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In-silco structure prediction of beta amyloid: A novel protein in alzhemers, on different aspects

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ABSTRACT

Alzheimer's disease (AD) that are relevant to the design and interpretation of clinical treatment trials. Longitudinal data from patients tested with the Alzheimer's Disease Assessment Scale demonstrate that cognitive symptoms and non cognitive symptoms. Functional measures of activities of daily living are difficult to standardize for AD patients but are important for determining the overall clinical and economic impact of AD treatments. This project is a longitudinal data collected from patients with Alzheimer's disease (AD) that are relevant to the design and interpretation of clinical treatment trials. Using NCBI, done the data mining of beta amyloid and from phylogenetic analysis , infer that Musculus is closely related to beta amyloid. From Texshade and Boxshade alignments, observed that more conserved regions are present when compared different model organisms .The energy range before docking is Energy range: Emin = -132.04, Emax = -82.92 and after docking is Energy range: Emin = -134.00, Emax = -68.35.

Keywords: Alzheimers disease, NCBI, Beta amyloid, Clinical trials correlation.

INTRODUCTION

Alzheimer's disease is a progressive, degenerative disease of the brain, which causes thinking and memory to become seriously impaired. It is the most common form of dementia. (Dementia is a syndrome consisting of a number of symptoms that include loss of memory, judgment and reasoning, and changes in mood, behaviour and communication abilities. Related diseases include: Vascular Dementia, Fronto temporal Dementia, Creutzfeldt-Jakob Disease and Lewy body Dementia.). The disease was first identified by Dr. Alois Alzheimer in 1906. He described the two hallmarks of the disease: "plaques" - numerous tiny dense deposits scattered throughout

the brain which become toxic to brain cells at excessive levels and "tangles" which interfere with vital processes eventually "choking" off the living cells. As well, when brain cells degenerate and die, the brain markedly shrinks in some regions .

Amyloid beta (Aβ or A beta) is a peptide of 36–43 amino acids that appears to be the main constituent of amyloid plaques in the brains of Alzheimer's disease patients. Similar plaques appear in some variants of Lewy body dementia and ininclusion body myositis, a muscle disease. Aβ also forms aggregates coating cerebral blood vessels in cerebral amyloid angiopathy. These plaques are composed of a tangle of regularly ordered fibrillar aggregates called amyloid fibers, a protein fold shared by other peptides such as the prions associated with protein misfolding diseases. Recent research suggests that soluble oligomeric forms of the peptide are likely to be the causative agents in the development of Alzheimer's disease. Longitudinal data from patients tested with the Alzheimer's Disease Assessment Scale demonstrate that cognitive symptoms, including memory loss, dysphasia, and dyspraxia, worsen relentlessly over time with the rate of change depending upon baseline dementia severity. Noncognitive symptoms, such as agitation, depressed mood, and psychosis, are episodic, do not necessarily worsen over time, and tend not to be highly correlated with one another. The reliability of cognitive change measures increases with follow-up duration so that the likelihood of detecting drug effects on the rate of cognitive deterioration is greater with longer treatment trials [1-17].

MATERIALS AND METHODS

The Insilco Materials and Methods That Had Been Used in the the Insilco Structure Prediction of Beta Amyloid, A Novel Protein in Alzheimer’s, On Different Species are as follows:

1) CDD-BLAST (http://www.ncbi.nlm.nih.gov/BLAST/)
2) INTERPROSCAN (http://www.abi.ac.uk/interpro)
3) PFAM (http://www.pfam.sanger.ac.uk/)
4) COGs (http://www.ncbi.nih, gov/cog) [12-17].

Tools	Purpose
NCBI	Sequence Similarity search and sequence retrieval
PDB	Primary Database for 3D structures
BLAST	Sequence alignment
ClustalW	Phylogenetic analysis
TEXSHADE	Shows Conserved, Identical and Similar Residues(Local alignment)
Clustal Distance Matrix	Phylogenetic Analysis
Protparam	Primary Structure Analysis
HNN	Secondary Structure Analysis

National Centre for Biotechnology Information-
This is a primary database. It is majorly used for sequence retrieval and similarity based searches. It develops software tools for analyzing Genomic data and disseminates biomedical information affecting human health and disease.

Blast
BLAST-The BLAST program was designed by Eugene Myers, Stephen Altschul, Warren Gish, David J. Lipman and Webb Miller at the NIH and was published in J. Mol. Biol. in 1990.

