

Supplementary Materials: tRNA Core Hypothesis for the Transition from the RNA World to the Ribonucleoprotein World

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BLASTX 2.2.27+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: G67NCMY9013

Database: Non-redundant UniProtKB/SwissProt sequences
454,086 sequences; 169,309,753 total letters

Query= 1

Length=121

Score	E		(Bits)	Value
Sequences producing significant alignments:				

sp A8ABM5.1 EF1A_IGNH4	RecName: Full=Elongation factor 1-alpha...	29.3	1.2
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ALIGNMENTS

>sp|A8ABM5.1|EF1A_IGNH4 RecName: Full=Elongation factor 1-alpha; Short=EF-1-alpha; AltName: Full=Elongation factor Tu; Short=EF-Tu
Length=442

Score = 29.3 bits (64), Expect = 1.2, Method: Composition-based stats.
Identities = 15/38 (39%), Positives = 24/38 (63%), Gaps = 5/38 (13%)
Frame = -1

Query	103	SSLAVGFEP-----THSVNSRIFQLQQGVEPVLARVPE	5
		S++AVG+ P T SV SRI +++Q ++P +V E	
Sbjct	341	SAIAVGYPVIHAHTASVASRIIEIKQKIDPRTGKVIE	378

Query= 2

Length=136

Score	E		(Bits)	Value
Sequences producing significant alignments:				

sp A8ABM5.1 EF1A_IGNH4	RecName: Full=Elongation factor 1-alpha...	28.1	3.8
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sp Q29293.1 RL3_PIG	RecName: Full=60S ribosomal protein L3	26.6	8.4
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ALIGNMENTS

>sp|A8ABM5.1|EF1A_IGNH4 RecName: Full=Elongation factor 1-alpha; Short=EF-1-alpha; AltName:
Full=Elongation factor Tu; Short=EF-Tu
Length=442

Score = 28.1 bits (61), Expect = 3.8, Method: Composition-based stats.
Identities = 17/44 (39%), Positives = 25/44 (57%), Gaps = 7/44 (16%)
Frame = -1

```
Query   121   IWYGPAHHFAVGFE-----THSVNSRIFQLQQGVPEVLARVPE   5
          IW+  A    AVG+ P      T SV SRI +++Q ++P   +V E
Sbjct   337   IWHPSA--IAVGYPVIHAHTASVASRIIEIKQKIDPRTGKVIE   378
```

>sp|Q29293.1|RL3_PIG RecName: Full=60S ribosomal protein L3
Length=130

Score = 26.6 bits (57), Expect = 8.4, Method: Compositional matrix adjust.
Identities = 10/19 (53%), Positives = 13/19 (68%), Gaps = 0/19 (0%)
Frame = +2

```
Query   47   LEDSAVNRMGRFESYGEV   103
          L D ++N +GRF  YGEV
Sbjct   106   LSDKSINPLGRFVHYGEVT   124
```

Query= 3

Length=138

Sequences producing significant alignments:	Score (Bits)	E Value
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sp B3PIT8.1 MNMG_CELJU RecName: Full=tRNA uridine 5-carboxyme...	27.3	6.7
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>sp|B3PIT8.1|MNMG_CELJU RecName: Full=tRNA uridine 5-carboxymethylaminomethyl
modification
enzyme MnmG; AltName: Full=Glucose-inhibited division
protein A
Length=638

Score = 27.3 bits (59), Expect = 6.7, Method: Composition-based stats.
Identities = 12/20 (60%), Positives = 15/20 (75%), Gaps = 0/20 (0%)
Frame = +1

```
Query   70   SLKGEPSSGEYACPQVRVES   129
          SLKGEP +GE A  QV +E+
Sbjct   525   SLKGEPLAGEAAAEQVEIEA   544
```

Query= 4

Length=148

Sequences producing significant alignments:	Score (Bits)	E Value
sp B1I165.1 KTHY_DESAP RecName: Full=Thymidylate kinase; AltN...	27.3	4.8

ALIGNMENTS

>sp|B1I165.1|KTHY_DESAP RecName: Full=Thymidylate kinase; AltName: Full=dTMP kinase
Length=221

Score = 27.3 bits (59), Expect = 4.8, Method: Compositional matrix adjust.
Identities = 12/27 (44%), Positives = 18/27 (67%), Gaps = 0/27 (0%)
Frame = -3

Query	116	NSRIFQLQRSGGTQPGPADRRILLNSG	36
		N R+ + GGT+ G A RR+LL++G	
Sbjct	32	NHRVLVTREPGGTRIGEAVRRVLLDTG	58

Query= 5

Length=138

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q8Y003.1 RGMG_RALSO RecName: Full=Putative ribose/galactos...	27.7	5.0

ALIGNMENTS

>sp|Q8Y003.1|RGMG_RALSO RecName: Full=Putative ribose/galactose/methyl galactoside import

ATP-binding protein
Length=518

Score = 27.7 bits (60), Expect = 5.0, Method: Compositional matrix adjust.
Identities = 11/28 (39%), Positives = 16/28 (57%), Gaps = 0/28 (0%)
Frame = -1

Query	120	PWQVMSELIWVRRDSTRTCGQAYSPELR	37
		P+ ++E IW+RR+ CG ELR	
Sbjct	116	PYMTVAENIWIRREPRNRCGLVDHAELR	143

Query= 7

Length=131

Sequences producing significant alignments:	Score (Bits)	E Value
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sp Q2NQF4.1 DAPF_SODGM RecName: Full=Diaminopimelate epimeras...	26.6	8.4
--	------	-----

ALIGNMENTS

>sp|Q2NQF4.1|DAPF_SODGM RecName: Full=Diaminopimelate epimerase; Short=DAP epimerase
Length=274

Score = 26.6 bits (57), Expect = 8.4, Method: Compositional matrix adjust.
Identities = 13/31 (42%), Positives = 16/31 (52%), Gaps = 0/31 (0%)
Frame = -3

Query	102	SPPLVRRDSTRTCGQAYSPELRGSNPY*PEF	10
		SP ++RR S R CG + L PY PE	
Sbjct	26	SPEMIRRLSDRHCGVGFQQLLVVEPPYDPEL	56

Query= 8

Length=133

Sequences producing significant alignments:	Score (Bits)	E Value
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sp Q8EDG1.1 CDD_SHEON RecName: Full=Cytidine deaminase; AltNa...	28.1	2.9
sp Q0HHI5.1 CDD_SHESM RecName: Full=Cytidine deaminase; AltNa...	28.1	2.9
sp Q0HTT9.1 CDD_SHESR RecName: Full=Cytidine deaminase; AltNa...	28.1	2.9
sp A0KYD1.1 CDD_SHESA RecName: Full=Cytidine deaminase; AltNa...	28.1	2.9
sp A8H5H1.1 CDD_SHEPA RecName: Full=Cytidine deaminase; AltNa...	27.7	4.4

ALIGNMENTS

>sp|Q8EDG1.1|CDD_SHEON RecName: Full=Cytidine deaminase; AltName: Full=Cytidine aminohydrolase;

Short=CDA

Length=296

Score = 28.1 bits (61), Expect = 2.9, Method: Composition-based stats.
Identities = 14/35 (40%), Positives = 21/35 (60%), Gaps = 0/35 (0%)
Frame = -3

Query	125	LQGPSAVRDVILNAERIERPWQVMSELI*GGRTRI	21
		L G S + D+I+NA Q M+EL+ GG+ +I	
Sbjct	112	LSGESQIVDMIVNASPCGHCRQFMNELVDGGQIKI	146

>sp|Q0HHI5.1|CDD_SHESM RecName: Full=Cytidine deaminase; AltName: Full=Cytidine aminohydrolase;

Short=CDA

Length=296

Score = 28.1 bits (61), Expect = 2.9, Method: Composition-based stats.
Identities = 14/35 (40%), Positives = 21/35 (60%), Gaps = 0/35 (0%)

Frame = -3

```
Query 125 LQGPSAVRDVILNAERIERPWQVMSELI*GGRTRI 21
          L G S + D+I+NA          Q M+EL+ GG+ +I
Sbjct 112 LSGESQIVDMIVNASPCGHCRCQFMNELVEGGQIKI 146
```

>sp|Q0HTT9.1|CDD_SHEsr RecName: Full=Cytidine deaminase; AltName: Full=Cytidine aminohydrolase;

Short=CDA

Length=296

Score = 28.1 bits (61), Expect = 2.9, Method: Composition-based stats.
Identities = 14/35 (40%), Positives = 21/35 (60%), Gaps = 0/35 (0%)
Frame = -3

```
Query 125 LQGPSAVRDVILNAERIERPWQVMSELI*GGRTRI 21
          L G S + D+I+NA          Q M+EL+ GG+ +I
Sbjct 112 LSGESQIVDMIVNASPCGHCRCQFMNELVEGGQIKI 146
```

>sp|A0KYD1.1|CDD_SHEsa RecName: Full=Cytidine deaminase; AltName: Full=Cytidine aminohydrolase;

Short=CDA

Length=296

Score = 28.1 bits (61), Expect = 2.9, Method: Composition-based stats.
Identities = 14/35 (40%), Positives = 21/35 (60%), Gaps = 0/35 (0%)
Frame = -3

```
Query 125 LQGPSAVRDVILNAERIERPWQVMSELI*GGRTRI 21
          L G S + D+I+NA          Q M+EL+ GG+ +I
Sbjct 112 LSGESQIVDMIVNASPCGHCRCQFMNELVEGGQIKI 146
```

>sp|A8H5H1.1|CDD_SHEpa RecName: Full=Cytidine deaminase; AltName: Full=Cytidine aminohydrolase;

Short=CDA

Length=296

Score = 27.7 bits (60), Expect = 4.4, Method: Composition-based stats.
Identities = 13/35 (37%), Positives = 20/35 (57%), Gaps = 0/35 (0%)
Frame = -3

```
Query 125 LQGPSAVRDVILNAERIERPWQVMSELI*GGRTRI 21
          L G S + D+I+NA          Q ++EL+ GG+ I
Sbjct 112 LSGESIIEDIIVNASPCGHCRCQFINELVDGGKVNI 146
```

Query= 9

Length=125

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp P06221.1 RPOL_BPSP6 RecName: Full=DNA-directed RNA polymerase	28.1	3.7
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ALIGNMENTS

>sp|P06221.1|RPOL_BPSP6 RecName: Full=DNA-directed RNA polymerase
Length=874

Score = 28.1 bits (61), Expect = 3.7, Method: Composition-based stats.
Identities = 14/27 (52%), Positives = 16/27 (59%), Gaps = 0/27 (0%)
Frame = -2

Query	115	SAVQVSSHELQNESNDLGKLCNLSEG	35
		S V V S L +SNDLGK L +EG	
Sbjct	414	SRVYVQSSTLSPQSNDLGKALLRFTEG	440

Query= 10

Length=111

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp Q8FS33.1 RPOA_COREF RecName: Full=DNA-directed RNA polymer...	26.9	6.2
sp A4QBQ7.1 RPOA_CORGB RecName: Full=DNA-directed RNA polymer...	26.6	8.0
sp Q8NSV2.1 RPOA_CORGL RecName: Full=DNA-directed RNA polymer...	26.6	8.2
sp Q6NJ63.1 RPOA_CORDI RecName: Full=DNA-directed RNA polymer...	26.6	9.0

ALIGNMENTS

>sp|Q8FS33.1|RPOA_COREF RecName: Full=DNA-directed RNA polymerase subunit alpha;
Short=RNAP
subunit alpha; AltName: Full=RNA polymerase subunit alpha;
AltName: Full=Transcriptase subunit alpha
Length=338

Score = 26.9 bits (58), Expect = 6.2, Method: Composition-based stats.
Identities = 12/22 (55%), Positives = 15/22 (68%), Gaps = 0/22 (0%)
Frame = -3

Query	85	VRDVILNCRGFVQSSQGVEPVL	20
		V D+ILN +G V SS EPV+	
Sbjct	73	VSDIILNIKGLVLSSDSDEPVI	94

>sp|A4QBQ7.1|RPOA_CORGB RecName: Full=DNA-directed RNA polymerase subunit alpha;
Short=RNAP
subunit alpha; AltName: Full=RNA polymerase subunit alpha;
AltName: Full=Transcriptase subunit alpha
Length=338

Score = 26.6 bits (57), Expect = 8.0, Method: Composition-based stats.
Identities = 12/25 (48%), Positives = 17/25 (68%), Gaps = 0/25 (0%)
Frame = -3

Query 85 VRDVILNCRGFVQSSQGVEPVLARV 11
 V D+ILN +G V SS EPV+ ++
 Sbjct 73 VSDIILNIKGLVLSSDSDEPVVMQL 97

>sp|Q8NSV2.1|RPOA_CORGL RecName: Full=DNA-directed RNA polymerase subunit alpha;
 Short=RNAP
 subunit alpha; AltName: Full=RNA polymerase subunit alpha;
 AltName: Full=Transcriptase subunit alpha
 Length=338

Score = 26.6 bits (57), Expect = 8.2, Method: Composition-based stats.
 Identities = 12/25 (48%), Positives = 17/25 (68%), Gaps = 0/25 (0%)
 Frame = -3

Query 85 VRDVILNCRGFVQSSQGVEPVLARV 11
 V D+ILN +G V SS EPV+ ++
 Sbjct 73 VSDIILNIKGLVLSSDSDEPVVMQL 97

>sp|Q6NJ63.1|RPOA_CORDI RecName: Full=DNA-directed RNA polymerase subunit alpha;
 Short=RNAP
 subunit alpha; AltName: Full=RNA polymerase subunit alpha;
 AltName: Full=Transcriptase subunit alpha
 Length=338

Score = 26.6 bits (57), Expect = 9.0, Method: Composition-based stats.
 Identities = 12/22 (55%), Positives = 15/22 (68%), Gaps = 0/22 (0%)
 Frame = -3

Query 85 VRDVILNCRGFVQSSQGVEPVL 20
 V D+ILN +G V SS EPV+
 Sbjct 73 VSDIILNIKGLVLSSDSDEPVV 94

Query= 12
 Length=126

Sequences producing significant alignments:	Score (Bits)	E Value
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sp P49327.3 FAS_HUMAN RecName: Full=Fatty acid synthase; Incl...	28.5	2.6
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ALIGNMENTS

>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
 Full=[Acyl-carrier-protein]
 S-acetyltransferase; Includes: RecName:
 Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
 RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:
 RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
 Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
 dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
 reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein]
 hydrolase
 Length=2511

Score = 28.5 bits (62), Expect = 2.6, Method: Compositional matrix adjust.
 Identities = 12/27 (44%), Positives = 17/27 (63%), Gaps = 0/27 (0%)
 Frame = -3

Query 124 FTLQGPSAVRDVILNRWLRSIWYGPAH 44
 +TLQ + V DV+++RWLR G H

Sbjct 1067 YTLQDKAQVADVVSRLRVTVAGGVH 1093

Query= 13

Length=131

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp Q03396.1 L_SV5WR RecName: Full=RNA-directed RNA polymerase...	29.6	1.3
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ALIGNMENTS

>sp|Q03396.1|L_SV5WR RecName: Full=RNA-directed RNA polymerase L; Short=Protein L;

AltName: Full=Large structural protein; AltName: Full=Replicase;

AltName: Full=Transcriptase; Includes: RecName: Full=RNA-directed

RNA polymerase; Includes: RecName: Full=mRNA (guanine-N(7)-)-methyltransferase;

Includes: RecName: Full=mRNA

guanylyltransferase

Length=2255

Score = 29.6 bits (65), Expect = 1.3, Method: Composition-based stats.

