

Programming for Biology Protein Evolution / Similarity Searching

What BLAST Does / Why BLAST works

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Protein Evolution/ Similarity Searching

- 9:00 – Homology and Expectation value
- 10:30 – Similarity searching workshop I
- 1:30 – Practical Similarity Searching, improving sensitivity
- 3:00 – Workshop II – investigating scoring matrices with scripts

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Goals of this lecture:

- understand why and how homology is inferred; the meaning of “expectation value”
- significance \Rightarrow homology, but no-significance \nRightarrow non-homology
- understand sequence similarity, and why protein comparison is more sensitive than DNA sequence comparison

Similarity searching is POWERFUL, but not MAGIC. There are characteristic errors, and simple strategies to reduce them.

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Why is this material important?

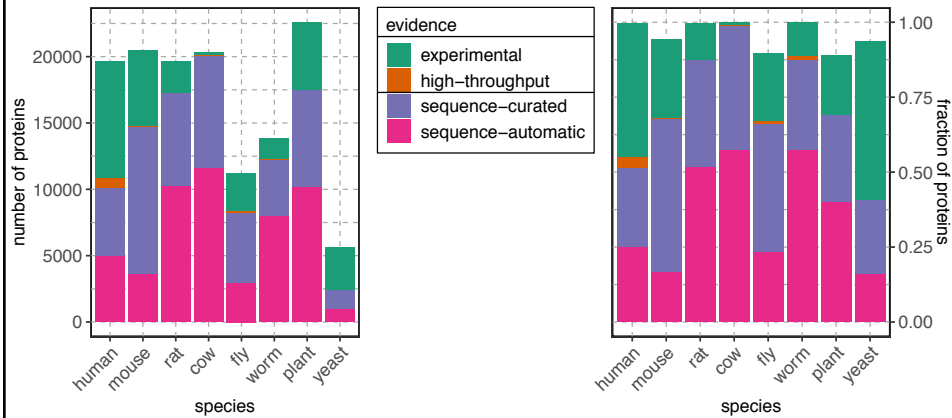
- Most information in biological databases is based on a BLAST search
 - all functional information except for a few model organisms (mostly rats, mice, humans, and yeast)
 - Most genetic information except for *E. coli*, yeast, *Drosophila*
- That information is (usually) *correct*, but *incomplete*
- My goal: to show you what to trust, and when to be skeptical, when using sequence names/annotations, functions, etc.
 - Trust E()-values for proteins to infer homology (common structure)
 - Understand that search results and alignment boundaries are often incomplete – the absence of a result is not a negative result
 - this can be very difficult to accept

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Biological (functional) knowledge is based on sequence comparison



Gene Ontology evidence codes for reference proteomes

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Effective Similarity Searching

1. Always search protein databases (possibly with translated DNA)
 2. Use E()-values, not percent identity, to infer homology
 - $E() < 0.001$ is significant in a single search
-
1. Search smaller (comprehensive) databases
 2. Change the scoring matrix for:
 - short sequences (exons, reads)
 - short evolutionary distances (mammals, vertebrates, a-proteobacteria)
 - high identity (>50% alignments) to reduce over-extension
 3. All methods (pairwise, HMM, PSSM) miss homologs, and find homologs the other methods miss

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Sequence Similarity - Conclusions

- Homologous sequences share a common ancestor, but most sequences are non-homologous
- Always compare Protein Sequences
- Sequence Homology can be reliably inferred from statistically significant similarity (non-homology cannot from non-similarity)
- Homologous proteins share common structures, but not necessarily common functions
- Sequence statistical significance estimates are accurate (verify this yourself) $10^{-6} < E() < 10^{-3}$ is statistically significant
- Scoring matrices set evolutionary look back horizons - not every discovery is distant
- PSI-BLAST can be more sensitive, but with lower statistical accuracy

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Establishing homology from statistically significant similarity

Why BLAST works

- For most proteins, homologs are easily found over long evolutionary distances (500 My – 2 By) using standard approaches (BLAST, FASTA)
- Difficult for distant relationships or very short domains
- Most default search parameters are optimized for distant relationships and work well

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Protein Evolution and Sequence Similarity

Similarity Searching I

- What is Homology and how do we recognize it?
- How do we measure sequence similarity – alignments and scoring matrices?
- DNA vs protein comparison

Similarity Searching II

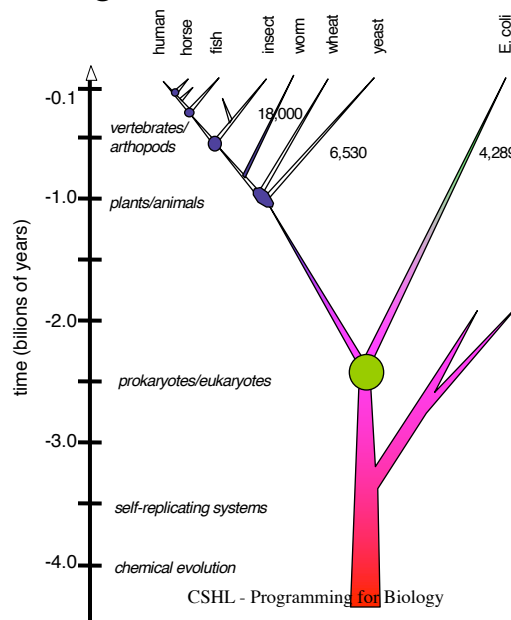
- More effective similarity searching
 - Smaller databases
 - Appropriate scoring matrices
 - Using annotation/domain information

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Homologues share a common ancestor

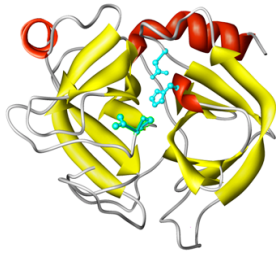


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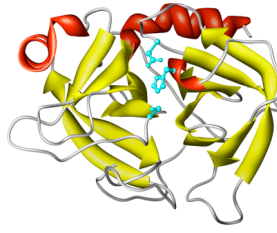
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When do we infer homology?

