

BLASTP 2.10.0+

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.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

RID: SA820JPM014

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
234,979,574 sequences; 84,697,594,569 total letters

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Query= ORF7

Length=376

Sequences producing significant alignments:	Score (Bits)	E Value	Max Ident
YP_009519162.1 hypothetical protein [Caulerpa verticillata]	335	3e-111	61%
YP_009472820.1 hypothetical protein [Caulerpa manorensis]	259	1e-80	42%
YP_009519448.1 hypothetical protein [Rhipiliopsis peltata]	206	1e-59	56%
AYC64487.1 hypothetical protein [Pseudochlorodesmis sp. HV01306c]	197	9e-58	54%
AOP19087.1 hypothetical protein [Halimeda discoidea]	184	2e-53	58%
YP_009306362.1 hypothetical protein [Caulerpa cliftonii]	106	4e-21	31%
YP_009519140.1 hypothetical protein [Caulerpa verticillata]	97.4	8e-21	48%
ARR28454.1 hypothetical protein [Caulerpa okamurae]	89.7	2e-17	34%
AYC64090.1 hypothetical protein [Johnson-sea-linkia profunda]	89.7	1e-15	27%
AOP19034.1 hypothetical protein [Halimeda discoidea]	89.4	2e-15	34%
YP_009472588.1 hypothetical protein [Rhipilia penicilloides]	88.6	4e-15	28%
YP_009130586.1 putative DNA primase [Tydemania expeditionis]	86.7	7e-15	29%
YP_009326773.1 hypothetical protein [Caulerpa racemosa]	86.3	2e-14	28%
YP_009472859.1 hypothetical protein [Caulerpa manorensis]	85.5	4e-14	28%
YP_009518867.1 hypothetical protein [Boodleopsis pusilla]	83.2	2e-13	31%
WP_106459521.1 DUF3854 domain-containing protein [Aphanothece ...]	74.3	2e-10	30%
OQX20052.1 hypothetical protein BWK76_02530 [Desulfobulbaceae ...]	73.2	4e-10	29%
WP_106459359.1 DUF3854 domain-containing protein [Aphanothece ...]	72.0	1e-09	29%
WP_106872064.1 MULTISPECIES: hypothetical protein [unclassified ...]	60.5	5e-06	28%
WP_048670661.1 toprim domain-containing protein [Candidatus Co ...]	57.4	5e-05	29%
WP_117948860.1 hypothetical protein [Faecalibacterium prausnit ...]	56.6	8e-05	27%
ASC70311.1 hypothetical protein XM38_012480 [Halomicronema hon ...]	55.1	2e-04	27%
WP_137455024.1 hypothetical protein [Halomicronema hongdechloris]	55.1	3e-04	27%
WP_005329991.1 phage/plasmid primase P4 family domain [Coryneb ...]	53.9	5e-04	24%
WP_080099994.1 hypothetical protein [Vibrio cholerae]	53.9	6e-04	26%
EKY32300.1 hypothetical protein OSU_2061 [Vibrio cholerae PS15]	53.5	8e-04	26%
WP_015537438.1 phage/plasmid primase, P4 family, C-terminal do ...]	52.8	0.001	25%
WP_097783161.1 hypothetical protein [Faecalibacterium prausnit ...]	52.4	0.002	25%
CVI73287.1 hypothetical protein NDGK_02952 [Clostridiales bact ...]	51.2	0.002	25%
HBJ06247.1 TPA: hypothetical protein [Erysipelotrichaceae bact ...]	50.8	0.004	29%