Identities = 15/30 (50%), Positives = 17/30 (57%), Gaps = 3/30 (10%)

Frame = -3

Query 114	PGPADRRILLN---SDGFDPSGTAQPTTRG	34
	P P +RR+LLN D FDPS Q T G	
Sbjct 507	PNPFNRRLLLNLFLGDDKFDPSVELQYVTSG	536

Query= 14

Length=125

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp Q9VQC4.1 GLCTK_DROME RecName: Full=Glycerate kinase	28.5	2.2
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ALIGNMENTS

>sp|Q9VQC4.1|GLCTK_DROME RecName: Full=Glycerate kinase

Length=487

Score = 28.5 bits (62), Expect = 2.2, Method: Compositional matrix adjust.

Identities = 11/21 (52%), Positives = 15/21 (71%), Gaps = 0/21 (0%)

Frame = -1

Query 86	LICSGHSAVQVSSHELGGRT	24
	LIC G ++VS H LGGR++	
Sbjct 369	LICGGEPIKVS GHGLGGRSQ	389

Query= 15

Length=148

	Score (Bits)	E Value
Sequences producing significant alignments:		

sp Q4QLD1.1 HIS82_HAEI8 RecName: Full=Histidinol-phosphate am...	27.3	6.9
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ALIGNMENTS

```
>sp|Q4QLD1.1|HIS82_HAEI8 RecName: Full=Histidinol-phosphate aminotransferase 2;
AltName:
Full=Imidazole acetol-phosphate transaminase 2
Length=366
```

Score = 27.3 bits (59), Expect = 6.9, Method: Composition-based stats.
 Identities = 14/39 (36%), Positives = 23/39 (59%), Gaps = 0/39 (0%)
 Frame = -1

```
Query 133 NPDRLRTGVFS*TQGVEPVLARVPERLAVGFEPTHSVNSR 17
          NP+  TG F  +Q +E  LA+VPE + V  +  ++  +R
Sbjct 163 NPNNPTGNFLTSQEIEDFLAKVPENVIVVLDEAYTEFTR 201
```

Query= 16

Length=143

	Score (Bits)	E Value
Sequences producing significant alignments:		

sp Q30ZW0.1 TPIS_DESDG RecName: Full=Triosephosphate isomeras...	28.1	3.4
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ALIGNMENTS

```
>sp|Q30ZW0.1|TPIS_DESDG RecName: Full=Triosephosphate isomerase; Short=TIM;
AltName:
Full=Triose-phosphate isomerase
Length=250
```

Score = 28.1 bits (61), Expect = 3.4, Method: Composition-based stats.
 Identities = 13/29 (45%), Positives = 20/29 (69%), Gaps = 1/29 (3%)
 Frame = -2

```
Query 103 LSEGVEPVLARV-PERLAVGFEPTHSVNS 20
          LSEG+  V A + PERLA+ +EP  ++ +
Sbjct 148 LSEGLSGVPAGIAPERLAIAYEPVWAIGT 176
```

Query= 17

Length=156

	Score (Bits)	E Value
Sequences producing significant alignments:		

sp B3PIT8.1 MNMG_CELJU RecName: Full=tRNA uridine 5-carboxyme...	27.3	7.5
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ALIGNMENTS

>sp|B3PIT8.1|MNMG_CELJU RecName: Full=tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG; AltName: Full=Glucose-inhibited division protein A
Length=638

Score = 27.3 bits (59), Expect = 7.5, Method: Composition-based stats.
Identities = 12/20 (60%), Positives = 15/20 (75%), Gaps = 0/20 (0%)
Frame = +1

Query 88 SLKGEPSSGEYACPQVRVES 147
SLKGEP +GE A QV +E+
Sbjct 525 SLKGEPLAGEAAAEQVEIEA 544

Query= 18

Length=148

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q1AW66.1 PYRH_RUBXD RecName: Full=Uridylate kinase; Short=...	27.3	5.7

ALIGNMENTS

>sp|Q1AW66.1|PYRH_RUBXD RecName: Full=Uridylate kinase; Short=UK; AltName: Full=Uridine monophosphate kinase; Short=UMP kinase; Short=UMPK
Length=255

Score = 27.3 bits (59), Expect = 5.7, Method: Composition-based stats.
Identities = 15/35 (43%), Positives = 17/35 (49%), Gaps = 0/35 (0%)
Frame = +3

Query 42 SNPTARVQENTPVRRSGLSPSGPPLRNSG*YGFDP 146
S A E P+RR L SG L +G YG DP
Sbjct 4 SARAAETSELGPLRRVVLKLSGESLAGNGGYGIDP 38

Query= 19

Length=134

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q29293.1 RL3_PIG RecName: Full=60S ribosomal protein L3	26.9	4.5

ALIGNMENTS

>sp|Q29293.1|RL3_PIG RecName: Full=60S ribosomal protein L3
Length=130

Score = 26.9 bits (58), Expect = 4.5, Method: Compositional matrix adjust.

Identities = 9/23 (39%), Positives = 15/23 (65%), Gaps = 0/23 (0%)
 Frame = +2

Query 8 LEDSAVNRMGRFESYGESSGEYA 76
 L D ++N +GRF YGE + ++
 Sbjct 106 LSDKSINPLGRFVHYGEVTNDFV 128

Query= 20

Length=129

			Score	E
Sequences producing significant alignments:			(Bits)	Value
sp Q5GS39.1 GPDA_WOLTR	RecName: Full=Glycerol-3-phosphate deh...	28.1	3.4	
sp P61749.1 GPDA_WOLPM	RecName: Full=Glycerol-3-phosphate deh...	26.9	6.5	
sp C0R3K2.1 GPDA_WOLWR	RecName: Full=Glycerol-3-phosphate deh...	26.9	6.6	

ALIGNMENTS

>sp|Q5GS39.1|GPDA_WOLTR RecName: Full=Glycerol-3-phosphate dehydrogenase
 [NAD(P)+]; AltName:
 Full=NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
 Length=327

Score = 28.1 bits (61), Expect = 3.4, Method: Composition-based stats.
 Identities = 13/35 (37%), Positives = 20/35 (57%), Gaps = 0/35 (0%)
 Frame = -3

Query 124 TLQGSAVRDVILNCRGFVQSSLAVGFEPTHSVNS 20
 TL GP+ + D+I+ C +L+ GF+ S NS
 Sbjct 234 TLLGPACLGDLIMTCTSLNSRNLSFGFKIGSSNNS 268

>sp|P61749.1|GPDA_WOLPM RecName: Full=Glycerol-3-phosphate dehydrogenase
 [NAD(P)+]; AltName:
 Full=NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
 Length=327

Score = 26.9 bits (58), Expect = 6.5, Method: Composition-based stats.
 Identities = 12/34 (35%), Positives = 20/34 (59%), Gaps = 0/34 (0%)
 Frame = -3

Query 124 TLQGSAVRDVILNCRGFVQSSLAVGFEPTHSVN 23
 TL GP+ + D+I+ C +L+ GF+ +S N
 Sbjct 234 TLLGPACLGDLIMTCTSLNSRNLSFGFKIGNSDN 267

>sp|C0R3K2.1|GPDA_WOLWR RecName: Full=Glycerol-3-phosphate dehydrogenase
 [NAD(P)+]; AltName:
 Full=NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
 Length=327

Score = 26.9 bits (58), Expect = 6.6, Method: Composition-based stats.
 Identities = 12/34 (35%), Positives = 20/34 (59%), Gaps = 0/34 (0%)
 Frame = -3

Query 124 TLQGSAVRDVILNCRGFVQSSLAVGFEPTHSVN 23
 TL GP+ + D+I+ C +L+ GF+ +S N
 Sbjct 234 TLLGPACLGDLIMTCTSLNSRNLSFGFKIGNSDN 267

Query= 21

Length=136

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp Q29293.1 RL3_PIG RecName: Full=60S ribosomal protein L3	26.6	8.2
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ALIGNMENTS

>sp|Q29293.1|RL3_PIG RecName: Full=60S ribosomal protein L3
Length=130

Score = 26.6 bits (57), Expect = 8.2, Method: Compositional matrix adjust.
Identities
= 10/19 (53%), Positives = 13/19 (68%), Gaps = 0/19 (0%)
Frame = +2

```
Query   8      LEDSAVNRMGRFESYGEVV   64
        L D ++N +GRF  YGEV
Sbjct  106  LSDKSINPLGRFVHYGEVT   124
```

Query= 22

Length=144

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp P49327.3 FAS_HUMAN RecName: Full=Fatty acid synthase; Incl...	28.9	2.4
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ALIGNMENTS

>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
Full=[Acyl-carrier-protein]
S-acetyltransferase; Includes: RecName:
Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein]
hydrolase
Length=2511

Score = 28.9 bits (63), Expect = 2.4, Method: Compositional matrix adjust.
Identities = 12/27 (44%), Positives = 17/27 (63%), Gaps = 0/27 (0%)
Frame = -3

```
Query  142    FTLQGPSAVRDVILNRWLRSIWYGPAH   62
        +TLQ + V DV+++RWLR      G  H
Sbjct  1067  YTLQDKAQVADVVSRLRVTVAGGVH   1093
```

Query= 23

Length=149

Sequences producing significant alignments:	Score (Bits)	E Value
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sp Q03396.1 L_SV5WR RecName: Full=RNA-directed RNA polymerase...	28.9	2.4
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ALIGNMENTS

>sp|Q03396.1|L_SV5WR RecName: Full=RNA-directed RNA polymerase L; Short=Protein L;

AltName: Full=Large structural protein; AltName: Full=Replicase;

AltName: Full=Transcriptase; Includes: RecName: Full=RNA-directed

RNA polymerase; Includes: RecName: Full=mRNA (guanine-N(7)-)-methyltransferase;

Includes: RecName: Full=mRNA

guanylyltransferase

Length=2255

Score = 28.9 bits (63), Expect = 2.4, Method: Composition-based stats.

Identities = 15/29 (52%), Positives = 17/29 (59%), Gaps = 3/29 (10%)

Frame = -3

Query	132	PGPADRRILLN---SDGFDPSGTAQPTTS	55
		P P +RR+LLN D FDPS Q TS	
Sbjct	507	PNPFNRRLLLNLFLGDDKFDPSVELQYVTS	535

Query= 24

Length=122

Sequences producing significant alignments:	Score (Bits)	E Value
---	-----------------	------------

sp Q29293.1 RL3_PIG RecName: Full=60S ribosomal protein L3	26.2	8.5
--	------	-----

ALIGNMENTS

>sp|Q29293.1|RL3_PIG RecName: Full=60S ribosomal protein L3

Length=130

Score = 26.2 bits (56), Expect = 8.5, Method: Composition-based stats.