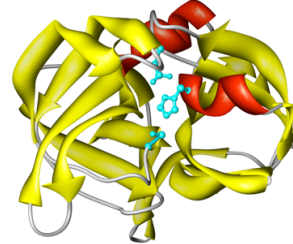
Homology \Leftrightarrow structural similarity
? sequence similarity



Bovine trypsin (5ptp)
Structure: $E() < 10^{-23}$;
RMSD 0.0 Å
Sequence: $E() < 10^{-84}$
100% 223/223



S. griseus trypsin (1sgt)
 $E() < 10^{-14}$ RMSD 1.6 Å
 $E() < 10^{-19}$ 36%; 226/223



S. griseus protease A (2sga)
 $E() < 10^{-4}$; RMSD 2.6 Å
 $E() < 2.6$ 25%; 199/181

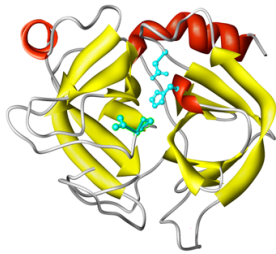
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When can we infer non-homology?

Non-homologous proteins have
different structures



Bovine trypsin (5ptp)
Structure: $E() < 10^{-23}$
RMSD 0.0 Å
Sequence: $E() < 10^{-84}$
100% 223/223



Subtilisin (1sbt)
 $E() > 100$
 $E() < 280$; 25% 159/275
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Cytochrome c4 (1etp)
 $E() > 100$
 $E() < 5.5$; 23% 171/190

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Homology is confusing I: Homology defined Three(?) Ways

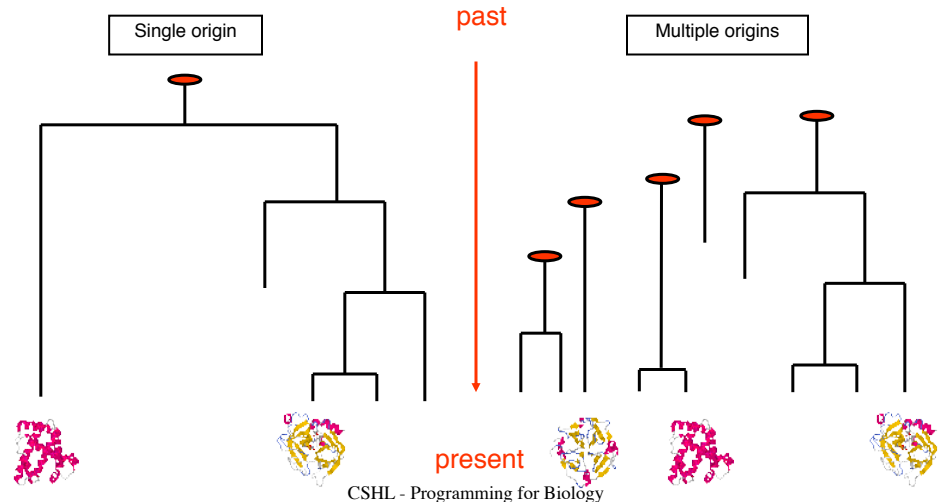
- Proteins/genes/DNA that share a common ancestor
- Specific positions/columns in a multiple sequence alignment that have a 1:1 relationship over evolutionary history
 - sequences are *50% homologous* ???
- Specific (morphological/functional) characters that share a recent divergence (clade)
 - bird/bat/butterfly wings are/are not homologous

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Homology is confusing II: Are All Sequences Homologous? **No Homology without excess similarity**



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Homology from sequence similarity

- Sequences are inferred to share a common ancestor based on statistically significant **excess** similarity. Any evidence of **excess** similarity can be used to infer homology
- Lack of sequence evidence **cannot** be used to infer non-homology.
 - Proteins with different structures are non-homologous
- There are always two alternative hypotheses: homology (common ancestry), or independence – one must weigh the evidence for each hypothesis (independence is the *null* hypothesis).

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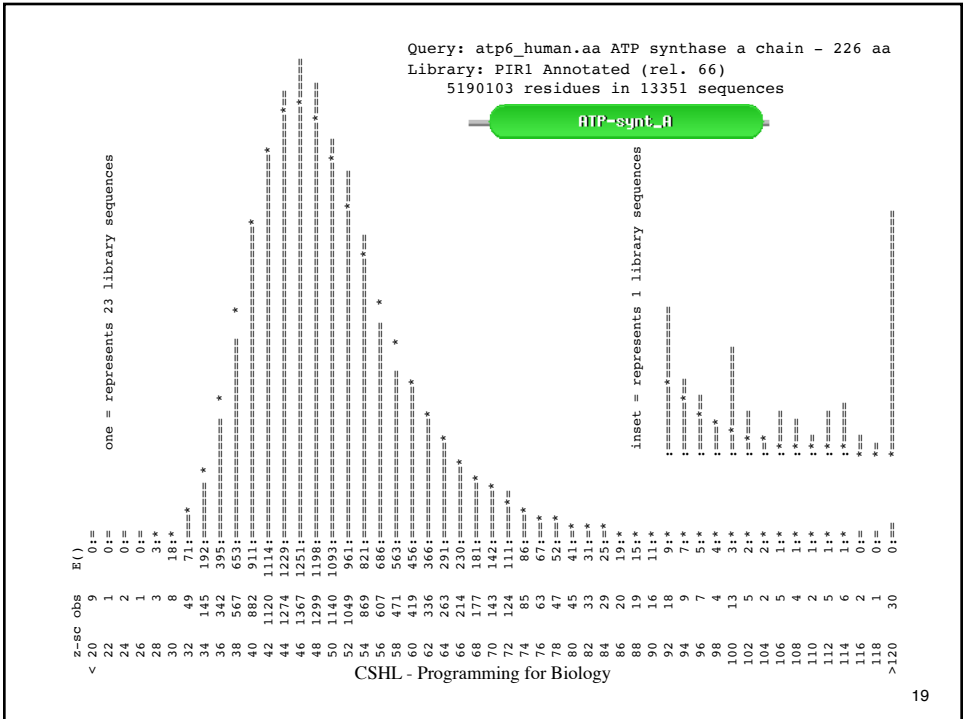
E. coli proteins vs Human – Ancient Protein Domains