TAD79303.1	hypothetical protein EA001_04585 [Oscillatoriales c...	51.2	0.004	27%
YP_009519502.1	hypothetical protein [Rhipiliopsis peltata]	47.4	0.005	33%
PXX83167.1	hypothetical protein DLY76_13175 [Staphylococcus wa...	50.8	0.005	27%
WP_089826771.1	DNA primase [Clostridiales bacterium CHKCI001]	50.1	0.006	26%
WP_122135129.1	hypothetical protein [Staphylococcus warneri]	50.4	0.006	27%
WP_058709749.1	hypothetical protein [Staphylococcus warneri]	50.4	0.007	27%
WP_117726019.1	hypothetical protein [Staphylococcus warneri]	50.4	0.007	27%
WP_099533992.1	DUF3854 domain-containing protein [Limnothrix s...	50.4	0.008	25%
WP_122135133.1	hypothetical protein [Staphylococcus warneri]	50.4	0.008	27%
OCQ94853.1	hypothetical protein BCR12_14730 [Limnothrix sp. P1...	50.4	0.008	25%
YP_009519361.1	hypothetical protein [Pseudocodium devriesii]	48.5	0.009	32%
WP_051669969.1	hypothetical protein [Methylomonas sp. LW13]	49.7	0.011	27%
WP_050044965.1	DUF3854 domain-containing protein [Tolypothrix ...	49.7	0.014	25%
BAY87916.1	primase P4 [Calothrix parasitica NIES-267]	49.7	0.015	24%
WP_087545683.1	hypothetical protein [Nostocales cyanobacterium...	49.3	0.015	27%
WP_096661640.1	DUF3854 domain-containing protein [Calothrix pa...	49.7	0.016	24%
WP_134356385.1	toprim domain-containing protein [Nitrosococcus...	48.9	0.021	26%
WP_114735354.1	hypothetical protein [Vibrio cholerae]	48.9	0.025	24%
WP_148519512.1	hypothetical protein [Vibrio cholerae]	48.5	0.029	24%
WP_082755228.1	hypothetical protein [Bradyrhizobium diazoeffic...	48.5	0.032	27%
YP_009519210.1	hypothetical protein [Caulerpa verticillata]	48.1	0.036	36%
AL050062.1	E1 protein [Deltapapillomavirus 5]	47.8	0.046	29%
WP_081712488.1	hypothetical protein [Gordonia amicalis]	47.4	0.060	30%
WP_076343410.1	hypothetical protein [Paludisphaera borealis]	47.4	0.079	26%
WP_143052189.1	hypothetical protein [Halobacterium jilantaiense]	47.0	0.090	26%
BBD63650.1	hypothetical protein NIES2109_65250 [Nostoc sp. HK-01]	47.0	0.10	27%
YP_009519427.1	hypothetical protein [Rhipiliopsis peltata]	46.2	0.12	38%
WP_015014502.1	phage/plasmid primase [Acidovorax sp. KKS102]	45.4	0.27	27%
WP_069652414.1	toprim domain-containing protein [Aeromonas cav...	45.4	0.28	26%
TMQ25139.1	NTP-binding protein [Deltaproteobacteria bacterium]	45.1	0.32	27%
WP_099869324.1	NTP-binding protein [Mycobacterium heckeshornense]	44.7	0.44	27%
WP_071700079.1	hypothetical protein [Mycobacterium heckeshorne...	44.7	0.49	27%
WP_055185464.1	hypothetical protein [Faecalibacterium prausnit...	43.9	0.79	27%
WP_117554111.1	hypothetical protein [Faecalibacterium prausnit...	43.9	0.81	27%
WP_120020883.1	hypothetical protein [Faecalibacterium sp. AF10...	43.9	0.85	23%
WP_080793152.1	hypothetical protein [Corynebacterium sp. Marse...	43.5	0.93	21%
AVP41438.1	DNA primase [Streptomyces phage Yara]	43.9	0.95	28%
WP_146372635.1	DUF3854 domain-containing protein [Planctomycet...	43.5	1.0	25%
AXQ00533.1	E1 protein [Okapia johnstoni papillomavirus 1]	43.5	1.1	28%
WP_103918394.1	hypothetical protein [Thiotrichales bacterium H...	43.5	1.1	25%
WP_127066654.1	hypothetical protein [Cellulosilyticum sp. WCF-2]	43.1	1.1	25%
WP_025988927.1	hypothetical protein [Mycobacteroides abscessus]	43.5	1.2	27%
SHP30503.1	phage/plasmid primase, P4 family, C-terminal domain...	43.5	1.2	27%
WP_145718318.1	hypothetical protein [Mesorhizobium tianshanense]	43.5	1.2	30%
WP_074243874.1	unnamed protein product	43.5	1.2	27%
WP_052617223.1	hypothetical protein [Mycobacteroides abscessus]	43.5	1.2	26%
CPS32393.1	phage/plasmid primase%2C P4 family%2C C-terminal do...	43.5	1.3	27%
QEA05367.1	hypothetical protein KBTEX_01688 [uncultured organism]	43.1	1.3	25%
CPU37683.1	bacteriophage protein [Mycobacteroides abscessus]	43.5	1.3	27%
WP_052536874.1	hypothetical protein [Mycobacteroides abscessus]	43.5	1.3	27%
WP_074269985.1	hypothetical protein [Mycobacteroides abscessus]	43.1	1.4	27%
WP_100451585.1	hypothetical protein [Mycobacteroides abscessus]	43.1	1.4	27%
WP_100460742.1	hypothetical protein [Mycobacteroides abscessus]	43.1	1.5	24%
WP_119570835.1	hypothetical protein [Mycobacteroides abscessus]	43.1	1.5	27%
OGS01264.1	hypothetical protein A3G41_05925 [Elusimicrobia bac...	43.1	1.6	21%
SHP11590.1	phage/plasmid primase [Mycobacteroides abscessus su...	43.1	1.7	27%
YP_009508736.1	E1 protein [Giraffa camelopardalis papillomavir...	42.7	1.7	28%
SHP06125.1	bacteriophage protein [Mycobacteroides abscessus su...	42.4	2.6	24%
WP_144681351.1	hypothetical protein [Desulfohalobium alkaliphilus]	42.4	2.6	30%
WP_074232794.1	hypothetical protein [Mycobacteroides abscessus]	42.4	2.8	24%
WP_098923763.1	hypothetical protein [Faecalibacterium prausnit...	42.0	2.9	23%
SKI81432.1	bacteriophage protein [Mycobacteroides abscessus su...	42.4	3.0	24%
WP_064996905.1	hypothetical protein [Mycolicibacter heraklione...	42.0	3.6	26%
PKM60256.1	DNA primase [Firmicutes bacterium HGW-Firmicutes-4]	42.0	3.9	25%