Identities = 10/18 (56%), Positives = 13/18 (72%), Gaps = 0/18 (0%)

Frame = +2

Query	8	LEDSAVNRMGRFESYGEV	61
		L D ++N +GRF YGEV	
Sbjct	106	LSDKSINPLGRFVHYGEV	123

Query= 25

Length=136

Sequences producing significant alignments:	Score (Bits)	E Value
---	-----------------	------------

sp Q29293.1 RL3_PIG RecName: Full=60S ribosomal protein L3	26.9	5.8
--	------	-----

ALIGNMENTS

>sp|Q29293.1|RL3_PIG RecName: Full=60S ribosomal protein L3
Length=130

Score = 26.9 bits (58), Expect = 5.8, Method: Compositional matrix adjust.
Identities = 10/19 (53%), Positives = 13/19 (68%), Gaps = 0/19 (0%)
Frame = +2

Query 8 LEDSAVNRMGRFESYGEV 64
L D ++N +GRF YGEV
Sbjct 106 LSDKSINPLGRFVHYGEVT 124

Query= 26

Length=143

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp B7VIS0.1 GLND_VIBSL RecName: Full=[Protein-PII] uridylyltr...	27.7	5.1
--	------	-----

ALIGNMENTS

>sp|B7VIS0.1|GLND_VIBSL RecName: Full=[Protein-PII] uridylyltransferase;
Short=PII uridylyl-transferase;
AltName: Full=UTase; AltName: Full=Uridylyl-removing
enzyme
Length=873

Score = 27.7 bits (60), Expect = 5.1, Method: Composition-based stats.
Identities = 16/37 (43%), Positives = 19/37 (51%), Gaps = 2/37 (5%)
Frame = +3

Query 6 SWKIRLLTEWVGSNPTAKLMRRHLHCGVTATDKFRHN 116
SWK LL E S T + +RR L V D+ RHN
Sbjct 591 SWKRTLLAELFHS--TQRALRRGLENPVDVRDIRHN 625

Query= 27

Length=133

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp A9B5T5.1 SYK_HERA2 RecName: Full=Lysine--tRNA ligase; AltN...	29.3	1.5
--	------	-----

ALIGNMENTS

>sp|A9B5T5.1|SYK_HERA2 RecName: Full=Lysine--tRNA ligase; AltName: Full=Lysyl-
tRNA synthetase;
Short=LysRS
Length=492

Score = 29.3 bits (64), Expect = 1.5, Method: Composition-based stats.
Identities = 20/43 (47%), Positives = 25/43 (58%), Gaps = 8/43 (19%)

Frame = -2

```
Query 126  ESNDL-----GKLCLNLSEGVEPVLARVPERRFTLQGPSAVRD 13
          E NDL      GKL      + G+EP  ARVP+R  TL    +AVR+
Sbjct  2    ELNDLQQTRYGKLQALQAAGIEPYPARVPQRTHTL---TAVRE 41
```

Query= 28

Length=124

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp B3PIT8.1 MNMG_CELJU RecName: Full=tRNA uridine 5-carboxyme...	32.0	0.18
--	------	------

ALIGNMENTS

```
>sp|B3PIT8.1|MNMG_CELJU RecName: Full=tRNA uridine 5-carboxymethylaminomethyl
modification
enzyme MnmG; AltName: Full=Glucose-inhibited division
protein A
Length=638
```

Score = 32.0 bits (71), Expect = 0.18, Method: Composition-based stats.
 Identities = 15/31 (48%), Positives = 20/31 (65%), Gaps = 0/31 (0%)
 Frame = +1

```
Query 31  SLKGEPSSGEYACPQVRVESLRTGWTERIPD 123
          SLKGEP +GE A  QV +E+    G+ +R  D
Sbjct 525  SLKGEPLAGEAAAEQVEIEAKYAGYIDRQQD 555
```

Query= 29

Length=134

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp B2RKK1.1 LEPA_PORG3 RecName: Full=Elongation factor 4; Sho...	28.1	3.4
sp Q7MV56.1 LEPA_PORGI RecName: Full=Elongation factor 4; Sho...	27.7	4.2

ALIGNMENTS

```
>sp|B2RKK1.1|LEPA_PORG3 RecName: Full=Elongation factor 4; Short=EF-4; AltName:
Full=Ribosomal
back-translocase LepA
Length=595
```

Score = 28.1 bits (61), Expect = 3.4, Method: Composition-based stats.
 Identities = 12/37 (32%), Positives = 20/37 (54%), Gaps = 3/37 (8%)
 Frame = -2

```
Query 124  DPSGTAQPTTAERIERPW---QVMSELIWVHPSRTFC 23
          +PSG +PT + IE P+    V++    ++ P  T  C
Sbjct 385  NPSGLPEPTLIDHIEEPFIRASVITNTAYIGPIMTLC 421
```

```
>sp|Q7MV56.1|LEPA_PORGI RecName: Full=Elongation factor 4; Short=EF-4; AltName:
```

Full=Ribosomal
back-translocase LepA
Length=595

Score = 27.7 bits (60), Expect = 4.2, Method: Composition-based stats.
Identities = 12/37 (32%), Positives = 20/37 (54%), Gaps = 3/37 (8%)
Frame = -2

Query 124 DPSGTAQPTTAERIERPW---QVMSELIWVHPSRTFC 23
+PSG +PT + IE P+ V++ ++ P T C
Sbjct 385 NPSGLLEPTLIDHIEEPFIRASVITNTAYIGPIMTLC 421

Query= 30

Length=124

Sequences producing significant alignments:			Score (Bits)	E Value
sp B1JKQ0.1 PYRF_YERPY	RecName: Full=Orotidine 5'-phosphate d...	28.5	2.2	
sp P58644.1 PYRF_YERPE	RecName: Full=Orotidine 5'-phosphate d...	28.5	2.2	
sp Q66AI1.1 PYRF_YERPS	RecName: Full=Orotidine 5'-phosphate d...	28.1	2.3	
sp A8FVN0.1 PYRF_SHESH	RecName: Full=Orotidine 5'-phosphate d...	28.1	2.8	
sp B4RDU2.1 FMT_PHEZH	RecName: Full=Methionyl-tRNA formyltran...	27.3	4.6	
sp A4WAY2.1 PYRF_ENT38	RecName: Full=Orotidine 5'-phosphate d...	26.6	7.6	
sp A1JM26.1 PYRF_YERE8	RecName: Full=Orotidine 5'-phosphate d...	26.6	8.9	

ALIGNMENTS

>sp|B1JKQ0.1|PYRF_YERPY RecName: Full=Orotidine 5'-phosphate decarboxylase;
AltName:
Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
Length=245

Score = 28.5 bits (62), Expect = 2.2, Method: Composition-based stats.
Identities = 13/36 (36%), Positives = 18/36 (50%), Gaps = 0/36 (0%)
Frame = -2

Query 117 RDSTRTCGQAYSPELCRGFVQSSRFTLQGPSAVRDV 10
+D+ SP+ CR V FTL GP +RD+
Sbjct 26 KDAALAFADQVSPQDCRLKVGKEMFTLYGPELIRDL 61

>sp|P58644.1|PYRF_YERPE RecName: Full=Orotidine 5'-phosphate decarboxylase;
AltName:
Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
sp|Q1CJ05.1|PYRF_YERPN RecName: Full=Orotidine 5'-phosphate decarboxylase;
AltName:
Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
sp|Q1C7L9.1|PYRF_YERPA RecName: Full=Orotidine 5'-phosphate decarboxylase;
AltName:
Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
sp|A4TJ45.1|PYRF_YERPP RecName: Full=Orotidine 5'-phosphate decarboxylase;
AltName:
Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
sp|A9R8T1.1|PYRF_YERPG RecName: Full=Orotidine 5'-phosphate decarboxylase;
AltName:
Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
Length=245

Score = 28.5 bits (62), Expect = 2.2, Method: Composition-based stats.
 Identities = 13/36 (36%), Positives = 18/36 (50%), Gaps = 0/36 (0%)
 Frame = -2

Query 117 RDSTRTCGQAYSPELCRGFVQSSRFTLQGPSAVRDV 10
 +D+ SP+ CR V FTL GP +RD+
 Sbjct 26 KDAALAFADQVSPQDCRLKVGKEMFTLYGPELIRDL 61

>sp|Q66AI1.1|PYRF_YERPS RecName: Full=Orotidine 5'-phosphate decarboxylase;
 AltName:
 Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
 sp|A7FI10.1|PYRF_YERP3 RecName: Full=Orotidine 5'-phosphate decarboxylase;
 AltName:
 Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
 sp|B2K4I4.1|PYRF_YERPB RecName: Full=Orotidine 5'-phosphate decarboxylase;
 AltName:
 Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
 Length=245

Score = 28.1 bits (61), Expect = 2.3, Method: Composition-based stats.
 Identities = 13/36 (36%), Positives = 18/36 (50%), Gaps = 0/36 (0%)
 Frame = -2

Query 117 RDSTRTCGQAYSPELCRGFVQSSRFTLQGPSAVRDV 10
 +D+ SP+ CR V FTL GP +RD+
 Sbjct 26 KDAALAFADQVSPQDCRLKVGKEMFTLYGPELIRDL 61

>sp|A8FVN0.1|PYRF_SHESH RecName: Full=Orotidine 5'-phosphate decarboxylase;
 AltName:
 Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
 Length=234

Score = 28.1 bits (61), Expect = 2.8, Method: Composition-based stats.
 Identities = 11/24 (46%), Positives = 15/24 (63%), Gaps = 0/24 (0%)
 Frame = -2

Query 81 PELCRGFVQSSRFTLQGPSAVRDV 10
 P++CR V FTL GP V+D+
 Sbjct 27 PQMCRLKVGKEMFTLFGPELVKDI 50

>sp|B4RDU2.1|FMT_PHEZH RecName: Full=Methionyl-tRNA formyltransferase
 Length=308

Score
 = 27.3 bits (59), Expect = 4.6, Method: Composition-based stats.
 Identities = 14/34 (41%), Positives = 20/34 (59%), Gaps = 0/34 (0%)
 Frame = -3

Query 113 TQPGPADRRILLNSVGDSFSPAGSPFKDLLLLGT 12
 T+ GP + LL++ D+ PAG D LL+GT
 Sbjct 239 TEKGPVRVKALLSAFEDAEGPAGETLDDRLLVGT 272

>sp|Q11GT5.1|DNLJ_MESSB RecName: Full=DNA ligase; AltName:
 Full=Polydeoxyribonucleotide
 synthase [NAD(+)]
 Length=703

Score = 27.3 bits (59), Expect = 6.5, Method: Composition-based stats.
 Identities = 11/18 (61%), Positives = 14/18 (78%), Gaps = 0/18 (0%)
 Frame = +2

```

Query   68   RQSSGEYACPQVRVESLR   121
          R+  SGE+ACP   R+E  LR
Sbjct   442  RRCSGEFACPFQRIEHLR   459

```

```

>sp|A4WAY2.1|PYRF_ENT38 RecName: Full=Orotidine 5'-phosphate decarboxylase;
AltName:
Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
Length=246

```

```

Score = 26.6 bits (57), Expect = 7.6, Method: Compositional matrix adjust.
Identities = 15/36 (42%), Positives = 16/36 (44%), Gaps = 0/36 (0%)
Frame = -2

```

```

Query   117  RDSTRTCGQAYSPELCRGFVQSSRFTLQGPSAVRDV   10
          RDS          P CR V      FTL GP VRD+
Sbjct   26   RDSALAFVDLIDPRDCRLKVGKEMFTLFGPQIVRDL   61

```

```

>sp|A1JM26.1|PYRF_YERE8 RecName: Full=Orotidine 5'-phosphate decarboxylase;
AltName:
Full=OMP decarboxylase; Short=OMPDCase; Short=OMPdecase
Length=246

```

```

Score = 26.6 bits (57), Expect = 8.9, Method: Composition-based stats.
Identities = 13/36 (36%), Positives = 17/36 (47%), Gaps = 0/36 (0%)
Frame = -2

```

```

Query   117  RDSTRTCGQAYSPELCRGFVQSSRFTLQGPSAVRDV   10
          +D+          +P CR V      FTL GP VRD+
Sbjct   26   KDAALAFADRVNPRDCRLKVGKEMFTLYGPQLVRDL   61

```

Query= 31

Length=119

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q9UMX2.1 OAZ3_HUMAN RecName: Full=Ornithine decarboxylase ...	27.7	2.9
sp Q9CP62.1 MTNN_PASMU RecName: Full=5'-methylthioadenosine/S...	27.7	3.5

ALIGNMENTS

```

>sp|Q9UMX2.1|OAZ3_HUMAN RecName: Full=Ornithine decarboxylase antizyme 3;
Short=AZ3;
Short=ODC-Az 3
Length=187

```

```

Score = 27.7 bits (60), Expect = 2.9, Method: Compositional matrix adjust.
Identities = 12/28 (43%), Positives = 15/28 (54%), Gaps = 0/28 (0%)
Frame = -2

```

```

Query   118  QNESNDLGKLCNLNLSVSGIRSVQPVHPS   35
          QN+ ND G L      S G      V+P HP+
Sbjct   134  QNDRNDRGALLRAFSYMGFEVVRPDHPA   161

```

```

>sp|Q9CP62.1|MTNN_PASMU RecName: Full=5'-methylthioadenosine/S-
adenosylhomocysteine nucleosidase;
Short=MTA/SAH nucleosidase; Short=MTAN; AltName:
Full=5'-methylthioadenosine nucleosidase; Short=MTA nucleosidase;

```

AltName: Full=S-adenosylhomocysteine nucleosidase; Short=AdoHcy
nucleosidase; Short=SAH nucleosidase; Short=SRH
nucleosidase
Length=229

Score = 27.7 bits (60), Expect = 3.5, Method: Composition-based stats.
Identities = 14/33 (42%), Positives = 19/33 (58%), Gaps = 2/33 (6%)
Frame = -1

Query 119 AERI--ERPWQVMSELICVGDSFSPAGSPFKDL 27
AE+I ++ QV LIC GDSF G+P +
Sbjct 129 AEKIAVQQQQQVKRGLICSGDSFIQGGTPLAQI 161

Query= 32

Length=144

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q0V6M5.1 LCPS_PHANO RecName: Full=Bifunctional lycopene cy...	27.3	7.3

ALIGNMENTS

>sp|Q0V6M5.1|LCPS_PHANO RecName: Full=Bifunctional lycopene cyclase/phytoene synthase;

Includes: RecName: Full=Lycopene beta-cyclase; AltName: Full=Lycopene cyclase; Includes: RecName: Full=Phytoene synthase

Length=585

Score = 27.3 bits (59), Expect = 7.3, Method: Composition-based stats.
Identities = 13/29 (45%), Positives = 18/29 (62%), Gaps = 1/29 (3%)
Frame = +2