expect	%_id	alen	E coli descr	Human descr	sp_name
2.7e-206	53.8	944	glycine decarboxylase, P	Glycine dehydrogenase [de	GCSP_HUMAN
1.2e-176	59.5	706	methylmalonyl-CoA mutase	Methylmalonyl-CoA mutase,	MUTA_HUMAN
3.8e-176	50.6	803	glycogen phosphorylase [E	Glycogen phosphorylase, l	PHS1_HUMAN
9.9e-173	55.6	1222	B12-dependent homocystein	5-methyltetrahydrofolate-	METH_HUMAN
1.8e-165	41.8	1031	carbamoyl-phosphate synth	Carbamoyl-phosphate synth	CPSM_HUMAN
5.6e-159	65.7	542	glucosephosphate isomeras	Glucose-6-phosphate isome	G6PI_HUMAN
8.1e-143	53.7	855	aconitate hydratase 1 [Esch	Iron-responsive element b	IRE1_HUMAN
2.5e-134	73.0	459	membrane-bound ATP syntha	ATP synthase beta chain,	ATPB_HUMAN
3.3e-121	55.8	550	succinate dehydrogenase,	Succinate dehydrogenase [DHSA_HUMAN
1.5e-113	60.6	401	putative aminotransferase	Cysteine desulfurase, mit	NFS1_HUMAN
4.4e-111	60.9	460	fumarase C= fumarate hydr	Fumarate hydratase, mitoc	FUMH_HUMAN
1.5e-109	56.1	474	succinate-semialdehyde de	Succinate semialdehyde de	SSDH_HUMAN
3.6e-106	44.7	789	maltodextrin phosphorylas	Glycogen phosphorylase, m	PHS2_HUMAN
1.4e-102	53.1	484	NAD+-dependent betaine al	Aldehyde dehydrogenase, E	DHAG_HUMAN
3.8e-98	53.0	449	pyridine nucleotide trans	NAD(P) transhydrogenase,	NNTM_HUMAN
5.8e-96	49.9	489	glycerol kinase [Escheric	Glycerol kinase, testis s	GKP2_HUMAN
2.1e-95	66.8	328	glyceraldehyde-3-phosphat	Glyceraldehyde 3-phosphat	G3P2_HUMAN
5.0e-91	62.5	368	alcohol dehydrogenase cla	Alcohol dehydrogenase cla	ADHX_HUMAN
6.7e-91	56.5	393	protein chain elongation	Elongation factor Tu, mit	EFTU_HUMAN
9.5e-91	56.6	392	protein chain elongation	Elongation factor Tu, mit	EFTU_HUMAN
2.2e-89	59.1	369	methionine adenosyltransf	S-adenosylmethionine synt	METK_HUMAN
6.5e-88	53.3	422	enolase [Escherichia coli	Alpha enolase (2-phospho-	ENOA_HUMAN
9.2e-88	43.3	536	NAD-linked malate dehydro	NADP-dependent malic enzy	MAOX_HUMAN
7.3e-86	55.5	389	2-amino-3-ketobutyrate Co	2-amino-3-ketobutyrate co	KBL_HUMAN
5.2e-83	44.4	543	degrades sigma32, integra	AFG3-like protein 2 (Para	AF32_HUMAN

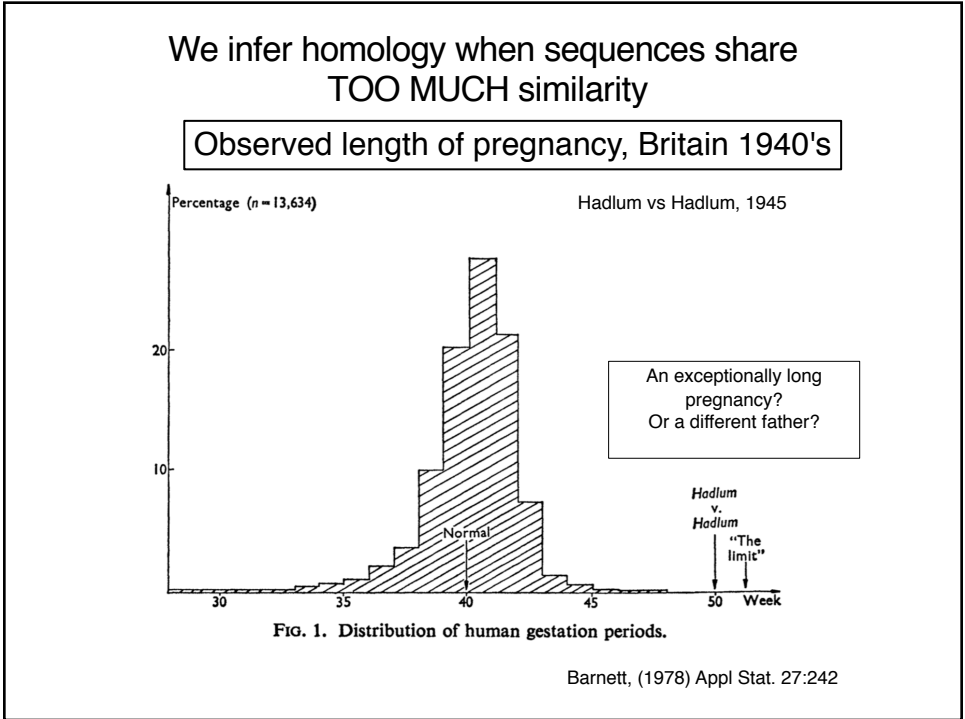
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Inferring Homology from Statistical Significance