WP_006347292.1 NTP-binding protein [Streptomyces tsukubensis]	41.2	4.8	25%
PZV21913.1 DNA primase [Snowella sp.]	41.6	5.1	28%
KUL51672.1 NTP-binding protein [Streptomyces sp. NRRL S-1521]	41.2	5.3	26%
KFG75654.1 hypothetical protein FM21_05885 [Streptomyces luteus]	41.2	5.4	26%
WP_107063888.1 NTP-binding protein [Streptomyces luteus]	41.2	5.6	26%
ALL29332.1 E1 [Bovine papillomavirus type 14]	41.2	5.7	29%

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Query= ORF8

Length=660

Sequences producing significant alignments:	Score (Bits)	E Value	Max Ident
YP_009326860.1 hypothetical protein [Caulerpa racemosa]	253	1e-74	43%
AY045732.1 hypothetical protein [Caulerpa cupressoides]	182	3e-49	40%
YP_009519211.1 hypothetical protein [Caulerpa verticillata]	176	4e-43	30%
YP_009519359.1 hypothetical protein [Pseudocodium devriesii]	152	3e-36	29%
YP_009519163.1 hypothetical protein [Caulerpa verticillata]	136	4e-34	62%
YP_009326773.1 hypothetical protein [Caulerpa racemosa]	151	4e-34	26%
YP_009519209.1 hypothetical protein [Caulerpa verticillata]	137	1e-33	52%
YP_009472855.1 hypothetical protein [Caulerpa manorensis]	147	5e-33	26%
AYC64085.1 hypothetical protein [Johnson-sea-linkia profunda]	145	6e-33	25%
WP_008287183.1 bifunctional 3'-5' exonuclease/DNA polymerase [...]	136	6e-30	26%
WP_121011606.1 bifunctional 3'-5' exonuclease/DNA polymerase [...]	132	1e-28	26%
WP_121922680.1 bifunctional 3'-5' exonuclease/DNA polymerase [...]	129	1e-27	30%
WP_028949995.1 bifunctional 3'-5' exonuclease/DNA polymerase [...]	128	2e-27	26%
EGS31161.1 DNA-directed DNA polymerase [Peptoniphilus sp. oral...]	126	3e-27	27%
WP_012673655.1 bifunctional 3'-5' exonuclease/DNA polymerase [...]	127	5e-27	26%
MAV17669.1 DNA polymerase I [Gammaproteobacteria bacterium]	127	1e-26	31%
WP_072469393.1 DNA polymerase I [Urinacoccus massiliensis]	125	6e-26	27%
WP_034440597.1 DNA polymerase I [Tissierellia bacterium S5-A11]	125	7e-26	27%
WP_097041874.1 DNA polymerase I [Terribacillus aidingensis]	125	1e-25	26%
WP_099208946.1 DNA polymerase I [Urinacoccus sp. Marseille-P3926]	124	1e-25	27%
WP_068868882.1 DNA polymerase I [Planococcus plakortidis]	124	1e-25	28%
AKE21663.1 DNA polymerase A family protein [Francisella tulare...]	118	2e-25	30%
WP_131748623.1 DNA polymerase I [Anaerococcus prevotii]	124	2e-25	27%
WP_095220162.1 DNA polymerase I [Terribacillus saccharophilus]	124	2e-25	26%
WP_095272594.1 DNA polymerase I [Terribacillus saccharophilus]	124	2e-25	26%
RUM46834.1 bifunctional 3'-5' exonuclease/DNA polymerase [Hydr...]	122	2e-25	26%
AYC64023.1 hypothetical protein [Halimeda micronesica]	112	2e-25	45%
WP_095232974.1 DNA polymerase I [Terribacillus saccharophilus]	123	2e-25	26%
WP_095260824.1 DNA polymerase I [Terribacillus saccharophilus]	123	3e-25	26%
WP_095226616.1 DNA polymerase I [Terribacillus saccharophilus]	123	3e-25	26%
WP_095222178.1 DNA polymerase I [Virgibacillus sp. 7505]	123	3e-25	26%
WP_077308099.1 DNA polymerase I [Terribacillus halophilus]	123	4e-25	26%
WP_142330819.1 DNA polymerase I [Bacillus thuringiensis]	122	4e-25	26%
WP_121300248.1 DNA polymerase I [Planococcus citreus]	122	5e-25	28%
WP_069718151.1 DNA polymerase I [Bacillus solimangrovi]	122	6e-25	26%
PFP11927.1 DNA polymerase I [Bacillus thuringiensis]	122	6e-25	26%
PMP76048.1 bifunctional 3'-5' exonuclease/DNA polymerase [Sulf...]	121	6e-25	24%
PFE06921.1 DNA polymerase I [Bacillus cereus]	121	1e-24	26%
OON59049.1 DNA polymerase I [Klebsiella pneumoniae]	118	1e-24	26%
WP_040955141.1 DNA polymerase I [Virgibacillus sp. SK37]	121	1e-24	24%
WP_141532717.1 DNA polymerase I [Bacillus cereus]	121	1e-24	26%
WP_093879404.1 DNA polymerase I [Terribacillus saccharophilus]	121	1e-24	25%
TKJ03686.1 DNA polymerase I [Bacillus cereus]	119	1e-24	26%
WP_141525460.1 DNA polymerase I [Bacillus cereus]	121	1e-24	26%
WP_140386899.1 MULTISPECIES: DNA polymerase I [Bacillus cereus...]	121	1e-24	26%
PFL69735.1 DNA polymerase I [Bacillus cereus]	121	1e-24	26%
PFB29359.1 DNA polymerase I [Bacillus cereus]	121	1e-24	26%