Query 41 VNQWWAGPYQMDRSHLL*LEDSAVNRMGR 127
+N W PY+ DR+ L L+D AV R+ R
Sbjct 268 INALWVSPYKYDRARLAGLQD-AVLRLKR 295

Query= 33

Length=148

Sequences producing significant alignments:	Score (Bits)	E Value
sp A8ABM5.1 EF1A_IGNH4 RecName: Full=Elongation factor 1-alpha...	29.6	1.1

ALIGNMENTS

>sp|A8ABM5.1|EF1A_IGNH4 RecName: Full=Elongation factor 1-alpha; Short=EF-1-alpha; AltName:

Full=Elongation factor Tu; Short=EF-Tu

Length=442

Score = 29.6 bits (65), Expect = 1.1, Method: Composition-based stats.
Identities = 17/46 (37%), Positives = 25/46 (54%), Gaps = 5/46 (11%)
Frame = -3

```

Query   146  AVGFEP-----THSVNSRIFQLQQGVEPVLARVPERRSGGTQPGPA   24
          AVG+ P      T SV SRI +++Q ++P   +V E      +PG A
Sbjct   344  AVGYTPVIHAHTASVASRIIEIKQKIDPRTGKVIEENPSFLKPGDA   389

```

Query= 34

Length=116

		Score	E
		(Bits)	Value

sp Q9FY99.2 G6PD2_ARATH	RecName: Full=Glucose-6-phosphate 1-d...	27.3	5.4
sp B2SX19.1 GPDA_BURPP	RecName: Full=Glycerol-3-phosphate deh...	26.6	8.5

ALIGNMENTS

```

>sp|Q9FY99.2|G6PD2_ARATH RecName: Full=Glucose-6-phosphate 1-dehydrogenase 2,
chloroplastic;
Short=G6PD2; Short=G6PDH2; Flags: Precursor
Length=596

```

Score = 27.3 bits (59), Expect = 5.4, Method: Compositional matrix adjust.
 Identities = 13/25 (52%), Positives = 14/25 (56%), Gaps = 0/25 (0%)
 Frame = -2

```

Query   106  SFSPARGSNPY*PEFLSGGPEGLNP   32
          SFSP G      FLS P+GLNP
Sbjct   20   SFSPVNGDRHRSLSFLSASPQGLNP   44

```

```

>sp|B2SX19.1|GPDA_BURPP RecName: Full=Glycerol-3-phosphate dehydrogenase
[NAD(P)+]; AltName:
Full=NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
Length=332

```

Score = 26.6 bits (57), Expect = 8.5, Method: Compositional matrix adjust.
 Identities = 14/36 (39%), Positives = 20/36 (56%), Gaps = 2/36 (6%)
 Frame = -1

```

Query   116  CRGFVQSSQGV--EPVLARVPERRSGGTQPGPADRR   15
          C+GF SQ + + V A +PE +S G GP+ R
Sbjct   107  CKGFEADSQLMPHQVVAELPEHKSNGVLSGPSFAR   142

```

```

>sp|Q9I2N4.1|MODC_PSEAE RecName: Full=Molybdenum import ATP-binding protein ModC
Length=361

```

Score = 26.6 bits (57), Expect = 10.0, Method: Compositional matrix adjust.
 Identities = 11/18 (61%), Positives = 14/18 (78%), Gaps = 0/18 (0%)
 Frame = -1

```

Query   89   GVEPVLARVPERRSGGTQ   36
          G+E +L R+PER SGG Q
Sbjct   123  GIEHLLERMPERLSGGEQ   140

```

Query= 35

Length=138

Sequences producing significant alignments:	Score (Bits)	E Value
---	-----------------	------------

sp A7HIL1.1 Y4379_ANADF RecName: Full=Probable RNA methyltran...	26.9	7.6
sp Q8ZIN5.1 KHSE_YERPE RecName: Full=Homoserine kinase; Short...	26.9	7.9
sp Q2NVZ5.1 KHSE_SODGM RecName: Full=Homoserine kinase; Short...	26.9	8.5
sp A1JJC7.1 KHSE_YERE8 RecName: Full=Homoserine kinase; Short...	26.6	8.9

ALIGNMENTS

>sp|A7HIL1.1|Y4379_ANADF RecName: Full=Probable RNA methyltransferase
 Ana109_4379
 Length=336

Score = 26.9 bits (58), Expect = 7.6, Method: Compositional matrix adjust.
 Identities = 11/24 (46%), Positives = 17/24 (71%), Gaps = 0/24 (0%)
 Frame = -1

Query	102	GAERIERPWQVMSELIWVRDSTR	31
		G R R W++++L+ VR DSTR	
Sbjct	120	GLARSLRAWWEIVAQLLHVRADSTR	143

>sp|Q8ZIN5.1|KHSE_YERPE RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 sp|Q66ET8.1|KHSE_YERPS RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 sp|Q1C0K9.1|KHSE_YERPA RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 sp|Q1CMW6.1|KHSE_YERP3 RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 sp|A4TQG9.1|KHSE_YERPP RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 sp|A7FMF2.1|KHSE_YERP3 RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 sp|B2K3L2.1|KHSE_YERP3 RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 sp|A9R025.1|KHSE_YERPG RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 sp|B1JL13.1|KHSE_YERPY RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 Length=309

Score = 26.9 bits (58), Expect = 7.9, Method: Composition-based stats.
 Identities = 13/31 (42%), Positives = 19/31 (61%), Gaps = 0/31 (0%)
 Frame = -2

Query	131	RTRISPSS*AAQNESNDLGKLCNLNSGSGGT	39
		RT++ P AA+ + D+G L +SGSG T	
Sbjct	235	RTQLLPGFAAARQAAQDIGALACGISGSGPT	265

>sp|Q2NVZ5.1|KHSE_SODGM RecName: Full=Homoserine kinase; Short=HK; Short=HSK
 Length=310

Score = 26.9 bits (58), Expect = 8.5, Method: Composition-based stats.
 Identities = 15/39 (38%), Positives = 20/39 (51%), Gaps = 0/39 (0%)
 Frame = -2

Query	131	RTRISPSS*AAQNESNDLGKLCNLNSGSGGTQPGPADRR	15
		RTR+ P A+ D+G L +SGSG T DR+	
Sbjct	235	RTRLLPGFADARQAVGDIGALACGISGSGPTLFAICDRQ	273

>sp|A1JJC7.1|KHSE_YERE8 RecName: Full=Homoserine kinase; Short=HK; Short=HSK
Length=309

Score = 26.6 bits (57), Expect = 8.9, Method: Composition-based stats.
Identities = 13/31 (42%), Positives = 19/31 (61%), Gaps = 0/31 (0%)
Frame = -2

Query 131 RTRISPSS*AAQNESNDLGKLCNLNSGSGGT 39
RT++ P AA+ + D+G L +SGSG T
Sbjct 235 RTQLLPGFAAARQAAQDIGALACGISGSGPT 265

Query= 36

Length=146

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp Q9SW95.2 SYNC2_ARATH RecName: Full=Asparagine--tRNA ligase...	29.3	1.9
--	------	-----

ALIGNMENTS

>sp|Q9SW95.2|SYNC2_ARATH RecName: Full=Asparagine--tRNA ligase, cytoplasmic 2;
AltName:
Full=Asparaginyl-tRNA synthetase 2; Short=AsnRS 2
Length=638

Score = 29.3 bits (64), Expect = 1.9, Method: Composition-based stats.
Identities = 12/40 (30%), Positives = 17/40 (43%), Gaps = 0/40 (0%)
Frame = -3

Query 132 GPSAVRDVILNAERIERPWQVMSELIWVRDSTRTCGQAY 13
GP + D I NA + W V +E+ + D C Y
Sbjct 401 GPRFIADKIDNARHLAEKWNVETEMAFaelDDAMDCADEY 440

Query 23 PQVRVESLRTGWTERIPDSLGSRP 94
PQVR+ T W++R P +L S P
Sbjct 833 PQVRIAPTVTTWSDRTPALPSHP 856

Query= 37

Length=139

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp P49327.3 FAS_HUMAN RecName: Full=Fatty acid synthase; Incl...	29.6	1.2
--	------	-----

ALIGNMENTS

>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
Full=[Acyl-carrier-protein]
S-acetyltransferase; Includes: RecName:
Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:

RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
 Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
 dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
 reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein]
 hydrolase
 Length=2511

Score = 29.6 bits (65), Expect = 1.2, Method: Compositional matrix adjust.
 Identities = 14/37 (38%), Positives = 20/37 (54%), Gaps = 0/37 (0%)
 Frame = -3

Query 137 FTLQGPSAVRDVILNRWLRSIWYGPAHHWSGGTQPGP 27
 +TLQ + V DV+++RWLR G H T+ P
 Sbjct 1067 YTLQDKAQVADVVSRLRVTVAGGVHISGLHTESAP 1103

Query= 38

Length=117

Sequences producing significant alignments:	Score (Bits)	E Value
---	-----------------	------------

sp Q0V6M5.1 LCPS_PHANO RecName: Full=Bifunctional lycopene cy...	27.3	6.5
--	------	-----

ALIGNMENTS

>sp|Q0V6M5.1|LCPS_PHANO RecName: Full=Bifunctional lycopene cyclase/phytoene
 synthase;
 Includes: RecName: Full=Lycopene beta-cyclase; AltName: Full=Lycopene
 cyclase; Includes: RecName: Full=Phytoene synthase
 Length=585

Score = 27.3 bits (59), Expect = 6.5, Method: Compositional matrix adjust.
 Identities = 9/18 (50%), Positives = 13/18 (72%), Gaps = 0/18 (0%)
 Frame = +1

Query 58 WAGPYQMDRSHLAGL NES 111
 W PY+ DR+ LAGL ++
 Sbjct 272 WVSPYKYDRARLAGLQDA 289

Query= 39

Length=116

Sequences producing significant alignments:	Score (Bits)	E Value
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sp A1K5J1.1 SYE_AZOSB RecName: Full=Glutamate--tRNA ligase; A...	28.1	3.0
--	------	-----

ALIGNMENTS

>sp|A1K5J1.1|SYE_AZOSB RecName: Full=Glutamate--tRNA ligase; AltName: Full=Glutamyl-tRNA synthetase; Short=GluRS
Length=467

Score = 28.1 bits (61), Expect = 3.0, Method: Compositional matrix adjust.
Identities = 15/28 (54%), Positives = 18/28 (64%), Gaps = 1/28 (4%)
Frame = +3

Query 27 RSGLSP-SGPAHETTLALRSR*AGLNE 107
R G+ P +GPA E +AL DR A LNE
Sbjct 336 RRGVDPEAGPALEQVVALYKDRSANLNE 363

Query= 40

Length=126

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q2KA45.1 PUR5_RHIEC RecName: Full=Phosphoribosylformylglyc...	26.6	8.6

ALIGNMENTS

>sp|Q2KA45.1|PUR5_RHIEC RecName: Full=Phosphoribosylformylglycinamide cyclo-
ligase;
AltName: Full=AIR synthase; AltName: Full=AIRS; AltName: Full=Phosphoribosyl-
aminoimidazole
synthetase
Length=357

Score = 26.6 bits (57), Expect = 8.6, Method: Composition-based stats.
Identities = 15/39 (38%), Positives = 21/39 (54%), Gaps = 1/39 (3%)
Frame = +3

Query 9 FRHNLPRSFDSFCAAQ-ELGLIRVRPPSGGLGRTRWIEA 122
F N+PR AA+ +LG ++V P L RT +EA
Sbjct 259 FPEINIPRVLPEHLAAEIDLGA VKVPPVFSWLARTGGVEA 297

Query= 41

Length=143

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q8GXG1.2 ASPG2_ARATH RecName: Full=Probable isoaspartyl pe...	27.7	5.2

ALIGNMENTS

>sp|Q8GXG1.2|ASPG2_ARATH RecName: Full=Probable isoaspartyl peptidase/L-
asparaginase 2;
AltName: Full=L-asparagine amidohydrolase 2; Contains: RecName:
Full=Isoaspartyl peptidase/L-asparaginase 2 subunit alpha;
Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase
2 subunit beta; Flags: Precursor

Length=325

Score = 27.7 bits (60), Expect = 5.2, Method: Composition-based stats.
Identities = 13/24 (54%), Positives = 14/24 (58%), Gaps = 0/24 (0%)
Frame = -2

Query 76 G*QPNLPATAQNESNDLGKLCNL 5
G PNLPA Q E+ L CLNL
Sbjct 13 GIDPNLPAERQEEAKQLLTRCLNL 36

Query= 42

Length=151

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q8GXG1.2 ASPG2_ARATH RecName: Full=Probable isoaspartyl pe...	28.5	2.8

ALIGNMENTS

>sp|Q8GXG1.2|ASPG2_ARATH RecName: Full=Probable isoaspartyl peptidase/L-asparaginase 2;
AltName: Full=L-asparagine amidohydrolase 2; Contains: RecName:
Full=Isoaspartyl peptidase/L-asparaginase 2 subunit alpha;
Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase
2 subunit beta; Flags: Precursor
Length=325

Score = 28.5 bits (62), Expect = 2.8, Method: Composition-based stats.
Identities = 13/24 (54%), Positives = 14/24 (58%), Gaps = 0/24 (0%)
Frame = -1

Query 76 G*QPNLPATAQNESNDLGKLCNL 5
G PNLPA Q E+ L CLNL
Sbjct 13 GIDPNLPAERQEEAKQLLTRCLNL 36

Query= 43

Length=129

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q8GXG1.2 ASPG2_ARATH RecName: Full=Probable isoaspartyl pe...	28.5	2.2

