREDICTED: dnaJ homolog subfamily B member 6 isoform X1 [Wasmannia auropunctata]/
 Length = 329
Total Score: 141
 Score = 59 (31.4 bits)
 Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 83 RRVYDQY 89
 RRVYDQY
Sbjct: 99 RRVYDQY 105
 Score = 44 (23.9 bits)
 Identities = 8/13 (61%), Positives = 8/13 (61%)
Query: 26 YSREHTRPTRGFT 38
 Y R RP RGFT
Sbjct: 70 YQRAASRPGRGFT 82
 Score = 38 (20.9 bits)
 Identities = 5/9 (55%), Positives = 7/9 (77%)
Query: 192 GNYLRASQL 200
 G+YL AS +
Sbjct: 303 GDYLKASRI 311
>/:RLS30951.1 hypothetical protein DWH78_13845 [Planctomycetes bacterium]/
 Length = 1041
Total Score: 140
 Score = 51 (27.4 bits)
 Identities = 7/10 (70%), Positives = 8/10 (80%)
Query: 113 VDLAMMRDGV 122
 VD+ MM DGV
Sbjct: 796 VDIDMMEDGV 805
 Score = 50 (26.9 bits)
 Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 193 NYLRASQL 200
 NYLRA Q+
Sbjct: 1022 NYLRANQI 1029
 Score = 39 (21.4 bits)
 Identities = 5/8 (62%), Positives = 6/8 (75%)
Query: 99 EGLHMSKL 106
 EG MSK+
Sbjct: 501 EGMDMSKI 508
>/:KZS03838.1 Uncharacterized protein APZ42_033339 [Daphnia magna]/
 Length = 215
Total Score: 139
 Score = 61 (32.4 bits)
 Identities = 8/9 (88%), Positives = 8/9 (88%)
Query: 45 ASAYRHPSN 53
 AS YRHPSN
Sbjct: 121 ASSYRHPSN 129
 Score = 44 (23.9 bits)
 Identities = 6/7 (85%), Positives = 6/7 (85%)
Query: 165 WELRSSR 171
 W LRSSR
Sbjct: 158 WALRSSR 164
 Score = 34 (18.9 bits)
 Identities = 4/4 (100%), Positives = 4/4 (100%)
Query: 90 YRVF 93
 YRVF
Sbjct: 152 YRVF 155
>/:WP_057246641.1 hypothetical protein [Duganella sp. Root198D2]//:KRB92964.1 hypothetical protein ASE26_28660 [Duganella sp. Root198D2]/
 Length = 506
Total Score: 139
 Score = 49 (26.4 bits)
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 Identities = 6/11 (54%), Positives = 8/11 (72%)
Query: 12 YLRGLSSWARG 22
 ++RGL W RG
Sbjct: 265 FIRGLAGWPRG 275
 Score = 48 (25.9 bits)
 Identities = 6/6 (100%), Positives = 6/6 (100%)
Query: 189 RDDGNY 194
 RDDGNY
Sbjct: 418 RDDGNY 423
 Score = 42 (22.9 bits)
 Identities = 7/13 (53%), Positives = 9/13 (69%)
Query: 176 LANLLLRLMALRR 188
 LAN+L L +RR
Sbjct: 314 LANILVLLLLIRR 326
>/:WP_113617232.1 hypothetical protein [Chitinophaga flava]//:RBL88491.1 hypothetical protein DF182_18080 [Chitinophaga flava]/
 Length = 660
Total Score: 139
 Score = 64 (33.9 bits)
 Identities = 10/13 (76%), Positives = 12/13 (92%)
Query: 190 DDGNYLRASQLLL 202
 +DGNY RAS+LLL
Sbjct: 314 NDGNYNRASELLL 326
 Score = 38 (20.9 bits)
 Identities = 4/5 (80%), Positives = 5/5 (100%)
Query: 86 YDQYY 90
 YDQY+
Sbjct: 269 YDQYF 273
 Score = 37 (20.4 bits)
 Identities = 5/7 (71%), Positives = 6/7 (85%)
Query: 63 RSDGDNM 69
 RSD D+M
Sbjct: 200 RSDPDDM 206
>/:WP_102069824.1 alpha,alpha-trehalose-phosphate synthase (UDP-forming)
 [Pusillimonas sp. JR1/69-2-13]//:PLC54366.1 alpha,alpha-trehalose-phosphate synthase (UDP-forming)
 [Pusillimonas sp. JR1/69-2-13]/
 Length = 455
Total Score: 138
 Score = 68 (35.9 bits)
 Identities = 9/12 (75%), Positives = 10/12 (83%)