PMP60411.1	bifunctional 3'-5' exonuclease/DNA polymerase [Sulf...	120	2e-24	24%
WP_141558566.1	DNA polymerase I [Bacillus thuringiensis]	121	2e-24	26%
WP_142947063.1	DNA polymerase I [Bacillus cereus]	120	2e-24	26%
WP_141538298.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
PGW45597.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
AHA74189.1	DNA polymerase I [Bacillus thuringiensis YBT-1518]	120	2e-24	26%
WP_025117755.1	DNA polymerase I [Bacillus sp. H1m]	120	2e-24	26%
WP_140392562.1	DNA polymerase I [Bacillus cereus]	120	2e-24	26%
WP_080672436.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
WP_075716589.1	MULTISPECIES: DNA polymerase I [Bacillus cereus...	120	2e-24	26%
PEC73952.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
WP_022853929.1	DNA polymerase I [Thermodesulfatator atlanticus]	120	2e-24	28%
WP_053563570.1	MULTISPECIES: DNA polymerase I [Bacillus]	120	2e-24	26%
WP_063548740.1	MULTISPECIES: DNA polymerase I [Bacillus cereus...	120	2e-24	26%
TCL51840.1	DNA polymerase I [Thermolongibacillus altinsuensis]	120	2e-24	25%
WP_000412829.1	MULTISPECIES: DNA polymerase I [Bacillus]	120	2e-24	26%
WP_065229422.1	MULTISPECIES: DNA polymerase I [Bacillus cereus...	120	2e-24	26%
PEE64345.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
PES44316.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
PEF03997.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
WP_065485383.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
AVP46514.1	DNA polymerase I [Bacillus cereus]	120	2e-24	26%
WP_141505510.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
WP_142327068.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
PE001438.1	DNA polymerase I [Bacillus cereus]	120	2e-24	26%
WP_016512259.1	MULTISPECIES: DNA polymerase I [Bacillus]	120	2e-24	26%
WP_141484265.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
WP_078993673.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
WP_141550417.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
WP_113303084.1	DNA polymerase I [Bacillus cereus]	120	2e-24	26%
WP_132947547.1	DNA polymerase I [Thermolongibacillus altinsuen...	120	2e-24	25%
PEB73834.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
WP_080469882.1	DNA polymerase I [Bacillus cereus]	120	2e-24	26%
WP_145959744.1	DNA polymerase I [Bacillus cereus]	120	2e-24	26%
WP_141493449.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
COF45140.1	DNA polymerase I [Streptococcus pneumoniae]	118	2e-24	26%
PFJ62672.1	DNA polymerase I [Bacillus thuringiensis]	120	2e-24	26%
WP_080126339.1	DNA polymerase I [Bacillus cereus]	120	3e-24	26%
WP_038562164.1	DNA polymerase I [Terribacillus goriensis]	120	3e-24	25%
WP_080017654.1	MULTISPECIES: DNA polymerase I [Bacillus cereus...	120	3e-24	26%
PEG03856.1	DNA polymerase I [Bacillus cereus]	120	3e-24	26%
WP_142312045.1	DNA polymerase I [Bacillus cereus]	120	3e-24	26%
PDX94771.1	DNA polymerase I [Bacillus thuringiensis]	120	3e-24	26%
WP_144524277.1	DNA polymerase I [Bacillus thuringiensis]	120	3e-24	26%
WP_060486537.1	DNA polymerase I [Bacillus wiedmannii]	120	3e-24	26%
PED35322.1	DNA polymerase I [Bacillus cereus]	120	3e-24	26%
WP_102707368.1	DNA polymerase I [Terribacillus goriensis]	120	3e-24	25%
PHD63790.1	DNA polymerase I [Bacillus wiedmannii]	120	3e-24	26%
WP_142399372.1	DNA polymerase I [Bacillus wiedmannii]	120	3e-24	26%
WP_142309456.1	DNA polymerase I [Bacillus cereus]	120	3e-24	26%
PRT05698.1	DNA polymerase I [Bacillus wiedmannii]	120	3e-24	26%
WP_144463139.1	MULTISPECIES: DNA polymerase I [Bacillus]	120	3e-24	25%
WP_120075084.1	DNA polymerase I [Bacillus fortis]	120	3e-24	25%