ALIGNMENTS

>sp|Q8GXG1.2|ASPG2_ARATH RecName: Full=Probable isoaspartyl peptidase/L-asparaginase 2;
AltName: Full=L-asparagine amidohydrolase 2; Contains: RecName:
Full=Isoaspartyl peptidase/L-asparaginase 2 subunit alpha;
Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase
2 subunit beta; Flags: Precursor
Length=325

Score = 28.5 bits (62), Expect = 2.2, Method: Composition-based stats.
Identities = 13/24 (54%), Positives = 14/24 (58%), Gaps = 0/24 (0%)
Frame = -3

```

Query   76  G*QPNLPATAQNESNDLGKLCNL  5
          G  PNLPA  Q  E+  L   CLNL
Sbjct   13  GIDPNLPAERQEEAKQLLTRCLNL  36

```

Query= 44

Length=151

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp A3QDC9.1 CDD_SHELP RecName: Full=Cytidine deaminase; AltNa...	27.3	6.3
--	------	-----

ALIGNMENTS

>sp|A3QDC9.1|CDD_SHELP RecName: Full=Cytidine deaminase; AltName: Full=Cytidine aminohydrolase;

Short=CDA

Length=296

Score = 27.3 bits (59), Expect = 6.3, Method: Compositional matrix adjust.
 Identities = 13/42 (31%), Positives = 22/42 (52%), Gaps = 0/42 (0%)
 Frame = -3

```

Query   128  HSVNSRIFQLQRFTLQGPSAVRDVILNAERIERPWQVMSELI  3
          HSV++      +      L G + + D+I+NA      Q M+EL+
Sbjct   98  HSVHAEQSAISHAWLSGETGIEDIIVNASPCGHCRCQFMNELV  139

```

Query= 45

Length=146

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp B3PIT8.1 MNMG_CELJU RecName: Full=tRNA uridine 5-carboxyme...	27.3	7.0
--	------	-----

ALIGNMENTS

>sp|B3PIT8.1|MNMG_CELJU RecName: Full=tRNA uridine 5-carboxymethylaminomethyl modification

enzyme MnmG; AltName: Full=Glucose-inhibited division

protein A

Length=638

Score = 27.3 bits (59), Expect = 7.0, Method: Composition-based stats.
 Identities = 12/20 (60%), Positives = 15/20 (75%), Gaps = 0/20 (0%)
 Frame = +3

```

Query   78  SLKGEPSSGEYACPQVRVES  137
          SLKGEP +GE A  QV +E+
Sbjct   525  SLKGEPLAGEAAAEQVEIEA  544

```

Score = 27.3 bits (59), Expect = 6.0, Method: Composition-based stats.
Identities = 12/34 (35%), Positives = 23/34 (68%), Gaps = 3/34 (9%)
Frame = -1

```
Query 134 RWLRSIWYGPAHHWFTLQGPSAVRDVILNAERIE 33
          RW +S + G A H+FT+ P R+++L+ +++E
Sbjct 14 RWDQSTFLGRARHFFTVTDP---RNLLLSGKQLE 44
```

Query= 46

Length=138

Sequences producing significant alignments:	Score (Bits)	E Value
---	-----------------	------------

sp A1BGY2.1 KTHY_CHLPD RecName: Full=Thymidylate kinase; AltN...	28.1	2.6
sp Q8FLM0.1 SYL_COREF RecName: Full=Leucine--tRNA ligase; Alt...	27.3	6.4
sp B3EDD6.1 KTHY_CHLL2 RecName: Full=Thymidylate kinase; AltN...	26.9	6.8
sp Q9A842.1 DNLJ_CAUCR RecName: Full=DNA ligase; AltName: Ful...	26.9	9.9

ALIGNMENTS

>sp|A1BGY2.1|KTHY_CHLPD RecName: Full=Thymidylate kinase; AltName: Full=dTMP
kinase
Length=219

Score = 28.1 bits (61), Expect = 2.6, Method: Composition-based stats.
Identities = 18/42 (43%), Positives = 24/42 (57%), Gaps = 4/42 (10%)
Frame = -3

```
Query 136 GVEPVLARVPERRSGGTQPGPADRRILLNSQNESNDLGKLCL 11
          GVE V R P GGT+ R ILL S++E + +G+L L
Sbjct 28 GVESVTIREP----GGTEVAEKIRSILLESRHEISAVGELLL 65
```

>sp|Q8FLM0.1|SYL_COREF RecName: Full=Leucine--tRNA ligase; AltName: Full=Leucyl-
tRNA
synthetase; Short=LeuRS
Length=957

Score = 27.3 bits (59), Expect = 6.4, Method: Composition-based stats.
Identities = 11/22 (50%), Positives = 14/22 (64%), Gaps = 0/22 (0%)
Frame = -2

```
Query 86 STRTCGQAYSPELAERIERPWQ 21
          S ++ Y+PELA IER WQ
Sbjct 11 SAQSLAYRYTPELANAIEREWQ 32
```

>sp|B3EDD6.1|KTHY_CHLL2 RecName: Full=Thymidylate kinase; AltName: Full=dTMP
kinase
Length=219

Score = 26.9 bits (58), Expect = 6.8, Method: Composition-based stats.
Identities = 13/31 (42%), Positives = 20/31 (65%), Gaps = 0/31 (0%)
Frame = -3

```
Query 103 RRSGGTQPGPADRRILLNSQNESNDLGKLCL 11
          R GGT+ R+ILL S++E + +G+L L
Sbjct 35 REPGGTEVAEKIRQILLESRHEISPIGELLL 65
```

Query= 47

Length=156

Sequences producing significant alignments:	Score (Bits)	E Value
sp A3MXT2.1 HEM12_PYRCJ RecName: Full=Glutamyl-tRNA reductase...	30.8	0.53
sp B1I165.1 KTHY_DESAP RecName: Full=Thymidylate kinase; AltN...	27.7	5.0
sp Q8FLM0.1 SYL_COREF RecName: Full=Leucine--tRNA ligase; Alt...	27.3	7.1
sp B3EDD6.1 KTHY_CHLL2 RecName: Full=Thymidylate kinase; AltN...	26.9	9.1

ALIGNMENTS

>sp|A3MXT2.1|HEM12_PYRCJ RecName: Full=Glutamyl-tRNA reductase 2; Short=GluTR 2
Length=391

Score = 30.8 bits (68), Expect = 0.53, Method: Compositional matrix adjust.
Identities = 12/37 (32%), Positives = 20/37 (54%), Gaps = 0/37 (0%)
Frame = -2

Query	119	PNLPATAVRRDSTRTCGQAYSPELAERIERPWQVMSE	9
		PNLP V+ + R + Y+ E A +E+ W ++ E	
Sbjct	270	PNLPVAVVKIEDLRELAEEYNRRERAGEVEKAWAIVDE	306

>sp|B1I165.1|KTHY_DESAP RecName: Full=Thymidylate kinase; AltName: Full=dTMP
kinase
Length=221

Score = 27.7 bits (60), Expect = 5.0, Method: Composition-based stats.
Identities = 12/28 (43%), Positives = 18/28 (64%), Gaps = 0/28 (0%)
Frame = -3

Query	124	NSRIFQLQRSGGTQPGPADRRILLNSQN	41
		N R+ + GGT+ G A RR+LL++ N	
Sbjct	32	NHRVLVTREPGGTRIGEAVRRVLLDTGN	59

>sp|Q8FLM0.1|SYL_COREF RecName: Full=Leucine--tRNA ligase; AltName: Full=Leucyl-
tRNA
synthetase; Short=LeuRS
Length=957

Score = 27.3 bits (59), Expect = 7.1, Method: Composition-based stats.
Identities = 11/22 (50%), Positives = 14/22 (64%), Gaps = 0/22 (0%)
Frame = -2

Query	86	STRTCGQAYSPELAERIERPWQ	21
		S ++ Y+PELA IER WQ	
Sbjct	11	SAQSLAYRYTPELANAIEREWQ	32

>sp|B3EDD6.1|KTHY_CHLL2 RecName: Full=Thymidylate kinase; AltName: Full=dTMP
kinase
Length=219

Score = 26.9 bits (58), Expect = 9.1, Method: Composition-based stats.
Identities = 13/32 (41%), Positives = 21/32 (66%), Gaps = 0/32 (0%)
Frame = -3

```

Query   106   LQRSGGTQPGPADRRILLNSQNESNDLGKLCL   11
          L+  GGT+      R+ILL S++E + +G+L L
Sbjct   34   LREPGGTEVAEKIRQILLESRHEISPIGELLL   65

```

Query= 48

Length=139

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q8FLM0.1 SYL_COREF RecName: Full=Leucine--tRNA ligase; Alt...	27.7	5.9
sp Q966C6.3 RL7A_CAEEL RecName: Full=60S ribosomal protein L7a	26.9	8.3
sp Q04462.2 SYVC_RAT RecName: Full=Valine--tRNA ligase; AltNa...	26.9	9.0

ALIGNMENTS

```

>sp|Q8FLM0.1|SYL_COREF RecName: Full=Leucine--tRNA ligase; AltName: Full=Leucyl-
tRNA
synthetase; Short=LeuRS
Length=957

```

Score = 27.7 bits (60), Expect = 5.9, Method: Composition-based stats.
 Identities = 11/22 (50%), Positives = 14/22 (64%), Gaps = 0/22 (0%)
 Frame = -3

```

Query   86   STRTCGQAYSPELAERIERPWQ   21
          S ++      Y+PELA IER WQ
Sbjct   11   SAQSLAYRYTPELANAIEREWQ   32

```

```

>sp|Q966C6.3|RL7A_CAEEL RecName: Full=60S ribosomal protein L7a
Length=265

```

Score = 26.9 bits (58), Expect = 8.3, Method: Composition-based stats.
 Identities = 11/29 (38%), Positives = 15/29 (52%), Gaps = 0/29 (0%)
 Frame = -1

```

Query   103   HWSGGTQPGPADRRILLNSQNESNDLGKL   17
          HW GG      +D + L + + DLGKL
Sbjct   237   HWGGGVMSAKSDAKKLKIERARARDLGKL   265

```

```

>sp|Q04462.2|SYVC_RAT RecName: Full=Valine--tRNA ligase; AltName: Full=Valyl-
tRNA synthetase;
Short=ValRS
Length=1264

```

Score = 26.9 bits (58), Expect = 9.0, Method: Compositional matrix adjust.
 Identities = 11/30 (37%), Positives = 17/30 (57%), Gaps = 0/30 (0%)
 Frame = -3

```

Query   113   PSPPLVRRDSTRTCGQAYSPELAERIERPW   24
          P+PP ++D + T +YSP+ E PW
Sbjct   283   PTPPGKKDVSGTMPDSYSPQYVEAAWYPW   312

```

Query= 49

Length=138

Sequences producing significant alignments:	Score (Bits)	E Value
---	-----------------	------------

sp P16084.1 BGLS_BUTFI RecName: Full=Beta-glucosidase A; AltN...	30.0	0.99
--	------	------

ALIGNMENTS

>sp|P16084.1|BGLS_BUTFI RecName: Full=Beta-glucosidase A; AltName: Full=Beta-D-glucoside
glucohydrolase; AltName: Full=Cellobiase; AltName: Full=Gentiobiase
Length=830

Score = 30.0 bits (66), Expect = 0.99, Method: Composition-based stats.
Identities = 15/33 (45%), Positives = 17/33 (52%), Gaps = 0/33 (0%)
Frame = -3

Query	124	QCKCRLMSWSGGTQPGPADRRILLNSQNESNDL	26
		Q LM+W GG + G A RILL N S L	
Sbjct	227	QISSVLMWQGGIEGGLAAARILLGKVNPSGKL	259

Query= 50

Length=129

Sequences producing significant alignments:	Score (Bits)	E Value
---	-----------------	------------

sp Q8DLB7.1 PYRD_THEEB RecName: Full=Dihydroorotate dehydroge...	26.6	8.7
--	------	-----

ALIGNMENTS

>sp|Q8DLB7.1|PYRD_THEEB RecName: Full=Dihydroorotate dehydrogenase (quinone);
AltName:
Full=DHodehase; Short=DHOD; Short=DHODase; AltName: Full=Dihydroorotate
oxidase
Length=364

Score = 26.6 bits (57), Expect = 8.7, Method: Composition-based stats.
Identities = 10/29 (34%), Positives = 15/29 (52%), Gaps = 0/29 (0%)
Frame = +3

Query	21	LPRSFDSEFCGWTERIPDSCSWKIRLLTEW	107
		L + F S CGW + C+W + L +W	
Sbjct	25	LHQQLSLCGWLNQDRSLCTWLRQQLQW	53

Query= 51

Length=134

Sequences producing significant alignments:	Score (Bits)	E Value
---	-----------------	------------

sp P49327.3 FAS_HUMAN RecName: Full=Fatty acid synthase; Incl...	28.5	2.7
--	------	-----

ALIGNMENTS

>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName: Full=[Acyl-carrier-protein] S-acetyltransferase; Includes: RecName: Full=[Acyl-carrier-protein] S-malonyltransferase; Includes: RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes: RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase; Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein] dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein] reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein] hydrolase
Length=2511

Score = 28.5 bits (62), Expect = 2.7, Method: Compositional matrix adjust.
Identities = 12/27 (44%), Positives = 17/27 (63%), Gaps = 0/27 (0%)
Frame = -3

Query 132 FTLQGPSAVRDVILNRWLR SIWYGPAH 52
+TLQ + V DV+++RWLR G H
Sbjct 1067 YTLQDKAQVADV VVSRWLRVT VAGGVH 1093

Query= 52

Length=139

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q165T7.1 G6PI_ROSDO RecName: Full=Glucose-6-phosphate isom...	28.9	1.9