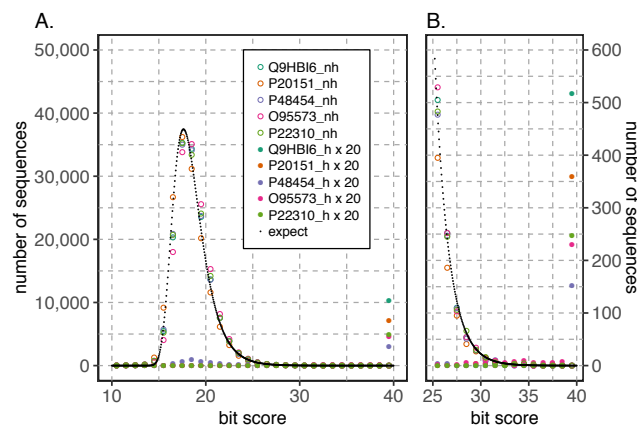
- Real **UNRELATED** sequences have similarity scores that are indistinguishable from **RANDOM** sequences
- If a similarity is NOT **RANDOM**, then it must be NOT **UNRELATED**
- Therefore, NOT **RANDOM** (statistically significant) similarity must reflect **RELATED** sequences

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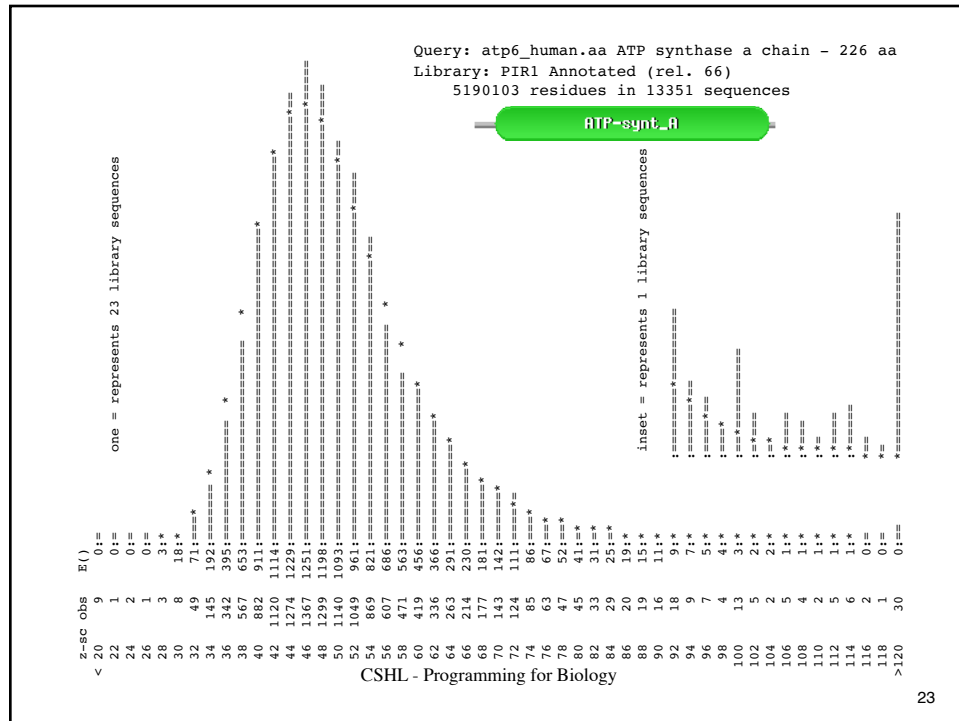
21

Homology inferences are reliable because similarity statistics are accurate (I)
(we know how unrelated sequences behave)



Distributions of similarity scores in searches with 5 human enzymes. Open circles (_nh) show scores for non-homologs. Closed circles show homolog (_h) scores.

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Query: atp6_human.aa ATP synthase a chain - 226 aa
Library: 5190103 residues in 13351 sequences

The best scores are:

sp	seq	len	s-w bits	E(13351)	%_id	%_sim	alen
sp P00846	ATP6_HUMAN ATP synthase a chain (AT (226)	1400	325.8	5.8e-90	1.000	1.000	226
sp P00847	ATP6_BOVIN ATP synthase a chain (AT (226)	1157	270.5	2.5e-73	0.779	0.951	226
sp P00848	ATP6_MOUSE ATP synthase a chain (AT (226)	1118	261.7	1.2e-70	0.757	0.916	226
sp P00849	ATP6_XENLA ATP synthase a chain (AT (226)	745	176.8	4.0e-45	0.533	0.847	229
sp P00851	ATP6_DROYA ATP synthase a chain (AT (224)	473	115.0	1.7e-26	0.378	0.721	222
sp P00854	ATP6_YEAST ATP synthase a chain pre (259)	428	104.7	2.3e-23	0.353	0.694	232
sp P00852	ATP6_EMENI ATP synthase a chain pre (256)	365	90.4	4.8e-19	0.304	0.691	230
sp P14862	ATP6_COACHE ATP synthase a chain (AT (257)	353	87.7	3.2e-18	0.313	0.650	214
sp P68526	ATP6_TRITI ATP synthase a chain (AT (386)	309	77.6	5.1e-15	0.289	0.651	235
sp P05499	ATP6_TOBAC ATP synthase a chain (AT (395)	309	77.6	5.2e-15	0.283	0.635	233
sp P07925	ATP6_MAIZE ATP synthase a chain (AT (291)	283	71.7	2.3e-13	0.311	0.667	180
sp P0AB98	ATP6_ECOLI ATP synthase a chain (AT (271)	178	47.9	3.2e-06	0.233	0.585	236
sp P0C2Y5	ATPI_ORYSA Chloroplast ATP synth (A (247)	144	40.1	0.00062	0.242	0.580	231
sp P06452	ATPI_PEA Chloroplast ATP synthase a (247)	143	39.9	0.00072	0.250	0.586	232
sp P27178	ATP6_SYNY3 ATP synthase a chain (AT (276)	142	39.7	0.00095	0.265	0.571	170
sp P06451	ATPI_SPIOL Chloroplast ATP synthase (247)	138	38.8	0.0016	0.242	0.580	231
sp P08444	ATP6_SYNP6 ATP synthase a chain (AT (261)	127	36.3	0.0095	0.263	0.557	167
sp P69371	ATPI_ATRBE Chloroplast ATP synthase (247)	126	36.0	0.01	0.221	0.571	231
sp P06289	ATPI_MARPO Chloroplast ATP synthase (248)	126	36.0	0.011	0.240	0.575	167
sp P30391	ATPI_EUGGR Chloroplast ATP synthase (251)	123	35.4	0.017	0.257	0.579	214
sp P19568	TLCA_RICPR ADP,ATP carrier protein (498)	122	35.0	0.043	0.243	0.579	152
sp P24966	CYB_TAYTA Cytochrome b (379)	113	33.0	0.13	0.234	0.532	158
sp P03892	NU2M_BOVIN NADH-ubiquinone oxidored (347)	107	31.7	0.31	0.261	0.479	211
sp P68092	CYB_STEAT Cytochrome b (379)	104	31.0	0.54	0.277	0.547	137
sp P03891	NU2M_HUMAN NADH-ubiquinone oxidored (347)	103	30.8	0.58	0.201	0.537	149
sp P00156	CYB_HUMAN Cytochrome b (380)	102	30.5	0.74	0.268	0.585	205
sp P15993	AROP_ECOLI Aromatic amino acid tr (457)	103	30.7	0.78	0.234	0.622	111
sp P24965	CYB_TRANA Cytochrome b (379)	101	30.3	0.87	0.234	0.563	158
sp P29631	CYB_POMTE Cytochrome b (308)	99	29.9	0.95	0.274	0.584	113
sp P24953	CYB_CAPHI Cytochrome b (379)	99	29.8	1.2	0.236	0.564	140

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Alberts is wrong about sequence similarity (three times in three claims)

“With such a large number of proteins in the database, the search programs find *many nonsignificant matches*, resulting in a background noise level that makes it very difficult to pick out all but the closest relatives. Generally speaking, *one requires a 30% identity* in sequence to consider that two proteins match. However, we know the function of many short signature sequences (“fingerprints”), and *these are widely used to find more distant relationships*.”

– Alberts, Molecular Biology of the Cell (5th ed) p. 139

- Sequences producing statistically significant alignments ALWAYS share a common structure
- Many significant alignments share < 30% identity (<25% identity is routine, and <20% identity can be significant)
- In the absence of significant similarity, “fingerprints” should never be trusted to infer homology.

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ATP-synt_0

```
>sp|P00846|ATP6_HUMAN ATP synthase subunit a; F-ATPase protein 6
>sp|P0AB98|ATP6_ECOLI ATP synthase subunit a; F-ATPase subunit 6
Length=271

Score = 47.9 bits (178), Expect = 3e-06
Identities = 55/199 (27%), Positives = 113/199 (56%), Gaps = 37/199 (18%)

Query 8 SFIAPTILGLPAAVLIILFPPLLIPTSKYLINNRLITQOWLIKLTQKMMTMHNTKGRT 67
      S +LGL ++++LF + + + ++ T + +I + + + M++ K +
Sbjct 45 SMFFSVVLGL---LFLVLFVRSVAKKATSG-VPGKFQTAIELVIGFVNGSVKDMYHGKSKL 100

Query 68 WSLMLVSLIIFIATTNLLGLLP-----HSF-----TPTTQLSMNLAMAIPLWAG 111
      + + +++ +++ NL+ LLP H + P+ +++ L+MA+ ++
Sbjct 101 IAPLALTIFVWVFLMNLMDLLPIDLLPYIAEHVGLPALRVVPSADVNVTLMSMALGVF-- 158

Query 112 TVIMGFRSKIKNALAHFLPQGTPTPL-----IPMLVIIETISLLIQPMALAVRLTANITA 166
      +++ F S + F + T P+ IP+ +I+E +SLL +P++L +RL N+ A
Sbjct 159 -ILILFYSIKMKGIGGFTKELTLQPFNHWFIPVNLILEGVSLLSKPVSLGLRLFGNMYA 217

Query 167 GHLLMHLIGSATLAMSTINLPSTLIIFTILILLTILEIAVALIQAYVFTLLVSLYL 222
      G L+ LI S L IF ILI+ +QA++F +L +YL
Sbjct 218 GELIFILIAGLLPWWSQWILNVPWAIFHILIIT-----LQAFIFMVLTVIYL 264
```

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The PAM250 matrix

[illegible]

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Query: atp6_human.aa ATP synthase a chain - 226 aa
Library: 5190103 residues in 13351 sequences