Query: 84 RVYDQYYRVFSD 95
 R YDQYYR FS+
Sbjct: 72 REYDQYYRGFSN 83
 Score = 38 (20.9 bits)
 Identities = 10/20 (50%), Positives = 11/20 (55%)
Query: 95 DVMREGLHMSKLTHSPGRVD 114
 D REGL+ KL S R D
Sbjct: 247 DALREGLQHRKLIVSVDRLD 266
 Score = 32 (17.9 bits)
 Identities = 4/5 (80%), Positives = 5/5 (100%)
Query: 157 GLLER 161
 GL+ER
Sbjct: 270 GLIER 274
>/:XP_012255663.1 dnaJ homolog subfamily B member 6-like isoform X1 [Athalia rosae]//:XP_020707900.1 dnaJ homolog subfamily B member 6-like
 isoform X1 [Athalia rosae]/
 Length = 327
Total Score: 138
 Score = 59 (31.4 bits)
 Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 83 RRVYDQY 89
 RRVYDQY
Sbjct: 99 RRVYDQY 105
 Score = 40 (21.9 bits)
 Identities = 6/7 (85%), Positives = 6/7 (85%)
Query: 32 RPTRGFT 38
 RP RGFT
Sbjct: 76 RPGRGFT 82
 Score = 39 (21.4 bits)
 Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 99 EGLHM 103
 EGLHM
Sbjct: 108 EGLHM 112
>/:WP_094301623.1 cobalamin biosynthesis protein [Azospirillum brasilense]//:OYD86375.1 cobalamin biosynthesis protein
 [Azospirillum brasilense]/
 Length = 335
Total Score: 137
 Score = 48 (25.9 bits)
 Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 72 APLTHRHVF 80
 APLT RH F
Sbjct: 142 APLTRRHAF 150
 Score = 45 (24.4 bits)
 Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 13 LRGLSSWAR 21
 LRG S WAR
Sbjct: 113 LRGRSAWAR 121
 Score = 44 (23.9 bits)
 Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 117 MMRDG 121
 MMRDG
Sbjct: 252 MMRDG 256
>/:WP_131518914.1 glycerophosphodiester phosphodiesterase [Kribbella sp.
 YM53]//:TCC39131.1 glycerophosphodiester phosphodiesterase
 [Kribbella sp. YM53]/
 Length = 321
Total Score: 137
 Score = 49 (26.4 bits)
 Identities = 7/10 (70%), Positives = 8/10 (80%)
Query: 182 RLMALRRRDD 191
 R+ ALR RDD
Sbjct: 163 RILALRLRDD 172
 Score = 45 (24.4 bits)
 Identities = 7/11 (63%), Positives = 7/11 (63%)
Query: 21 RGATAYSREHT 31
 RGA Y EHT
Sbjct: 7 RGASGYRPEHT 17
 Score = 43 (23.4 bits)
 Identities = 6/9 (66%), Positives = 7/9 (77%)
Query: 77 RHVFDDRRV 85
 R VF DRR+
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Sbjct: 61 RPVFADRRI 69
>/:NDC61331.1 bifunctional diaminohydroxyphosphoribosyl-
aminopyrimidine deaminase/5-amino-6-(5-phosphoribosylami-
no)uracil reductase RibD
 [Betaproteobacteria bacterium]/
 Length = 357
Total Score: 136
 Score = 55 (29.4 bits)
 Identities = 7/8 (87%), Positives = 7/8 (87%)
Query: 137 HHTRVGPD 144
 HHTR GPD
Sbjct: 341 HHTRLGPD 348
 Score = 43 (23.4 bits)
 Identities = 6/6 (100%), Positives = 6/6 (100%)
Query: 21 RGATAY 26
 RGATAY
Sbjct: 62 RGATAY 67
 Score = 38 (20.9 bits)
 Identities = 6/8 (75%), Positives = 6/8 (75%)
Query: 111 GRVDLAMM 118
 G VDLA M
Sbjct: 267 GKVDLAAM 274
>/:TMF77358.1 hypothetical protein E6I15_04945 [Chloroflexi
bacterium]/ Length = 456
Total Score: 136
 Score = 49 (26.4 bits)
 Identities = 6/14 (42%), Positives = 10/14 (71%)
Query: 68 NMRSAPLTHRHVFD 81
 +MR P+ RH++D