ALIGNMENTS

>sp|Q165T7.1|G6PI_ROSDO RecName: Full=Glucose-6-phosphate isomerase; Short=GPI; AltName: Full=Phosphoglucose isomerase; Short=PGI; AltName: Full=Phosphohexose isomerase; Short=PHI
Length=530

Score = 28.9 bits (63), Expect = 1.9, Method: Composition-based stats.
Identities = 13/29 (45%), Positives = 17/29 (59%), Gaps = 0/29 (0%)
Frame = +3

Query 24 PRSFDSFCSGGLGRTRWIEAI*VQENTPV 110
PR+FD+F GG R +A +EN PV
Sbjct 267 PRAFDAFLRGQAMDRHFQAADWRENLPV 2

Query= 53

Length=112

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q0V6M5.1 LCPS_PHANO RecName: Full=Bifunctional lycopene cy...	27.3	6.2

ALIGNMENTS

>sp|Q0V6M5.1|LCPS_PHANO RecName: Full=Bifunctional lycopene cyclase/phytoene synthase;

Includes: RecName: Full=Lycopene beta-cyclase; AltName: Full=Lycopene cyclase; Includes: RecName: Full=Phytoene synthase
Length=585

Score = 27.3 bits (59), Expect = 6.2, Method: Compositional matrix adjust.
Identities = 9/18 (50%), Positives = 13/18 (72%), Gaps = 0/18 (0%)
Frame = +2

Query 53 WAGPYQMDRSHLAGLNES 106
W PY+ DR+ LAGL ++
Sbjct 272 WVSPYKYDRARLAGLQDA
289

Query= 54

Length=116

Score E
Sequences producing significant alignments: (Bits) Value

sp|Q1QX56.2|PLSX_CHRSD RecName: Full=Phosphate acyltransferase... 26.9 6.7

ALIGNMENTS

>sp|Q1QX56.2|PLSX_CHRSD RecName: Full=Phosphate acyltransferase; AltName: Full=Acyl-ACP phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate acyltransferase; AltName: Full=Phosphate-acyl-ACP acyltransferase
Length=379

Score = 26.9 bits (58), Expect = 6.7, Method: Compositional matrix adjust.
Identities = 12/32 (38%), Positives = 20/32 (63%), Gaps = 0/32 (0%)
Frame = -1

Query 104 LNPDLRTGVFS*TQGVEPVLARVPERLSGIRS 9
++PDL ++ + +E L +P+RLSG RS
Sbjct 29 MHPDLEIQMYGPRALEDELETLPKRLSGYRS 60

Query= 55

Length=129

Score E
Sequences producing significant alignments: (Bits) Value

sp|Q2T1H1.2|GPDA_BURTA RecName: Full=Glycerol-3-phosphate deh... 29.3 1.4
sp|Q5S2C3.2|PIR_ARATH RecName: Full=Protein PIR; AltName: Ful... 26.9 8.7

ALIGNMENTS

>sp|Q2T1H1.2|GPDA_BURTA RecName: Full=Glycerol-3-phosphate dehydrogenase [NAD(P)+]; AltName: Full=NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
Length=332

Score = 29.3 bits (64), Expect = 1.4, Method: Composition-based stats.
Identities = 15/35 (43%), Positives = 19/35 (54%), Gaps = 6/35 (17%)
Frame = -3


```

Query  121  LQGPSAVRDVILNSP*DSNLPIRLTAESSYSCRG  17
          L GPS  R+V          LP+ LT  S+S +CRG
Sbjct  135  LSGPSFAREVA-----QGLPVALTVASASAACRG  163

```

```

>sp|Q5S2C3.2|PIR_ARATH RecName: Full=Protein PIR; AltName: Full=PIR of plants;
AltName:
Full=Protein KLUNKER; Short=AtSRA1; AltName: Full=Protein
PIROGI
Length=1282

```

Score = 26.9 bits (58), Expect = 8.7, Method: Composition-based stats.
 Identities = 15/38 (39%), Positives = 19/38 (50%), Gaps = 1/38 (3%)
 Frame = +1

```

Query  4      WTERIPDSCSWKIRLLTEWVGSNPTASLGSRP*QQKVL  117
          WT RI + C+WK          G P AS GS  +KV+
Sbjct  413  WTARIWEQCAWKFSRPCRDAGETPEAS-GSYSDYEKVV  449

```

Query= 56

Length=134

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q29293.1 RL3_PIG RecName: Full=60S ribosomal protein L3	27.3	4.0

ALIGNMENTS

```

>sp|Q29293.1|RL3_PIG RecName: Full=60S ribosomal protein L3
Length=130

```

Score = 27.3 bits (59), Expect = 4.0, Method: Compositional matrix adjust.
 Identities = 9/23 (39%), Positives = 15/23 (65%), Gaps = 0/23 (0%)
 Frame = +3

```

Query  33  LEDSAVNRMGRFESYGESSGEYA  101
          L D ++N +GRF  YGE + ++
Sbjct  106  LSDKSINPLGRFVHYGEVTNDFV  128

```

Query= 57

Length=122

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q29293.1 RL3_PIG RecName: Full=60S ribosomal protein L3	26.2	7.5

ALIGNMENTS

```

>sp|Q29293.1|RL3_PIG RecName: Full=60S ribosomal protein L3
Length=130

```

Score = 26.2 bits (56), Expect = 7.5, Method: Composition-based stats.
 Identities = 10/18 (56%), Positives = 13/18 (72%), Gaps = 0/18 (0%)
 Frame = +3

```

Query  33  LEDSAVNRMGRFESYGEV  86

```

L D ++N +GRF YGEV
Sbjct 106 LSDKSINPLGRFVHYGEV 123

Query= 58

Length=124

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp B3PIT8.1 MNMG_CELJU RecName: Full=tRNA uridine 5-carboxyme...	27.3	6.1
--	------	-----

ALIGNMENTS

>sp|B3PIT8.1|MNMG_CELJU RecName: Full=tRNA uridine 5-carboxymethylaminomethyl
modification
enzyme MnmG; AltName: Full=Glucose-inhibited division
protein A
Length=638

Score = 27.3 bits (59), Expect = 6.1, Method: Composition-based stats.
Identities = 12/20 (60%), Positives = 15/20 (75%), Gaps = 0/20 (0%)
Frame = +2

Query 56 SLKGEPSSGEYACPQVRVES 115
 SLKGEP +GE A QV +E+
Sbjct 525 SLKGEPLAGEAAAEQVEIEA 544

Query= 59

Length=119

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp B1KDM8.1 PYRD_SHEWM RecName: Full=Dihydroorotate dehydroge...	27.7	3.3
--	------	-----

ALIGNMENTS

>sp|B1KDM8.1|PYRD_SHEWM RecName: Full=Dihydroorotate dehydrogenase (quinone);
AltName:
Full=DHODEhase; Short=DHOD; Short=DHODase; AltName: Full=Dihydroorotate
oxidase
Length=340

Score = 27.7 bits (60), Expect = 3.3, Method: Composition-based stats.
Identities = 10/19 (53%), Positives = 13/19 (68%), Gaps = 0/19 (0%)
Frame = -2

Query 76 SGFTLQGPSAVRDVILNCR 20
 SGF QGP ++D+I CR
Sbjct 319 SGFIYQGPKLIKDIIEACR 337

Query= 60

Length=124

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp B1ZGG2.1 MNMG_METPB	RecName: Full=tRNA uridine 5-carboxyme...	28.1	3.8
sp Q8Y003.1 RGMG_RALSO	RecName: Full=Putative ribose/galactos...	26.9	8.2

ALIGNMENTS

>sp|B1ZGG2.1|MNMG_METPB RecName: Full=tRNA uridine 5-carboxymethylaminomethyl modification
enzyme MnmG; AltName: Full=Glucose-inhibited division
protein A
Length=624

Score = 28.1 bits (61), Expect = 3.8, Method: Compositional matrix adjust.
Identities = 16/40 (40%), Positives = 24/40 (60%), Gaps = 3/40 (8%)
Frame = +1

```
Query   7      TERIPDRVQEN---TPVRRSGLSPSGPR*VQT*LAKVVRF   117
      T+R+ D ++EN   +P+   G+S  GPR   +   KVVRF
Sbjct  248  TQRVHDLIRENLHRSPMYSGGISSRGPRYCPSIEDKVVRF   287
```

>sp|Q8Y003.1|RGMG_RALSO RecName: Full=Putative ribose/galactose/methyl galactoside import
ATP-binding protein
Length=518

Score = 26.9 bits (58), Expect = 8.2, Method: Compositional matrix adjust.
Identities = 11/29 (38%), Positives = 16/29 (55%), Gaps = 0/29 (0%)
Frame = -1

```
Query   106  PWQVMSELIWVRDSTRTCGQAYSPELCR   20
      P+  ++E IW+RR+   CG      EL R
Sbjct  116  PYMTVAENIWIWIRREPRNRCGLVDHAELRR   144
```

Query= 61

Length=116

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp P16084.1 BGLS_BUTFI	RecName: Full=Beta-glucosidase A; AltN...	28.1	3.0
------------------------	---	------	-----

ALIGNMENTS

>sp|P16084.1|BGLS_BUTFI RecName: Full=Beta-glucosidase A; AltName: Full=Beta-D-glucoside
glucohydrolase; AltName: Full=Cellobiase; AltName: Full=Gentiobiase
Length=830

Score = 28.1 bits (61), Expect = 3.0, Method: Composition-based stats.
 Identities = 14/30 (47%), Positives = 16/30 (53%), Gaps = 0/30 (0%)
 Frame = -3

```
Query 102 QCKCRLMSWSGGTQPGPADRRILLNSVGDS 13
          Q LM+W GG + G A RILL V S
Sbjct 227 QISSVLMAWQGGIEGGLAAARILLGKVNPS 256
```

Query= 62

Length=112

Sequences producing significant alignments:	Score (Bits)	E Value
sp P49327.3 FAS_HUMAN RecName: Full=Fatty acid synthase; Incl...	28.9	1.8
sp O27121.1 PGK_METTH RecName: Full=Phosphoglycerate kinase	27.7	3.7

ALIGNMENTS

```
>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
Full=[Acyl-carrier-protein]
S-acetyltransferase; Includes: RecName:
Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein]
hydrolase
Length=2511
```

Score = 28.9 bits (63), Expect = 1.8, Method: Compositional matrix adjust.
 Identities = 14/34 (41%), Positives = 22/34 (65%), Gaps = 1/34 (3%)
 Frame = -3

```
Query 110 FTLQGPSAVRDVILNRWLRSIWYGPAHHLSGIRS 9
          +TLQ + V DV+++RWLR G H+SG+ +
Sbjct 1067 YTLQDKAQVADVVSRLRVTVAG-GVHISGLHT 1099
```

```
>sp|O27121.1|PGK_METTH RecName: Full=Phosphoglycerate kinase
Length=411
```

Score = 27.7 bits (60), Expect = 3.7, Method: Compositional matrix adjust.
 Identities = 13/30 (43%), Positives = 18/30 (60%), Gaps = 4/30 (13%)
 Frame = -2

```
Query 78 RDPKQMASIHLVRPSPPL----VGDSFSPA 1
          RDP++ A HLVR PL + D+F+ A
Sbjct 134 RDPEEQAETHLVRKLAPLLDYFINDAFAAA 163
```

Query= 63

Length=136

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q0RRP6.1 RS13_FRAAA RecName: Full=30S ribosomal protein S13	26.2	9.1

ALIGNMENTS

>sp|Q0RRP6.1|RS13_FRAAA RecName: Full=30S ribosomal protein S13
Length=126

Score = 26.2 bits (56), Expect = 9.1, Method: Compositional matrix adjust.
Identities = 13/40 (33%), Positives = 20/40 (50%), Gaps = 0/40 (0%)
Frame = +1

Query	7	GLGRTRWIEAICRSGTRANTGSTPCCSWKIRLLTEWVGSN	126
		G+GRTR E + +G +T +I L EW+ +N	
Sbjct	24	GIGRTRSRET LAATGVNPDTRVRDLSEDEIVRLREWIDAN	63

Query= 64

Length=131

Sequences producing significant alignments:	Score (Bits)	E Value
sp A6X1X9.1 PLSX_OCHA4 RecName: Full=Phosphate acyltransferas...	27.7	4.5
sp A5VPV7.1 PLSX_BRUO2 RecName: Full=Phosphate acyltransferas...	27.3	5.5
sp Q57DX5.1 PLSX_BRUAB RecName: Full=Phosphate acyltransferas...	27.3	5.5
sp Q8YGH8.1 PLSX_BRUME RecName: Full=Phosphate acyltransferas...	27.3	5.5
sp Q8G1E1.1 PLSX_BRUSU RecName: Full=Phosphate acyltransferas...	27.3	5.5

ALIGNMENTS

>sp|A6X1X9.1|PLSX_OCHA4 RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
Length=352

Score = 27.7 bits (60), Expect = 4.5, Method: Composition-based stats.
Identities = 14/29 (48%), Positives = 18/29 (62%), Gaps = 0/29 (0%)
Frame = -1

Query	116	NPDLRTGVFS*TQGVEPV LARVPERQMAS	30
		+PD+R F VEPVLAR P+ + AS	
Sbjct	29	HPDIRFIFFG LPAQVEPV LARYPKLKAAS	57

>sp|A5VPV7.1|PLSX_BRUO2 RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
Length=346