Most popular program for sequence analysis. It uses heuristic methods to align a query sequence with all other sequences in the database .The objective is to find high-scoring ungapped segments among related sequences. The emphasis on speed is vital to making the algorithm practical on the huge genome databases currently available.

It is a service of the U.S. National Library of Medicine that includes over 18 million citations from MEDLINE and other life science journals. Includes links to full articles and other related resources.

Biology Workbench-
It's a web based tool for biologists. Database searching is integrated with access to a wide variety of analysis and modelling tools.

ClustalW-
Clustal is a progressive multiple alignment program available either as stand alone or on-line program .the stand-alone program, which run on UNIX and MACINTOSH has two variants, ClustalW and ClustalX. The W version provides a simple text based interface and X version provides a more user friendly graphical interface.ClustalW2 is a general purpose multiple sequence alignment program for DNA or proteins. It produces biologically meaningful multiple sequence alignments of divergent sequences. It calculates the best match for the selected sequences, and lines them up so that the identities, similarities and differences can be seen. Evolutionary relationships can be seen via viewing Cladograms or Phylograms.

Texshade-
It is a web implementation of TeXshade, a LaTeX style sheet which allows for alignment coloring via a series of LaTeX directives. The output is a DVI file which is converted to postscript files and then to gif file for web display. It is based on Local alignment of sequences.

Boxshade-
It produces shaded GIF and postscript plots of prealigned multiple sequences. It works by Global alignment of all sequences and show the conserved, identical and similar residues.

Clustal Distance Matrix-
The matrix contains data that shows relationships between a given set of elements (DNA and Protein sequences). Values in the matrix file show distance, similarity or identity between different sequences [18-31].

RESULTS AND DISCUSSION

Here the vertebrates used are dario rerio, mus musculus, rattus norvegicus, invertebrates used are anopheles gambiae str. Pest, drosophila melanogaster, microorganisms used in analysis of beta amyloid are neurospora crassa

Protein sequence analysis vertebrates:
amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) [Homo sapiens]
Sequence:
>amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) [Homo sapiens]
MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPS
GTKTCIDTKEGIL
QYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLV
PDKCKFLHQER
MDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNVDS
ADAEEDDSDVWW
GGADTDYADGSEDKVVEVAEEEEVAEVEEEEADDDEDDEDGDEVEEEAEEPYEEATER
TTSIATTTTTTT
ESVEEVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCM
AVCGSAMSQSLL
KTTQEPLARDPVKLPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQ
VMREWEEAERQA
KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYIT
ALQAVPPRPRHV
FNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSL
LYNVPAVAEEIQD
EVDELLQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQP
WHSFGADSVP
ANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLV
FFAEDVGSNKG
AIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYEN
PTYKFFEQMQN

Function:
BPTI/Kunitz family of serine protease inhibitors; Structure is a disulfide rich alpha+beta fold. BPTI (bovine pancreatic trypsin inhibitor) is an extensively studied model structure.

appa [Danio rerio]
amyloid beta (A4) precursor protein a [Danio rerio]
Organism : Dario rerio
Blosum 80
Expect threshold:1-10
Score = 444 bits (1021),
Expect = 3e-124,
Method: Compositional matrix adjust.

Identities = 222/319 (69%),
Positives = 255/319 (79%),
Gaps = 12/319 (3%)

Sequence:
appa [Danio rerio]
>MRSRELFILLMAVASTLAVEVPSDSGTGLLAEPQIAMFCGKLNMHINIQSGKWEPDPSG
SKSCIGNKEGI
LQYCQEVYPELQITNVVEANQPVSIWDWCKKSRKQCRSHMHIVVPYRCLVGEFVSDAL
LVPDKCKFLHQE
RMDMCESHLHWHTVAKESCGDRSMNLHDYGMLLPCGIDRFRGVEFVCCPADAGKESE
SAAVEEDDSDVWW
GGAEADYTENSMTRDAAAEPAVLEDDEDADEEEDEDQDGDGDRDEKIEEEEEEEERTQ
STSAALTSTTTT
TTESVEEVVRVPTPSSSPPDAVDRYLETPADENEHAHFLQAKESLETKHRERMSQVMRE
WEEAERQAKSL
PRNDKKAVIQHFQEKVEALEQESASERQQLVETHMARVEALLNDRRRLALESYLSALQ
ADPPRPRHVFSL
LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRVIEERMNQSLGLLYKV
PGVADDIQDQVE
LLQREQQEMSAQLANLQSDARVSYGNDALMPDSTAGLELLPAEDTQGFGFIHPESFNQP
NTHNQVEPVDA
RPVPDLDLATRPVSGLKPDDIPELRMEAEERHSEVYTRSWF