The best scores are:				(len)	s-w	bits	E(13351)	%_id	%_sim	alen
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sp	P00854	ATP6_YEAST	ATP synthase a chain pre	(259)	428	104.7	2.3e-23	0.353	0.694	232
sp	P00852	ATP6_EMENI	ATP synthase a chain pre	(256)	365	90.4	4.8e-19	0.304	0.691	230
sp	P14862	ATP6_COCHC	ATP synthase a chain	(257)	353	87.7	3.2e-18	0.313	0.650	214
sp	P68256	ATP6_TRITI	ATP synthase a chain	(386)	309	77.6	5.1e-15	0.289	0.651	235
sp	P05499	ATP6_TOBAC	ATP synthase a chain	(395)	309	77.6	5.2e-15	0.283	0.635	233
sp	P07925	ATP6_MAIZE	ATP synthase a chain	(291)	283	71.7	2.3e-13	0.311	0.667	180
sp	POA898	ATP6_ECOLI	ATP synthase a chain	(271)	178	47.9	3.2e-06	0.233	0.585	236
sp	P06255	ATP1_ORYSA	Chloroplast ATP synth (A	(247)	144	40.1	0.00062	0.242	0.580	231
sp	P06452	ATP1_PEA	Chloroplast ATP synthase a	(247)	143	39.9	0.00072	0.250	0.586	232
sp	P27158	ATP6_SYNY3	ATP synthase a chain	(276)	142	39.7	0.00095	0.265	0.571	170
sp	P06451	ATP1_SPTOL	Chloroplast ATP synthase	(247)	138	38.8	0.0016	0.242	0.580	231
sp	P08444	ATP6_SYNPF	ATP synthase a chain	(261)	127	36.3	0.0095	0.263	0.557	167
sp	P69371	ATP1_ATRBE	Chloroplast ATP synthase	(247)	126	36.0	0.01	0.221	0.571	231
sp	P06289	ATP1_MARPO	Chloroplast ATP synthase	(248)	126	36.0	0.011	0.240	0.575	167
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sp	P29631	CYB_POMTE	Cytochrome b	(308)	99	29.9	0.95	0.274	0.584	113
sp	P24953	CYB_CAPHI	Cytochrome b	(379)	99	29.8	1.2	0.236	0.564	140

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Query: atp6_ecoli.aa ATP synthase a - 271 aa
Library: 5190103 residues in 13351 sequences

The best scores are:

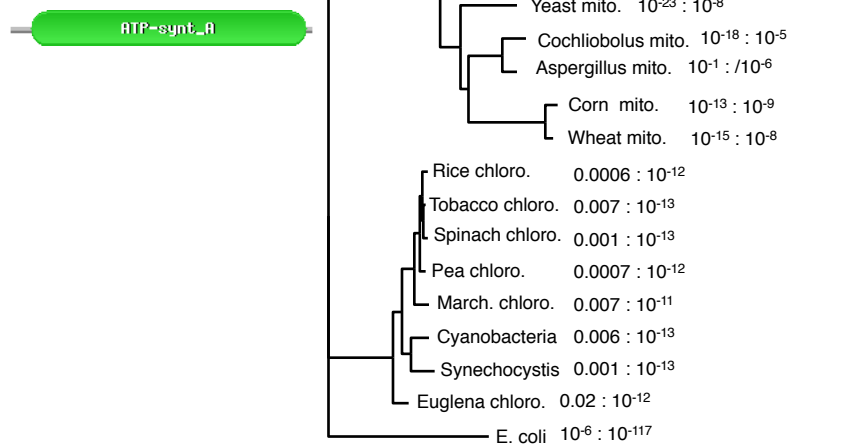
		(len)	s-w	bits	E(13351)	%_id	%_sim	alen
sp P0AB98 ATP6_ECOLI	ATP synthase a chain (AT	(271)	1774	416.8	3.e-117	1.000	1.000	271
sp P06451 ATPI_SPIOL	Chloroplast ATP synthase	(247)	274	70.4	5.8e-13	0.270	0.616	211
sp P69371 ATPI_ATRBE	Chloroplast ATP synthase	(247)	271	69.7	9.3e-13	0.270	0.607	211
sp P08444 ATP6_SYNP6	ATP synthase a chain (AT	(261)	271	69.7	9.9e-13	0.267	0.600	240
sp P06452 ATPI_PEA	Chloroplast ATP synthase a	(247)	266	68.5	2.1e-12	0.274	0.614	223
sp P30391 ATPI_EUGGR	Chloroplast ATP synthase	(251)	265	68.3	2.5e-12	0.298	0.596	225
sp P0C2Y5 ATPI_ORYSA	Chloroplast ATP synthase	(247)	260	67.2	5.4e-12	0.259	0.603	239
sp P27178 ATP6_SYNY3	ATP synthase a chain (AT	(276)	260	67.1	6.1e-12	0.264	0.578	258
sp P06289 ATPI_MARPO	Chloroplast ATP synthase	(248)	250	64.8	2.7e-11	0.261	0.621	211
sp P07925 ATP6_MAIZE	ATP synthase a chain (AT	(291)	215	56.7	8.7e-09	0.259	0.578	232
sp P68526 ATP6_TRITI	ATP synthase a chain (AT	(386)	209	55.3	3.1e-08	0.259	0.603	239
sp P00854 ATP6_YEAST	ATP synthase a chain pre	(259)	204	54.2	4.5e-08	0.235	0.578	277
sp P05499 ATP6_TOBAC	ATP synthase a chain (AT	(395)	189	50.7	7.8e-07	0.220	0.582	268
sp P00846 ATP6_HUMAN	ATP synthase a chain (AT	(226)	178	48.2	2.5e-06	0.237	0.589	236
sp P00852 ATP6_EMENI	ATP synthase a chain pre	(256)	178	48.2	2.8e-06	0.209	0.590	244
sp P00849 ATP6_XENLA	ATP synthase a chain (AT	(226)	173	47.1	5.5e-06	0.261	0.630	165
sp P00847 ATP6_BOVIN	ATP synthase a chain (AT	(226)	172	46.8	6.5e-06	0.233	0.581	236
sp P14862 ATP6_COACHE	ATP synthase a chain (AT	(257)	171	46.6	8.7e-06	0.204	0.608	265
sp P00848 ATP6_MOUSE	ATP synthase a chain (AT	(226)	166	45.5	1.7e-05	0.259	0.617	193
sp P00851 ATP6_DROYA	ATP synthase a chain (AT	(224)	139	39.2	0.0013	0.225	0.549	253
sp P24962 CYB_STELO	Cytochrome b	(379)	125	35.9	0.021	0.223	0.575	193
sp P09716 US17_HCMVA	Hypothetical protein HVL	(293)	109	32.3	0.21	0.260	0.565	131
sp P68092 CYB_STEAT	Cytochrome b	(379)	109	32.2	0.27	0.211	0.562	194
sp P24960 CYB_ODOHE	Cytochrome b	(379)	104	31.1	0.61	0.210	0.555	200
sp P03887 NUI1M_BOVIN	NADH-ubiquinone oxidored	(318)	98	29.7	1.3	0.287	0.545	167
sp P24992 CYB_ANTAM	Cytochrome b	(379)	99	29.9	1.4	0.192	0.565	193