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Query= ORF9

Length=651

Sequences producing significant alignments:	Score (Bits)	E Value	Max Ident
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AY045733.1 hypothetical protein [Caulerpa cupressoides]	760	0.0	65%
YP_009326774.1 hypothetical protein [Caulerpa racemosa]	681	0.0	59%
YP_009472822.1 hypothetical protein [Caulerpa manorensis]	662	0.0	64%
YP_009472858.1 hypothetical protein [Caulerpa manorensis]	551	0.0	56%
ARR28462.1 hypothetical protein [Caulerpa okamurae]	447	3e-150	70%
YP_009326795.1 hypothetical protein [Caulerpa racemosa]	282	4e-86	59%
YP_009326809.1 hypothetical protein [Caulerpa racemosa]	144	4e-35	68%
AY045724.1 putative DNA polymerase I [Caulerpa cupressoides]	88.6	1e-16	52%
YP_009472804.1 hypothetical protein [Caulerpa manorensis]	77.4	2e-12	49%
AYC64086.1 hypothetical protein [Johnson-sea-linkia profunda]	72.8	2e-09	25%
AYC64626.1 hypothetical protein [Halimeda minima]	68.9	6e-09	29%
AY045723.1 putative LAGLIDADG homing endonuclease [Caulerpa cu...]	60.1	6e-08	61%
YP_009519615.1 hypothetical protein [Udotea flabellum]	67.4	7e-08	26%
ARR28439.1 hypothetical protein [Caulerpa okamurae]	55.5	4e-05	43%
YP_009518872.1 hypothetical protein [Boodleopsis pusilla]	55.1	4e-04	25%
AYC64617.1 hypothetical protein [Halimeda minima]	54.3	7e-04	25%

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
excluding environmental samples from WGS projects

Posted date: Aug 30, 2019 12:43 AM

Number of letters in database: 84,697,594,569

Number of sequences in database: 234,979,574

Lambda K H
0.317 0.135 0.380

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 234979574

Number of Hits to DB: 90373741

Number of extensions: 155835

Number of successful extensions: 97294

Number of sequences better than 100: 4024

Number of HSP's better than 100 without gapping: 0

Number of HSP's gapped: 76902

Number of HSP's successfully gapped: 10950

Length of database: 84697594569

T: 21

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