Function:
Amyloid A4 extracellular domain
hippocampal amyloid precursor protein [Mus musculus]
amyloid beta (A4) precursor protein [Mus musculus]
Organism:Mus musculus
Blosum 80
Expect threshold:1
Score = 857 bits (1978),
Expect = 0.0,
Method: Compositional matrix adjust.
Identities = 400/409 (97%),
Positives = 403/409 (98%),
Gaps = 0/409 (0%)

Sequence:
hippocampal amyloid precursor protein [Mus musculus]
>MLPSLALLLLAAWTVRALEVPTDGNAGLLAEPQIAMFCGKLNMHMNVQNGKWESDP
SGTKTCIGTKEGIL
QYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHTHIVIPYRCLVGEFVSDALLV
PDKCKFLHQER

MDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDSVDS
ADAEEDDSDVWW
GGADTDYADGGEDKVVEVAEEEEVADVEEEEADDDEDVEDGDEVEEEAEEPYEEATE
RTTSTATTTTTTT
ESVEEVVRVPTTAASTPDAADKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMRE
WEEAERQAKNLPK
ADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQA
VPPRPHHVFNMLK
KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNVP
AVAEEIQDEVDEL
LQKEQNYSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEFSLDDLQPWHPF
GVDSVPANTEN
EVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFGHDSGFEVRHQKLVFFAED
VGSNKGAIIGL
MVGGVVIATVIVITLVMLKKKQYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYK
FFEQMQN

Function:
Amyloid A4 extracellular domain
ATPase involved in DNA repair [DNA replication, recombination, and repair]
Outer membrane protein (OmpH-like)

This family includes outer membrane proteins such as OmpH among others. Skp (OmpH) has been characterized as a molecular chaperone that interacts with unfolded proteins as they emerge in the periplasm from the Sec translocation machinery.
beta-amyloid precursor protein C-terminus

This is the amyloid, C-terminal, protein of the beta-Amyloid precursor protein (APP) which is a conserved and ubiquitous transmembrane glycoprotein strongly implicated in the pathogenesis of Alzheimer's disease but whose normal biological function is unknown. The C-terminal 100 residues are released and aggregate into amyloid deposits which are strongly implicated in the pathology of Alzheimer's disease plaque-formation. The domain is associated with family A4_EXTRA, pfam02177, further towards the N-terminus.

Rattus norvegicus
Organism:Rattus norvegicus
Blosum 80
Expect threshold:1
Score = 216 bits (492),
Expect = 1e-55,
Method: Compositional matrix adjust.
Identities = 99/198 (50%),
Positives = 145/198 (73%),
Gaps = 0/198 (0%)
Sequence:

>gi|171846588|gb|AAI61904.1| Aplp1 protein [Rattus norvegicus]
MGPSSPTTRGQGRRRGPPPLPLLLPLSLLLLRAQLAVGNLAGGSPSAAEAPGSAQVAGL
CGRLTLHRDLR
TGRWEPDPQRSRRCLLDPQRVLEYCRQMYPELHIARVEQAAQAIPMERWCGGTRSGRC
AHPHHEVVPFHC
LPGEFVSEALLVPEGCRFLHQERMDQCESSTRRHQEAQEACSSQGLILHGSGMLLPCGS
DRFRGVEYVCC
PPPATPNPSGMAVGDPSTRSWPLGGRAEGGEDEEEVESFPQPVDDYFVEPPQAEEEEEEE
EERAPPPSSH
TPVMVSRVTPTPRPTDGVDVYFGMPGEISEHEGFLRAKMDLEERRMRQINEVMREWA
MADSQSKNLPKAD
RQALNEHFQSILQTLEEQVSGERQRLVETHATRVIALINDQRRAALEGFLAALQGDPPQA
ERVLMALRRY
LRAEQKEQRHTLRHYQHVAAVDPEKAQQMRFQVQTHLQVVQERMNQSLGLLDQNPH
LAQELRPQIQELLH
AEHLGPSELEASVPGSSSEDKDAPVTLPKGSTDQESSSSGREKLTPLEQYEQKVNASAPR
GFPFHSSDIQ
RDELAPAGTGVSREALSGLLIMGAGGGSLIVLSLLLLRKKKPYGTISHGVVEVDPMLTLE
EQQLRELQRH
GYENPTYRFLEERP