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Homology is
Transitive
(on domains)



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Homology and Domains – Histone acetyltransferase KAT2B

The best scores are:

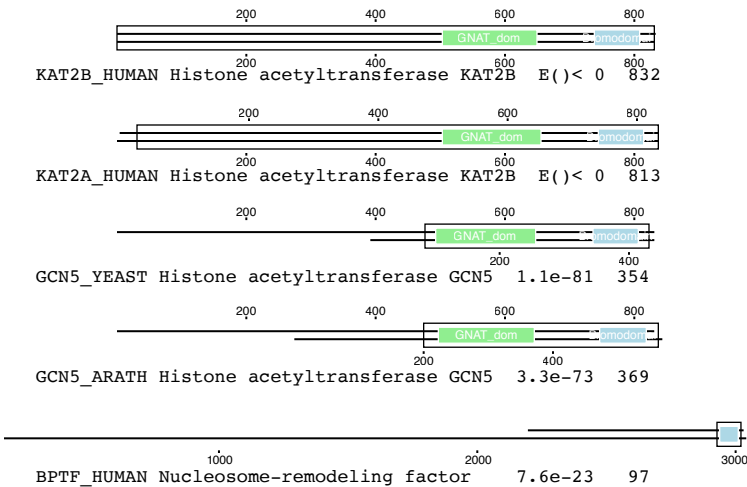
		s-w	bits	E(454402)	%_id	%_sim	alen
KAT2B_HUMAN	Histone acetyltransferase KAT2B (832)	3820	1456.	0	1.000	1.000	832
KAT2A_HUMAN	Histone acetyltransferase KAT2A (837)	2747	1049.	0	0.721	0.870	813
GCN5_SCHPO	Histone acetyltransferase gcn5 (454)	867	334.7	3e-90	0.483	0.768	354
GCN5_YEAST	Histone acetyltransferase GCN5 (439)	792	306.2	1.1e-81	0.469	0.760	354
GCN5_ORYSJ	Histone acetyltransferase GCN5 (511)	760	294.0	5.9e-78	0.436	0.755	376
GCN5_ARATH	Histone acetyltransferase GCN5; (568)	719	278.4	3.3e-73	0.434	0.740	369
BPTF_HUMAN	Nucleosome-remodeling factor sub (3046)	286	113.6	7.6e-23	0.495	0.804	97
NU301_DROME	Nucleosome-remodeling factor su (2669)	276	109.8	9.1e-22	0.511	0.819	94
CECR2_HUMAN	Cat eye syndrome critical regio (1484)	232	93.2	5e-17	0.371	0.790	105
BRD4_HUMAN	Bromodomain-containing protein 4 (1362)	214	86.4	5.2e-15	0.379	0.698	116
BRD4_MOUSE	Bromodomain-containing protein 4 (1400)	214	86.4	5.3e-15	0.379	0.698	116
BAZ2A_HUMAN	Bromodomain adjacent to zinc fi (1905)	211	85.2	1.7e-14	0.382	0.683	123
BAZ2A_XENLA	Bromodomain adjacent to zinc fi (1698)	206	83.3	5.5e-14	0.350	0.684	117
FSH_DROME	Homeotic protein female sterile; (2038)	205	82.9	8.8e-14	0.341	0.667	129
BAZ2A_MOUSE	Bromodomain adjacent to zinc fi (1889)	204	82.5	1e-13	0.368	0.680	125
BRDT_MACFA	Bromodomain testis-specific prot (947)	197	80.0	3e-13	0.367	0.697	109
BRD3_HUMAN	Bromodomain-containing protein 3 (726)	194	78.9	4.9e-13	0.362	0.664	116

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Homology and Domains – Histone deacetylase KAT2B

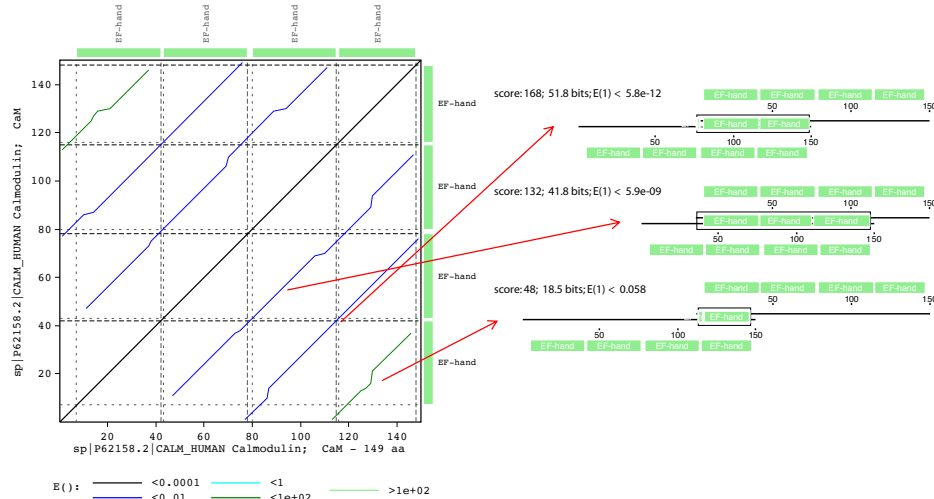


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LALIGN – Identifying mobile domains: mobile (duplicated) domains in local alignments