Sbjct: 183 DMREVPIPDRHIYD 196
 Score = 44 (23.9 bits)
 Identities = 8/14 (57%), Positives = 9/14 (64%)
Query: 49 RHPSNTHRGAGAVR 62
 RH + RGAG VR
Sbjct: 13 RHSDDRPRGAGSVR 26
 Score = 43 (23.4 bits)
 Identities = 5/7 (71%), Positives = 6/7 (85%)
Query: 83 RRVYDQY 89
 RR+YD Y
Sbjct: 334 RRIYDKY 340
>/:WP_115533291.1 alpha,alpha-trehalose-phosphate synthase
(UDP-forming)
 [Paraburkholderia sp. DHOM06]//:RDU99316.1
 alpha,alpha-trehalose-phosphate synthase (UDP-forming)
 [Paraburkholderia sp. DHOM06]/
 Length = 458
Total Score: 136
 Score = 68 (35.9 bits)
 Identities = 9/13 (69%), Positives = 11/13 (84%)
Query: 83 RRVYDQYYRVFSD 95
 RR Y+QYYR FS+
Sbjct: 73 RRDYEQYYRGFSN 85
 Score = 36 (19.9 bits)
 Identities = 5/8 (62%), Positives = 6/8 (75%)
Query: 184 MALRRRDD 191
 MA RR+D
Sbjct: 436 MAVLRRND 443
 Score = 32 (17.9 bits)
 Identities = 4/5 (80%), Positives = 5/5 (100%)
Query: 157 GLLER 161
 GL+ER
Sbjct: 273 GLIER 277
>/:XP_012135622.1 PREDICTED: dnaJ homolog subfamily B
member 6 isoform X1
 [Megachile rotundata]//:XP_012135623.1 PREDICTED: dnaJ
homolog subfamily B member 6 isoform X1 [Megachile
 rotundata]//:XP_012135625.1 PREDICTED: dnaJ homolog
subfamily B
 member 6 isoform X1 [Megachile rotundata]/
 Length = 313
Total Score: 136
 Score = 59 (31.4 bits)
 Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 83 RRVYDQY 89
 RRVYDQY
Sbjct: 99 RRVYDQY 105
 Score = 40 (21.9 bits)
 Identities = 6/7 (85%), Positives = 6/7 (85%)
Query: 32 RPTRGFT 38
 RP RGFT
Sbjct: 76 RPGRGFT 82
 Score = 37 (20.4 bits)
 Identities = 5/6 (83%), Positives = 6/6 (100%)
Query: 99 EGLHMS 104
 EGL+MS
Sbjct: 108 EGLQMS 113
>/:XP_012522221.1 dnaJ homolog subfamily B member 6 iso-
form X1 [Monomorium pharaonis]/ Length = 327
Total Score: 135
 Score = 59 (31.4 bits)
 Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 83 RRVYDQY 89
 RRVYDQY
Sbjct: 99 RRVYDQY 105
 Score = 44 (23.9 bits)
 Identities = 8/13 (61%), Positives = 8/13 (61%)
Query: 26 YSREHTRPTRGFT 38
 Y R RP RGFT
Sbjct: 70 YQRAASRPGRGFT 82
 Score = 32 (17.9 bits)
 Identities = 4/8 (50%), Positives = 6/8 (75%)
Query: 193 NYLRASQL 200
 +YL AS +
Sbjct: 302 DYLKASRI 309
>/:HEG86595.1 murein biosynthesis integral membrane protein
MurJ
 [Chthonomonadales bacterium]/
 Length = 575
Total Score: 134
 Score = 55 (29.4 bits)
 Identities = 9/10 (90%), Positives = 9/10 (90%)
Query: 183 LMALRRRDDG 192
 LMALRRR DG
Sbjct: 482 LMALRRRLDG 491
 Score = 47 (25.4 bits)
 Identities = 8/11 (72%), Positives = 8/11 (72%)
Query: 138 HTRVGPDHTRM 148
 H R GPD TRM
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Sbjct: 394 HGRFGPDDTRM 404
 Score = 32 (17.9 bits)
 Identities = 5/6 (83%), Positives = 5/6 (83%)
Query: 91 RVFSDV 96
 RVFS V
Sbjct: 141 RVFSTV 146
>/:WP_069321809.1 CatB-related O-acetyltransferase [Sphingomonas turrisvirgatae]//:ODP36543.1 hypothetical protein BFL28_05580
 [Sphingomonas turrisvirgatae]/
 Length = 220
Total Score: 134
 Score = 47 (25.4 bits)
 Identities = 8/14 (57%), Positives = 9/14 (64%)