Function:
beta-amyloid precursor protein C-terminus
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amyloid precursor protein [Gallus gallus]
Organism:Gallus gallus
Blosum 80
Expect threshold:1
>gb|AAC25052.1| amyloid precursor protein [Gallus gallus]
Length=534
Score = 863 bits (1993),
Expect = 0.0,
Method: Compositional matrix adjust.
Identities = 398/408 (97%),
Positives = 404/408 (99%),
Gaps = 0/408 (0%)
Sequence:
>gi|3282749|gb|AAC25052.1| amyloid precursor protein [Gallus gallus]

GMNLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNLDSADAEDDDSDVWWGGADADY
ADGSDDKVVEEQPE
EDEELTVVEDEDADDDDDDDGDEIEETEEEYEEATERTTSIATTTTTTTESVEEVVRVPT
TAASTPDAVD
KYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKAVIQ
HFQEKVESLEQEA
ANERQQLVETHMARVEAMLNDRRRIALENYITALQTVPPRPRHVFNMLKKYVRAEQK
DRQHTLKHFEHVR
MVDPKKAAQIRSQVMTHLRVIYERMNQSLSFLYNVPAVAEEIQDEVDELLQKEQNYSD
DVLANMISEPRI
SYGNDALMPSLTETKTTVELLPVDGEFSLDDLQPWHPFGVDSVPANTENEVEPVDARPA
ADRGLTTRPGS
GLTNVKTEEVSEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT
VIVITLVMLKKK
QYTSIHHGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN

Function:
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This is the amyloid, C-terminal, protein of the beta-Amyloid precursor protein (APP) which is a conserved and ubiquitous transmembrane glycoprotein strongly implicated in the pathogenesis of Alzheimer's disease but whose normal biological function is unknown. The C-terminal 100 residues are released and aggregate into amyloid deposits which are strongly implicated in the pathology of Alzheimer's disease plaque-formation. The domain is associated with family A4_EXTRA, pfam02177, further towards the N-terminus.

INVERTEBRATES:
AGAP002790-PA [Anopheles gambiae str. PEST]
>ref|XP_312126.4| AGAP002790-PA [Anopheles gambiae str. PEST]
gb|EAA07868.4| AGAP002790-PA [Anopheles gambiae str. PEST]
Length=877
Organism:Anopheles gambiae
Blosum 62
Expect threshold:10
Score = 135 bits (341),
Expect = 4e-32,
Method: Compositional matrix adjust.
Identities = 64/167 (38%),
Positives = 91/167 (54%),
Gaps = 9/167 (5%)

Sequence:
>gi|158290531|ref|XP_312126.4| AGAP002790-PA [Anopheles gambiae str. PEST]
TRAHSSSLLLARISSFHFLFYFSPSLQAASPRWEPQISVLCEAGQTYHPQFLSEEGRWTTD
LSIKVPGST

CLRDKMDLLDYCKKVYPGRDITNIVESSHYQKIGGWCRQGALNAAKCKGAQRWIKPFR
CLEGPFQSDALL
VPEGCLFDHIHNASRCWPFVRWNQTGAAACQDRNMQMRSFAMLLPCGISLFSGVEFVC
CPKHFKAGSIKI
QRLISPTNTIPQQQKHETVVMRPITCGHTHTHTHTSVHDEEEGGSVLRPAEDTDMLPALD
DGSDGASDNN
SEDDEEEDEMDDEEDEEMLGDEPIESEDDEYDSDEDFDSGSDKPAAGADTIDTGSAAWD
SFTTPPPPATG
NKDALKKQQQPDSLGAGMLYAAAGGYAAASSTERAAGGIELVTTPITAIPTPDPYFTHF
DPRNEHQSFKV
AQQRLEESHREKVTRVMKDWSDLEEKYQDMRLADPKSAQTFKQRMTARFQTSVQALE
EEGNSEKHQLAAM
HQQRVLAHINQRKREAMTCYTQALTEQPPSSHRVEKCLQKLLRALHKDRAHALSHYRH
LLGSGGTGGLEA
AASERPRTLERLVDIDRAVNQSMAMLKRYPELSVKLSQLMDDYIQALRSKDETPGSML
AMTEEAEAAILD
KYRMEIERKVSEKERQRLAEKQRKEQRAQEREKIREENAKGNGNHQGLLRGSGRDVST
SSTISQHFSEAI
ISRRSLWLFVVCVRPFARLINHHRVALSTLSHFRCCRSPQPTALPTVDDEAVQRAVEEVA
AAVAHQEAEP
KMQHVLAHDIGHGEPSYSVRREVYSSSGRDSKNVYFTVGFAGIALMAAVFVGVAVAK
WKASRSPHAQGFV
EVDQAVGAPVTPEERHVANMQINGYENPTYKYFEIKE