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Protein Evolution and Sequence Similarity

- What is Homology and how do we recognize it?
- How do we measure sequence similarity – alignments and scoring matrices?
- **DNA vs protein comparison**
- More effective similarity searching
 - Smaller databases
 - Appropriate scoring matrices
 - Using annotation/domain information

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DNA vs protein sequence comparison

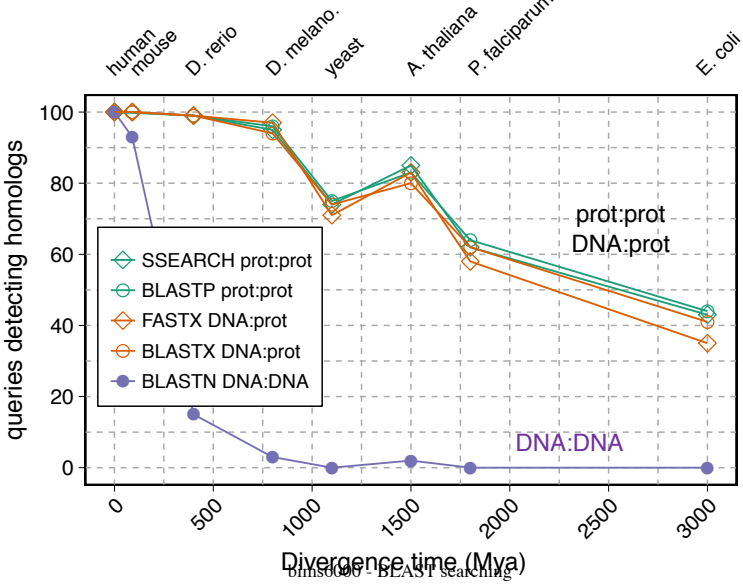
The best scores are:

		DNA	tfastx3	prot.
		E(188,018)	E(187,524)	E(331,956)
MDGST	D.melanogaster GST1-1	1.3e-164	4.1e-109	1.0e-109
MDGST1	M.domestica GST-1 gene	2e-77	3.0e-95	1.9e-76
LUCGLTR	Lucilia cuprina GST	1.5e-72	5.2e-91	3.3e-73
MDGST2A	M.domesticus GST-2 mRNA	9.3e-53	1.4e-77	1.6e-62
MDNF1	M.domestica nf1 gene. 10	4.6e-51	2.8e-77	2.2e-62
MDNF6	M.domestica nf6 gene. 10	2.8e-51	4.2e-77	3.1e-62
MDNF7	M.domestica nf7 gene. 10	6.1e-47	9.2e-77	6.7e-62
AGGST15	A.gambiae GST mRNA	3.1e-58	4.2e-76	4.3e-61
CVU87958	Culicoides GST	1.8e-41	4.0e-73	3.6e-58
AGG3GST11	A.gambiae GST1-1 mRNA	1.5e-46	2.8e-55	1.1e-43
BMO6502	Bombyx mori GST mRNA	1.1e-23	8.8e-50	5.7e-40
AGSUGST12	A.gambiae GST1-1 gene	2.3e-16	4.5e-46	5.1e-37
MOTGLUSTRA	Manduca sexta GST	5.7e-07	2.5e-30	8.0e-25
RLGSTARGN	R.leguminosarum gsa	0.0029	3.2e-13	1.4e-10
HUMGSTT2A	H. sapiens GSTT2	0.32	3.3e-10	2.0e-09
HSGSTT1	H.sapiens GSTT1 mRNA	7.2	8.4e-13	3.6e-10
ECAE000319	E. coli hypothet. prot.	—	4.7e-10	1.1e-09
MYMDCMA	Methyl. dichlorometh. DH	—	1.1e-09	6.9e-07
BCU19883	Burkholderia maleylacetate red.	—	1.2e-09	1.1e-08
NFU43126	Naegleria fowleri GST	—	3.2e-07	0.0056
SP505GST	Sphingomonas paucim	—	1.8e-06	0.0002
EN1838	H. sapiens maleylaceto. iso.	—	2.1e-06	5.9e-06
HSU86529	Human GSTZ1	—	3.0e-06	8.0e-06
SYCCPNC	Synechocystis GST	—	1.2e-05	9.5e-06
HSEF1GMR	H.sapiens EF1g mRNA	—	9.0e-05	0.00065

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Detectable homologs to human enzymes (DNA vs protein comparison)



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Why is protein comparison more sensitive?

- Larger alphabet: 20 aa vs 4 nt, means long alignments less likely by chance
- similarity scoring matrix
 - proteins have BLOSUM62: L ~ (V,I)
 - DNA typically match/mismatch A ≠ G
 - in 3rd codon position, DNA mismatch can be amino acid identity
- Smaller databases
- Better statistics
 - for proteins, $E() < 0.001$ is 1/1000 (unrelated looks like random)
 - for DNA, $E() < 10^{-10}$ a more reliable threshold (unrelated doesn't always look random)

fasta.bioch.virginia.edu/biol4230

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Effective Similarity Searching

1. Always search protein databases (possibly with translated DNA)
 2. Use E()-values, not percent identity, to infer homology
 - $E() < 0.001$ is significant in a single search (proteins)
-
1. Search smaller (comprehensive) databases
 2. Change the scoring matrix for:
 - short sequences (exons, reads)
 - short evolutionary distances (mammals, vertebrates, a-proteobacteria)
 - high identity (>50% alignments) to reduce over-extension
 3. All methods (pairwise, HMM, PSSM) miss homologs, and find homologs the other methods miss

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Computer lab:
fasta.bioch.virginia.edu/mol_evol

- Significant hits are homologous
- Non-significant hits? Homologous or not?
- Are *all* aligned residues homologous
- Are *unaligned* residues non-homologous
- Are domains really missing?

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