Score = 27.3 bits (59), Expect = 5.5, Method: Composition-based stats.
Identities = 14/29 (48%), Positives = 18/29 (62%), Gaps = 0/29 (0%)
Frame = -1

```
Query 116 NPDRLRTGVFS*TQGVEPVRLARVPERQMAS 30
          +PD+R F VEPVLAR P+ + AS
Sbjct 29 HPDIRFIFFGLPAQVEPVRLARYPKLKEAS 57
```

```
>sp|Q57DX5.1|PLSX_BRUAB RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
sp|Q2YNC0.1|PLSX_BRUA2 RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
sp|A9MAF5.1|PLSX_BRUC2 RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
sp|B0CLA1.1|PLSX_BRUSI RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
sp|B2S523.1|PLSX_BRUA1 RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
Length=346
```

Score = 27.3 bits (59), Expect = 5.5, Method: Composition-based stats.
Identities = 14/29 (48%), Positives = 18/29 (62%), Gaps = 0/29 (0%)
Frame = -1

```
Query 116 NPDRLRTGVFS*TQGVEPVRLARVPERQMAS 30
          +PD+R F VEPVLAR P+ + AS
Sbjct 29 HPDIRFIFFGLPAQVEPVRLARYPKLKEAS 57
```

```
>sp|Q8YGH8.1|PLSX_BRUME RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
sp|C0RIB2.1|PLSX_BRUMB RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
Length=346
```

Score = 27.3 bits (59), Expect = 5.5, Method: Composition-based stats.
Identities = 14/29 (48%), Positives = 18/29 (62%), Gaps = 0/29 (0%)
Frame = -1

```
Query 116 NPDRLRTGVFS*TQGVEPVRLARVPERQMAS 30
          +PD+R F VEPVLAR P+ + AS
Sbjct 29 HPDIRFIFFGLPAQVEPVRLARYPKLKEAS 57
```

```
>sp|Q8G1E1.1|PLSX_BRUSU RecName: Full=Phosphate acyltransferase; AltName:
Full=Acyl-ACP
phosphotransacylase; AltName: Full=Acyl-[acyl-carrier-protein]--phosphate
acyltransferase; AltName: Full=Phosphate-acyl-ACP
acyltransferase
Length=346
```

```
Score = 27.3 bits (59), Expect = 5.5, Method: Composition-based stats.
Identities = 14/29 (48%), Positives = 18/29 (62%), Gaps = 0/29 (0%)
Frame = -1
```

```
Query 116 NPDRLRTGVFS*TQGVEPVLLARVPERQMAS 30
          +PD+R F VEPVLAR P+ + AS
Sbjct 29 HPDIRFIFGLPAQVEPVLLARYPKLKEAS 57
```

Query= 65

Length=126

Sequences producing significant alignments:	Score (Bits)	E Value
sp P78605.1 OTC_TRAHI RecName: Full=Ornithine carbamoyltransf...	28.1	3.6
sp Q4R5T4.1 RNF32_MACFA RecName: Full=RING finger protein 32	26.9	7.3

ALIGNMENTS

```
>sp|P78605.1|OTC_TRAHI RecName: Full=Ornithine carbamoyltransferase,
mitochondrial;
AltName: Full=Ornithine transcarbamylase; Short=OTCase; Flags:
Precursor
Length=375
```

```
Score = 28.1 bits (61), Expect = 3.6, Method: Composition-based stats.
Identities = 14/29 (48%), Positives = 16/29 (55%), Gaps = 5/29 (17%)
Frame = +1
```

```
Query 31 EAICRSGTRANTGSTPSDKFRHNLPRSFD 117
          EA+CR G G+ P KF H LPR D
Sbjct 301 EALCREG-----GANPDWKFMHCLPRKQD 324
```

```
>sp|Q4R5T4.1|RNF32_MACFA RecName: Full=RING finger protein 32
Length=362
```

```
Score = 26.9 bits (58), Expect = 7.3, Method: Composition-based stats.
Identities = 12/17 (71%), Positives = 14/17 (82%), Gaps = 0/17 (0%)
Frame = +2
```

```
Query 44 AQELGLIRVRPPQISSD 94
          AQ+LGLI PPQ+SSD
Sbjct 92 AQKLGLIGPPPPQLSSD 108
```

Query= 66

Length=144

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp Q0V6M5.1 LCPS_PHANO RecName: Full=Bifunctional lycopene cy...	27.3	6.8
--	------	-----

ALIGNMENTS

>sp|Q0V6M5.1|LCPS_PHANO RecName: Full=Bifunctional lycopene cyclase/phytoene synthase;

Includes: RecName: Full=Lycopene beta-cyclase; AltName: Full=Lycopene cyclase; Includes: RecName: Full=Phytoene synthase

Length=585

Score = 27.3 bits (59), Expect = 6.8, Method: Compositional matrix adjust.
Identities = 18/44 (41%), Positives = 23/44 (52%), Gaps = 3/44 (7%)
Frame = +3

Query	6	WAGPYQMDRSHLL*LEDSAVNRMGRFESYGEFRITSLTAEGP*R	137
		W PY+ DR+ L L+D AV R+ R F + S T GP R	
Sbjct	272	WVSPYKYDRARLAGLQD-AVLRLKR--KSRSFYLASATFPGPLR	312

Query= 67

Length=122

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp P45694.2 TKT_BACSU RecName: Full=Transketolase; Short=TK	28.5	2.8
---	------	-----

ALIGNMENTS

>sp|P45694.2|TKT_BACSU RecName: Full=Transketolase; Short=TK

Length=667

Score = 28.5 bits (62), Expect = 2.8, Method: Composition-based stats.
Identities = 13/36 (36%), Positives = 22/36 (61%), Gaps = 1/36 (3%)
Frame = -1

Query	113	FVQSSLAVGFE-PTHSVNSRIFQLQQMASIHLVRPS	9
		F S+AVG + PTH ++ L+ M ++ L+RP+	
Sbjct	459	FTHDSIavgEDGPTHEPVEQLASLRAMPNLSLIRPA	494

Query= 68

Length=136

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp Q47N76.1 SYFB_THEFY RecName: Full=Phenylalanine--tRNA liga...	28.5	2.9
--	------	-----

ALIGNMENTS

>sp|Q47N76.1|SYFB_THEFY RecName: Full=Phenylalanine--tRNA ligase beta subunit;
AltName:

Full=Phenylalanyl-tRNA synthetase beta subunit; Short=PheRS

Length=831

Score = 28.5 bits (62), Expect = 2.9, Method: Composition-based stats.
Identities = 15/33 (45%), Positives = 20/33 (61%), Gaps = 1/33 (3%)
Frame = +1

Query 34 AICCSWKIRLLTEWVGSNPTAKLMRRHLH-CGV 129
AIC + +R +T + + PT MRR LH CGV
Sbjct 220 AICSRVLRGVTGFDPAAPTPLWMRRRLHLCGV 252

Query= 69

Length=126

	Score	E
Sequences producing significant alignments:	(Bits)	Value
sp P49327.3 FAS_HUMAN RecName: Full=Fatty acid synthase; Incl...	29.6	1.2

ALIGNMENTS

>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
Full=[Acyl-carrier-protein]
S-acetyltransferase; Includes: RecName:
Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein]
hydrolase
Length=2511

Score = 29.6 bits (65), Expect = 1.2, Method: Compositional matrix adjust.
Identities = 12/30 (40%), Positives = 19/30 (63%), Gaps = 0/30 (0%)
Frame = -3

Query 94 ERRFTLQGPSAVRDVILNRWLRSIWYGAH 5
++ +TLQ + V DV+++RWLR G H
Sbjct 1064 QKLYTLQDKAQVADVVSRLRVTVAGGVH 1093

Query= 70

Length=144

	Score	E
Sequences producing significant alignments:	(Bits)	Value
sp P49327.3 FAS_HUMAN RecName: Full=Fatty acid synthase; Incl...	28.9	2.6

ALIGNMENTS

>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
Full=[Acyl-carrier-protein]
S-acetyltransferase; Includes: RecName:
Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein]

Query= 71

Length=139

	Score	E
Sequences producing significant alignments:	(Bits)	Value
sp P49327.3 FAS_HUMAN RecName: Full=Fatty acid synthase; Incl...	28.5	2.9
sp B3PIT8.1 MNMG_CELJU RecName: Full=tRNA uridine 5-carboxyme...	27.3	6.7

ALIGNMENTS

```
>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
Full=[Acyl-carrier-protein]
S-acetyltransferase; Includes: RecName:
Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
reductase; Includes: RecName: Full=Oleoyle-[acyl-carrier-protein]
hydrolase
Length=2511
```

Score = 28.5 bits (62), Expect = 2.9, Method: Compositional matrix adjust.
 Identities = 12/27 (44%), Positives = 17/27 (63%), Gaps = 0/27 (0%)
 Frame = -1

```
Query 85 FTLQGPSAVRDVILNRWLR SIWYGPAH 5
      +TLQ + V DV+++RWLR G H
Sbjct 1067 YTLQDKAQVADV VVSRWLRVTVAGGVH 1093
```

```
>sp|B3PIT8.1|MNMG_CELJU RecName: Full=tRNA uridine 5-carboxymethylaminomethyl
modification
enzyme MnmG; AltName: Full=Glucose-inhibited division
protein A
Length=638
```

Score = 27.3 bits (59), Expect = 6.7, Method: Composition-based stats.
 Identities = 12/20 (60%), Positives = 15/20 (75%), Gaps = 0/20 (0%)
 Frame = +2

```
Query 71 SLKGEPSSGEYAC PQVRVES 130
      SLKGEP +GE A QV +E+
Sbjct 525 SLKGEP LAGEAAA EQVEIEA 544
```

Query= 72

Length=134

	Score	E
Sequences producing significant alignments:	(Bits)	Value
sp P49327.3 FAS_HUMAN RecName: Full=Fatty acid synthase; Incl...	29.3	1.8

ALIGNMENTS

```
>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
Full=[Acyl-carrier-protein]
S-acetyltransferase; Includes: RecName:
Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:
```

RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
 Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
 dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
 reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein]
 hydrolase
 Length=2511

Score = 29.3 bits (64), Expect = 1.8, Method: Compositional matrix adjust.
 Identities = 12/27 (44%), Positives = 17/27 (63%), Gaps = 0/27 (0%)
 Frame = -2

Query 85 FTLQGSAVRDVILNRWLR SIWYGPAH 5
 +TLQ + V DV+++RWLR G H
 Sbjct 1067 YTLQDKAQVADV VVSRWLRVTVAGGVH 1093

Query= 73

Length=112

		Score	E
		(Bits)	Value
Sequences producing significant alignments:			
sp P49327.3 FAS_HUMAN	RecName: Full=Fatty acid synthase; Incl...	28.5	2.5

ALIGNMENTS

>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
 Full=[Acyl-carrier-protein]
 S-acetyltransferase; Includes: RecName:
 Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
 RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:
 RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
 Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
 dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
 reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein]
 hydrolase
 Length=2511

Score = 28.5 bits (62), Expect = 2.5, Method: Compositional matrix adjust.
 Identities = 12/27 (44%), Positives = 17/27 (63%), Gaps = 0/27 (0%)
 Frame = -1

Query 85 FTLQGSAVRDVILNRWLR SIWYGPAH 5
 +TLQ + V DV+++RWLR G H
 Sbjct 1067 YTLQDKAQVADV VVSRWLRVTVAGGVH 1093

Query= 74

Length=126

		Score	E
		(Bits)	Value
Sequences producing significant alignments:			
sp P49327.3 FAS_HUMAN	RecName: Full=Fatty acid synthase; Incl...	28.9	2.4

ALIGNMENTS

>sp|P49327.3|FAS_HUMAN RecName: Full=Fatty acid synthase; Includes: RecName:
 Full=[Acyl-carrier-protein]
 S-acetyltransferase; Includes: RecName:
 Full=[Acyl-carrier-protein] S-malonyltransferase; Includes:
 RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; Includes:

RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase;
 Includes: RecName: Full=3-hydroxyacyl-[acyl-carrier-protein]
 dehydratase; Includes: RecName: Full=Enoyl-[acyl-carrier-protein]
 reductase; Includes: RecName: Full=Oleoyl-[acyl-carrier-protein]
 hydrolase
 Length=2511

Score = 28.9 bits (63), Expect = 2.4, Method: Compositional matrix adjust.
 Identities = 12/27 (44%), Positives = 17/27 (63%), Gaps = 0/27 (0%)
 Frame = -3

Query 85 FTLQGPSAVRDVILNRWLRSIWYGPAH 5
 +TLQ + V DV+++RWLR G H
 Sbjct 1067 YTLQDKAQVADVVSRLRVTVAGGVH 1093

Query= 75

Length=139

Sequences producing significant alignments:			Score	E
			(Bits)	Value
sp Q9BI06.1 R27A1_ENTHI	RecName: Full=60S ribosomal protein L...		31.2	0.17
sp Q9BH80.1 R27A2_ENTHI	RecName: Full=60S ribosomal protein L...		30.8	0.27
sp Q9BI14.1 R27A3_ENTHI	RecName: Full=60S ribosomal protein L...		30.0	0.55
sp Q8Y003.1 RGMG_RALSO	RecName: Full=Putative ribose/galactos...		26.9	8.2

ALIGNMENTS

>sp|Q9BI06.1|R27A1_ENTHI RecName: Full=60S ribosomal protein L27a-1
 Length=149

Score = 31.2 bits (69), Expect = 0.17, Method: Composition-based stats.
 Identities = 13/41 (32%), Positives = 23/41 (56%), Gaps = 0/41 (0%)
 Frame = +3

Query 12 GPYQMDRSHLSSGEYACPQVRVESLRTQISSDITCQGRSIR 134
 G + M HL + +Y CP + V+SL + + DI Q ++ +
 Sbjct 54 GKHGMRVFHLKANKYYCPSINVDSLWLVGKDIQAQYKNAK 94