Query: 61 VRRSDGDNMRSAPL 74
 VRR +G MRS L
Sbjct: 22 VRRWEGGEMRSSTL 35
 Score = 46 (24.9 bits)
 Identities = 7/10 (70%), Positives = 8/10 (80%)
Query: 158 LLERSAWWEL 167
 +LE S WWEL
Sbjct: 178 ILEDSRWWEL 187
 Score = 41 (22.4 bits)
 Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 150 SECHR 154
 SECHR
Sbjct: 132 SECHR 136
>/:WP_156384232.1 hypothetical protein [Marmoricola sp. Leaf446]/
 Length = 313
Total Score: 134
 Score = 53 (28.4 bits)
 Identities = 10/14 (71%), Positives = 10/14 (71%)
Query: 121 GVDVHRLSGLAMRA 134
 GV VHR GLA RA
Sbjct: 97 GVVVHRVAGLAERA 110
 Score = 49 (26.4 bits)
 Identities = 6/6 (100%), Positives = 6/6 (100%)
Query: 144 DHTRMA 149
 DHTRMA
Sbjct: 235 DHTRMA 240
 Score = 32 (17.9 bits)
 Identities = 5/6 (83%), Positives = 5/6 (83%)
Query: 83 RRVYDQ 88
 RRV DQ
Sbjct: 90 RRVVDQ 95
>/:WP_051399855.1 ABC transporter ATP-binding protein [Amycolatopsis halophila]/ Length = 569
Total Score: 134
 Score = 63 (33.4 bits)
 Identities = 11/19 (57%), Positives = 12/19 (63%)
Query: 115 LAMMRDGVDVHRLSGLAMR 133
 +A M DGV V RL AMR
Sbjct: 226 IAVMKDGVIVERLPASAMR 244
 Score = 39 (21.4 bits)
 Identities = 8/16 (50%), Positives = 9/16 (56%)
Query: 2 TGGHDRNSGNYLRGLS 17
 T GHDR + RG S
Sbjct: 15 TAGHDRGARDVVRGVS 30
 Score = 32 (17.9 bits)
 Identities = 5/7 (71%), Positives = 5/7 (71%)
Query: 66 GDNMRSA 72
 GD MR A
Sbjct: 127 GDAMRRA 133
>/:AHB48716.1 succinate-semialdehyde dehydrogenase [Hyphomicrobium
 nitrativorans NL23]/
 Length = 508
Total Score: 133
 Score = 68 (35.9 bits)
 Identities = 10/14 (71%), Positives = 10/14 (71%)
Query: 28 REHTRPTRGFTVTH 41
 R H RPT FTVTH
Sbjct: 13 RPHIRPTHSFTVTH 26
 Score = 33 (18.4 bits)
 Identities = 6/8 (75%), Positives = 6/8 (75%)
Query: 105 KLTHSPGR 112
 KLT PGR
Sbjct: 340 KLTVGPGR 347
 Score = 32 (17.9 bits)
 Identities = 4/4 (100%), Positives = 4/4 (100%)
Query: 79 VFDD 82
 VFDD
Sbjct: 289 VFDD 292
>/:WP_156876682.1 ABC transporter permease subunit [Microbacterium luticocti]/
 Length = 335
Total Score: 133
 Score = 61 (32.4 bits)
 Identities = 7/12 (58%), Positives = 10/12 (83%)
Query: 78 HVFDDRRVYDQY 89
 ++FD+ R YDQY
Sbjct: 220 QIFDEPRMYDQY 231
 Score = 39 (21.4 bits)
 Identities = 6/6 (100%), Positives = 6/6 (100%)
Query: 57 GAGAVR 62
 GAGAVR
Sbjct: 188 GAGAVR 193
 Score = 33 (18.4 bits)
 Identities = 4/7 (57%), Positives = 6/7 (85%)
Query: 7 RNSGNYL 13
 RNSG ++
Sbjct: 39 RNSGTFI 45
>/:WP_119999131.1 bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD
 [Rhodobacteraceae bacterium]/
 Length = 361
Total Score: 133
 Score = 49 (26.4 bits)
 Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 20 ARGATAY 26
 ARGATAY
Sbjct: 57 ARGATAY 63
 Score = 44 (23.9 bits)
 Identities = 9/12 (75%), Positives = 9/12 (75%)
Query: 51 PSNTHRGAGAVR 62
 PS T RG GAVR
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Sbjct: 196 PSLTVRGLGAVR 207
 Score = 40 (21.9 bits)
 Identities = 6/11 (54%), Positives = 7/11 (63%)
Query: 163 AWWELRSSRLY 173
 A WE R RL+
Sbjct: 250 ARWEARGARLF 260
>/:WP_147454093.1 hypothetical protein [Tessaracoccus antarcticus]/
 Length = 293
Total Score: 133
 Score = 51 (27.4 bits)
 Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 23 ATAYSRE 29
 ATAYSRE
Sbjct: 217 ATAYSRE 223
 Score = 50 (26.9 bits)
 Identities = 5/7 (71%), Positives = 6/7 (85%)
Query: 160 ERSAWWE 166
 +RS WWE
Sbjct: 249 DRSSWWE 255
 Score = 32 (17.9 bits)
 Identities = 4/4 (100%), Positives = 4/4 (100%)
Query: 187 RRRD 190
 RRRD
Sbjct: 287 RRRD 290
>/:WP_125052186.1 ABC transporter permease [Streptomyces rimosus]//:GCD41334.1 peptide ABC transporter permease [Streptomyces rimosus subsp. paromomycinus]/
 Length = 311
Total Score: 133
 Score = 52 (27.9 bits)
 Identities = 8/10 (80%), Positives = 8/10 (80%)
Query: 58 AGAVRRSDGD 67
 AGA RR DGD
Sbjct: 12 AGAARRGDGD 21
 Score = 49 (26.4 bits)
 Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 111 GRVDLAMMR 119
 G VD AMMR
Sbjct: 137 GWVDAAMMR 145
 Score = 32 (17.9 bits)
 Identities = 5/6 (83%), Positives = 5/6 (83%)
Query: 185 ALRRRD 190
 ALR RD
Sbjct: 195 ALRSRD 200
>/:WP_087292204.1 hypothetical protein [Pseudoflavonifractor sp.
 An184]//:OUP49899.1 hypothetical protein B5F19_15395
 [Pseudoflavonifractor sp. An184]/
 Length = 468
Total Score: 132
 Score = 55 (29.4 bits)
 Identities = 7/8 (87%), Positives = 8/8 (100%)
Query: 151 ECHRDTGL 158
 +CHRDTGL
Sbjct: 446 DCHRDTGL 453
 Score = 44 (23.9 bits)
 Identities = 7/10 (70%), Positives = 8/10 (80%)
Query: 123 DVHRLSGLAM 132
 D+ RLSGL M
Sbjct: 377 DIARLSGLSM 386
 Score = 33 (18.4 bits)
 Identities = 2/4 (50%), Positives = 4/4 (100%)
Query: 164 WWEL 167
 WW++
Sbjct: 461 WWDI 464
>/:OHC49295.1 choline ABC transporter ATP-binding protein [Rhodobacteraceae bacterium GWF1_65_7]//:HBD91478.1 choline ABC transporter
 ATP-binding protein [Gemmobacter sp.]/
 Length = 346
Total Score: 132
 Score = 53 (28.4 bits)
 Identities = 6/7 (85%), Positives = 7/7 (100%)
Query: 117 MMRDGVD 123
 MMRDGV+
Sbjct: 311 MMRDGVE 317
 Score = 44 (23.9 bits)
 Identities = 8/11 (72%), Positives = 8/11 (72%)
Query: 59 GAVRRSDGDNM 69
 G VR SDGD M
Sbjct: 86 GEVRVSDGDRM 96
 Score = 35 (19.4 bits)
 Identities = 5/6 (83%), Positives = 5/6 (83%)
Query: 95 DVMREG 100
 DVMR G
Sbjct: 285 DVMRPG 290
>/:WP_147027147.1 helix-turn-helix domain-containing protein [Methylobacterium oxalidis]/ Length = 306
Total Score: 132
 Score = 50 (26.9 bits)
 Identities = 7/12 (58%), Positives = 8/12 (66%)
Query: 17 SSWARGATAYSR 28
 S W ATA+SR
Sbjct: 12 SAWGKAATAFSR 23
 Score = 45 (24.4 bits)
 Identities = 6/8 (75%), Positives = 6/8 (75%)
Query: 147 RMASECHR 154
 R A ECHR
Sbjct: 252 RVACECHR 259
 Score = 37 (20.4 bits)
 Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 73 PLTHR 77
 PLTHR
Sbjct: 205 PLTHR 209
>/:ERS86211.1 hypothetical protein Q672_15090 [Marinobacter sp. EVN1]/ Length = 328
Total Score: 132
 Score = 57 (30.4 bits)
 Identities = 8/11 (72%), Positives = 9/11 (81%)
Query: 154 RDTGLLERSAW 164
 R+TGLLER W