>sp|Q9BH80.1|R27A2_ENTHI RecName: Full=60S ribosomal protein L27a-2/4
 Length=149

Score = 30.8 bits (68), Expect = 0.27, Method: Composition-based stats.
 Identities = 12/41 (29%), Positives = 23/41 (56%), Gaps = 0/41 (0%)
 Frame = +3

Query 12 GPYQMDRSHLSSGEYACPQVRVESLRTQISSDITCQGRSIR 134
 G + M HL + +Y CP + V+SL + + D+ Q ++ +
 Sbjct 54 GKHGMRVFHLKANKYYCPSINVDSLWLVGKDVQAQYKNAK 94

>sp|Q9BI14.1|R27A3_ENTHI RecName: Full=60S ribosomal protein L27a-3
 Length=149

Score = 30.0 bits (66), Expect = 0.55, Method: Composition-based stats.
 Identities = 12/42 (29%), Positives = 24/42 (57%), Gaps = 0/42 (0%)
 Frame = +3

Query 12 GPYQMDRSHLSSGEYACPQVRVESLRTQISSDITCQGRSIRS 137
 G + M HL + +Y CP + V+SL + + D+ Q ++ ++

Sbjct 54 GKHGMRVFHLKANKYYCPSINVDSLWSLVGKDVQEYKNAKT 95

>sp|Q8Y003.1|RGMG_RALSO RecName: Full=Putative ribose/galactose/methyl
galactoside import
ATP-binding protein
Length=518

Score = 26.9 bits (58), Expect = 8.2, Method: Compositional matrix adjust.
Identities = 11/28 (39%), Positives = 16/28 (57%), Gaps = 0/28 (0%)
Frame = -1

Query 121 PWQVMSELIWVRDSTRTCGQAYSPELR 38
P+ ++E IW+RR+ CG ELR
Sbjct 116 PYMTVAENIWIRREPRNRCGLVDHAELR 143

Query= 76

Length=131

Sequences producing significant alignments:	Score (Bits)	E Value
sp P16084.1 BGLS_BUTFI RecName: Full=Beta-glucosidase A; AltN...	28.1	3.9

ALIGNMENTS

>sp|P16084.1|BGLS_BUTFI RecName: Full=Beta-glucosidase A; AltName: Full=Beta-D-
glucoside
glucohydrolase; AltName: Full=Cellobiase; AltName: Full=Gentiobiase
Length=830

Score = 28.1 bits (61), Expect = 3.9, Method: Composition-based stats.
Identities = 16/38 (42%), Positives = 19/38 (50%), Gaps = 2/38 (5%)
Frame = -3

Query 117 QCKCRMSWSGGTQPGPADRRILLNSDGFDPSTGTAQPT 4
Q LM+W GG + G A RILL +PSG T
Sbjct 227 QISSVLMAWQGGIEGGLAAARILLGK--VNPSGKLSDT 262

Query= 77

Length=104

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp Q0V6M5.1 LCPS_PHANO RecName: Full=Bifunctional lycopene cy...	26.9	7.7
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ALIGNMENTS

>sp|Q0V6M5.1|LCPS_PHANO RecName: Full=Bifunctional lycopene cyclase/phytoene synthase;

Includes: RecName: Full=Lycopene beta-cyclase; AltName: Full=Lycopene cyclase; Includes: RecName: Full=Phytoene synthase
Length=585

Score = 26.9 bits (58), Expect = 7.7, Method: Compositional matrix adjust.
Identities = 9/18 (50%), Positives = 13/18 (72%), Gaps = 0/18 (0%)
Frame = +3

Query	6	WAGPYQMDRSHLAGLNES	59
		W PY+ DR+ LAGL ++	
Sbjct	272	WVSPYKYDRARLAGLQDA	289

Query= 78

Length=117

	Score	E
Sequences producing significant alignments:	(Bits)	Value

sp Q0V6M5.1 LCPS_PHANO RecName: Full=Bifunctional lycopene cy...	28.5	2.1
sp P35341.1 L_SV41 RecName: Full=RNA-directed RNA polymerase ...	28.5	2.3

ALIGNMENTS

>sp|Q0V6M5.1|LCPS_PHANO RecName: Full=Bifunctional lycopene cyclase/phytoene synthase;

Includes: RecName: Full=Lycopene beta-cyclase; AltName: Full=Lycopene cyclase; Includes: RecName: Full=Phytoene synthase
Length=585

Score = 28.5 bits (62), Expect = 2.1, Method: Compositional matrix adjust.
Identities = 10/24 (42%), Positives = 15/24 (63%), Gaps = 0/24 (0%)
Frame = +3

Query	6	WAGPYQMDRSHLAGLNESPTFRR	77
		W PY+ DR+ LAGL ++ +R	
Sbjct	272	WVSPYKYDRARLAGLQDAVLR LKR	295

>sp|P35341.1|L_SV41 RecName: Full=RNA-directed RNA polymerase L; Short=Protein L;

AltName: Full=Large structural protein; AltName: Full=Replicase;
AltName: Full=Transcriptase; Includes: RecName: Full=RNA-directed RNA polymerase; Includes: RecName: Full=mRNA (guanine-N(7)-)-methyltransferase; Includes: RecName: Full=mRNA guanylyltransferase
Length=2269

Score = 28.5 bits (62), Expect = 2.3, Method: Composition-based stats.

Identities = 14/30 (47%), Positives = 19/30 (63%), Gaps = 1/30 (3%)
 Frame = -3

Query 100 PGPADDRILLNSVGD-SFSPARWLRSIWG 14
 P P +RR+LLN + D SF PA+ L + G
 Sbjct 509 PNPFNRRLLLLNFIEDPSFDPAKELEYVTSG 538

Query= 79

Length=104

	Score	E
Sequences producing significant alignments:	(Bits)	Value
sp Q0V6M5.1 LCPS_PHANO RecName: Full=Bifunctional lycopene cy...	26.6	9.1

ALIGNMENTS

>sp|Q0V6M5.1|LCPS_PHANO RecName: Full=Bifunctional lycopene cyclase/phytoene synthase;
 Includes: RecName: Full=Lycopene beta-cyclase; AltName: Full=Lycopene cyclase; Includes: RecName: Full=Phytoene synthase
 Length=585

Score = 26.6 bits (57), Expect = 9.1, Method: Composition-based stats.
 Identities = 9/18 (50%), Positives = 13/18 (72%), Gaps = 0/18 (0%)
 Frame = +3

Query 6 WAGPYQMDRSHLAGLNES 59
 W PY+ DR+ LAGL ++
 Sbjct 272 WVSPYKYDRARLAGLQDA 289

Query= 80

Length=126

	Score	E
Sequences producing significant alignments:	(Bits)	Value
sp Q6XQH7.2 L_OLVVA RecName: Full=RNA-directed RNA polymerase...	30.8	0.56

ALIGNMENTS

>sp|Q6XQH7.2|L_OLVVA RecName: Full=RNA-directed RNA polymerase L; Short=Protein L;
 AltName: Full=Large structural protein; AltName: Full=Replicase;
 AltName: Full=Transcriptase
 Length=2234

Score = 30.8 bits (68), Expect = 0.56, Method: Composition-based stats.
 Identities = 15/34 (44%), Positives = 20/34 (59%), Gaps = 0/34 (0%)
 Frame = -1

Query 126 AERIERPWQVMSELICSGHSAVQVSSHELDGFDP 25
 AE ER ++ SE +C V+VS HE+ FDP
 Sbjct 951 AELQERLSELWSEFMCMKIITVEVSLHEIKDFDP 984

Query= 81

Length=136

	Score (Bits)	E Value
Sequences producing significant alignments:		

sp Q29293.1 RL3_PIG RecName: Full=60S ribosomal protein L3	26.6	8.4
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ALIGNMENTS

>sp|Q29293.1|RL3_PIG RecName: Full=60S ribosomal protein L3
Length=130

Score = 26.6 bits (57), Expect = 8.4, Method: Compositional matrix adjust.
Identities = 10/19 (53%), Positives = 13/19 (68%), Gaps = 0/19 (0%)
Frame = +2

Query	47	LED	SAVN	RMGR	FESY	GEVV	103
		L	D	++N	+GRF	YGEV	
Sbjct	106	LSD	KSIN	PLGR	FVHY	GEVT	124

Query= 82

Length=138

	Score (Bits)	E Value
Sequences producing significant alignments:		

sp B3PIT8.1 MNMG_CELJU RecName: Full=tRNA uridine 5-carboxyme...	27.3	6.7
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ALIGNMENTS

>sp|B3PIT8.1|MNMG_CELJU
RecName: Full=tRNA uridine 5-carboxymethylaminomethyl modification
enzyme MnmG; AltName: Full=Glucose-inhibited division
protein A
Length=638

Score = 27.3 bits (59), Expect = 6.7, Method: Composition-based stats.
Identities = 12/20 (60%), Positives = 15/20 (75%), Gaps = 0/20 (0%)
Frame = +1

Query	70	SLK	GEP	SSGE	YACP	QVR	VES	129
		SLK	GEP	+GE	A	QV	+E+	
Sbjct	525	SLK	GEP	PLAGE	AAAAE	QVE	IEA	544

Query= 83

Length=130

	Score (Bits)	E Value
Sequences producing significant alignments:		

sp Q1AW66.1 PYRH_RUBXD RecName: Full=Uridylate kinase; Short=...	27.3	4.7
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ALIGNMENTS

>sp|Q1AW66.1|PYRH_RUBXD RecName: Full=Uridylate kinase; Short=UK; AltName: Full=Uridine monophosphate kinase; Short=UMP kinase; Short=UMPK
Length=255

Score = 27.3 bits (59), Expect = 4.7, Method: Composition-based stats.
Identities = 16/37 (43%), Positives = 20/37 (54%), Gaps = 3/37 (8%)
Frame = +3

Query 27 GVTARVQENT---PVRRSGLSPSGPPLRNSG*YGFDP 128
G +AR E + P+RR L SG L +G YG DP
Sbjct 2 GESARAAETSELGPLRRVVLKLSGESLAGNGGYGIDP 38

Query= 84

Length=116

Sequences producing significant alignments:	Score (Bits)	E Value
sp A4FPQ7.1 RL10_SACEN RecName: Full=50S ribosomal protein L10	27.7	3.2

ALIGNMENTS

>sp|A4FPQ7.1|RL10_SACEN RecName: Full=50S ribosomal protein L10
Length=177

Score = 27.7 bits (60), Expect = 3.2, Method: Composition-based stats.
Identities = 16/34 (47%), Positives = 21/34 (62%), Gaps = 1/34 (3%)
Frame = +3

Query 6 MRRHLHCGVTARVQENTPVRRSGLSPSGPAGLNE 107
+RR L G T RV +NT V+R+ SG GL+E
Sbjct 39 LRRALGEGTTYRVAKNTLVKRAA-EQSGVEGLDE 71

Query= 85

Length=103

Sequences producing significant alignments:	Score (Bits)	E Value
sp Q1R0H5.1 RL3_CHRSD RecName: Full=50S ribosomal protein L3	26.6	5.9
sp B4SKW3.1 RL3_STRM5 RecName: Full=50S ribosomal protein L3 ...	26.6	6.9

ALIGNMENTS

>sp|Q1R0H5.1|RL3_CHRSD RecName: Full=50S ribosomal protein L3
Length=212

Score = 26.6 bits (57), Expect = 5.9, Method: Compositional matrix adjust.
Identities = 10/22 (45%), Positives = 18/22 (82%), Gaps = 0/22 (0%)
Frame = -3

Query 74 PERLSGIRSVQPSGHSVAVQVSS 9
P R++ +++V+ G+SAVQV+S
Sbjct 32 PNRVTRVKTVESDGYSVAVQVTS 53

>sp|B4SKW3.1|RL3_STRM5 RecName: Full=50S ribosomal protein L3
 sp|B2FQ45.1|RL3_STRMK RecName: Full=50S ribosomal protein L3
 Length=216

Score = 26.6 bits (57), Expect = 6.9, Method: Compositional matrix adjust.
 Identities = 10/22 (45%), Positives = 17/22 (77%), Gaps = 0/22 (0%)
 Frame = -3

Query 77 VPERLSGIRSVQPSGHSVQVS 12
 P R++ I++V+ G+SAVQV+
 Sbjct 35 TPNRIAQIKTVETDGYSVQVT 56

Query= 86

Length=104

Sequences producing significant alignments:	Score (Bits)	E Value
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sp Q5MI53.1 TRPA_LEPBP RecName: Full=Tryptophan synthase alph...	26.9	4.9
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ALIGNMENTS

>sp|Q5MI53.1|TRPA_LEPBP RecName: Full=Tryptophan synthase alpha chain
 sp|B0SDM7.1|TRPA_LEPBA RecName: Full=Tryptophan synthase alpha chain
 Length=266

Score = 26.9 bits (58), Expect = 4.9, Method: Composition-based stats.
 Identities = 11/23 (48%), Positives = 13/23 (57%), Gaps = 0/23 (0%)
 Frame = +3

Query 21 HCGVTARLD*TNPRQVVGWAVPD 89
 HCG+T LD VVG +PD
 Sbjct 106 HCGITKFLDNAKDSGVVGLVIPD 128

Lambda	K	H
0.318	0.134	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 454086

Number of Hits to DB: 13772125358

Number of extensions: 328258447

Number of successful extensions: 452965

Number of sequences better than 10: 744

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 452955

Number of HSP's successfully gapped: 1292

Length of database: 169309753

T: 12

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (20.4 bits)

ka-blk-alpha gapped: 1.9

ka-blk-alpha ungapped: 0.7916

ka-blk-alpha_v gapped: 42.6028

ka-blk-alpha_v ungapped: 4.96466

ka-blk-sigma gapped: 43.6362