Sbjct: 308 RETGLLERRPW 318
 Score = 40 (21.9 bits)
 Identities = 6/9 (66%), Positives = 7/9 (77%)
Query: 114 DLAMMRDGV 122
 +L M RDGV
Sbjct: 201 NLLMVRDGV 209
```

```
 Score = 35 (19.4 bits)
 Identities = 5/9 (55%), Positives = 6/9 (66%)
Query: 79 VFDDRRVYD 87
 VF+ R YD
Sbjct: 43 VFEGMRAYD 51
>/:MAF67130.1 hypothetical protein [Planctomycetes bacterium]/
 Length = 494
Total Score: 132
 Score = 61 (32.4 bits)
 Identities = 8/10 (80%), Positives = 9/10 (90%)
Query: 26 YSREHTRPTR 35
 YSRE+T PTR
Sbjct: 5 YSREQTHPTR 14
 Score = 38 (20.9 bits)
 Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 184 MALRR 188
 MALRR
Sbjct: 140 MALRR 144
 Score = 33 (18.4 bits)
 Identities = 4/4 (100%), Positives = 4/4 (100%)
Query: 76 HRHV 79
 HRHV
Sbjct: 46 HRHV 49
>/:VEI03626.1 Galactokinase [Acidipropionibacterium jensenii]/
 Length = 430
Total Score: 132
 Score = 51 (27.4 bits)
 Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 185 ALRRRDD 191
 ALRRRDD
Sbjct: 97 ALRRRDD 103
 Score = 42 (22.9 bits)
 Identities = 5/7 (71%), Positives = 7/7 (100%)
Query: 109 SPGRVDL 115
 SPGRV++
Sbjct: 67 SPGRVNI 73
 Score = 39 (21.4 bits)
 Identities = 6/7 (85%), Positives = 6/7 (85%)
Query: 57 GAGAVRR 63
 GAG VRR
Sbjct: 11 GAGPVRR 17
WARNING: HSPs involving 1081 database sequences were not reported due to the limiting value of parameter B = 50.
Parameters:
 B=50
 E=1000
 V=50 cpus=1 echofilter filter=none hspmax=100 matrix=PAM30MS nogaps qres qtype sort_by_totalscore
 span1 stats ctxfactor=1.00
 Query ----- As Used ----- ----- Computed ----
 Frame MatID Matrix name Lambda K H Lambda K H +0 0 PAM30MS 0.347 0.279 1.80 same same same
 Query
 Frame MatID Length Eff.Length E S W T X E2 S2
 +0 0 203 203 8.1e+02 65 3 16 20 0.48 32
Statistics:
 Query Expected Observed HSPs
 Frame MatID High Score High Score Reportable
 +0 0 82 (41.1 bits) 83 (41.6 bits) 1619
 Query Neighborhd Word Excluded Failed Successful Overlaps
 Frame MatID Words Hits Hits Extensions Extensions Excluded +0 0 1753 5879083375 543106899 5290237746 45721107 1107281
 Database: /net/db/ncbi/2020_05/nr95-msblast
 Title: NCBI nr95 (MS-BLAST)
 Posted: 9:19:19 AM EDT Jun 12, 2020
 Created: 9:19:19 AM EDT Jun 12, 2020
 Format: XDF-1
 # of letters in database: 49,010,334,033
 # of sequences in database: 144,844,843
 # of database sequences satisfying E: 1131
 No. of states in DFA: 460 (98 KB)
 Total size of DFA: 165 KB (2078 KB)
 Time to generate neighborhood: 0.00u 0.00s 0.00t Elapsed: 00:00:00
 No. of threads or processors used: 1
 Search cpu time: 829.78u 144.71s 974.49t Elapsed: 00:23:23
 Total cpu time: 829.78u 145.01s 974.79t Elapsed: 00:23:24
 Start: Fri Feb 18 12:25:01 2022 End: Fri Feb 18 12:48:25 2022
WARNINGS ISSUED: 2
Additional Parsing Information
-------------------------------
Scoring Table Used 100, 1 peptides
HSP       Score
----------------
1         64
2         104
3         134
Color Coding and Additional Parsing Added by: Jeffrey Oegema, Scionics GmbH
```