Function:
chromosome segregation protein SMC, primarily archaeal type
SMC (structural maintenance of chromosomes) proteins bind DNA and act in organizing and segregating chromosomes for partition. SMC proteins are found in bacteria, archaea, and eukaryotes. It is found in a single copy and is homodimeric in prokaryotes, but six paralogs (excluded from this family) are found in eukarotes, where SMC proteins are heterodimeric. This family represents the SMC protein of archaea and a few bacteria (Aquifex, Synechocystis, etc); the SMC of other bacteria is described by TIGR02168. The N- and C-terminal domains of this protein are well conserved, but the central hinge region is skewed in composition and highly divergent.

EG:65F1.5 [Drosophila melanogaster]
>emb|CAA18093.1| EG:65F1.5 [Drosophila melanogaster]
Length=887
Organism:Drosophilla melanogaster
Blosum 62
Expect threshold:10

Score = 136 bits (342),
Expect = 1e-31,
Method: Compositional matrix adjust.

Identities = 70/193 (36%),
Positives = 100/193 (51%),
Gaps = 10/193 (5%)
Sequence:
>gi|3929671|emb|CAA18093.1| EG:65F1.5 [Drosophila melanogaster]
MCAALRRNLLLRSLWVVLAIGTAQVQAASPRWEPQIAVLCEAGQIYQPQYLSEEGRWV
TDLSKKTTGPTC
LRDKMDLLDYCKKAYPNRDITNIVESSHYQKIGGWCRQGALNAAKCKGSHRWIKPFRC
LGPFQSDALLVP
EGCLFDHIHNASRCWPFVRWNQTGAAACQERGMQMRSFAMLLPCGISVFSGVEFVCCP
KHFKTDEIHVKK
TDLPVMPAAQINSANDELVMNDEDDSNDSNYSKDANEDDLDDEDDLMGDDEEDDMV
ADEAATAGGSPNTG
SSGDSNSGSLDDINAEYDSGEEGDNYEEDGAGSESEAEVEASWDQSGGAKVMSLKSDS
SSPSSAPVAPAP
EKAPVKSESVTSTPQLSASAAAFVAANSGNSGTGAGAPPSTAQPTSDPYFTHFDPHYEH
QSYKVSQKRLE
ESHREKVTRVMKDWSDLEEKYQDMRLADPKAAQSFKQRMTARFQTSVQALEEEGNAE
KHQLAAMHQQRVL
AHINQRKREAMTCYTQALTEQPPNAHHVEKCLQKLLRALHKDRAHALAHYRHLLNSG
GPGGLEAAASERP
RTLERLIDIDRAVNQSMTMLKRYPELSAKIAQLMNDYILALRSKDDIPGSSLGMSEEAEA
GILDKYRVEI
ERKVAEKERLRLAEKQRKEQRAAEREKLREEKLRLEAKKVDDMLKSQVAEQQSQPTQS
STQSQAQQQQQE
KSLPGKELGPDAALVTAANPNLETTKSEKDLSDTEYGEATVSSTKVQTVLPTVDDDAVQ
RAVEDVAAAVA
HQEAEPQVQHFMTHDLGHRESSFSLRREFAQHAHAAKEGRNVYFTLSFAGIALMAAVF
VGVAVAKWRTSR
SPHAQGFIEVDQNVTTHHPIVREEKIVPNMQINGYENPTYKYFEVKE

Function:
beta-amyloid precursor protein C-terminus
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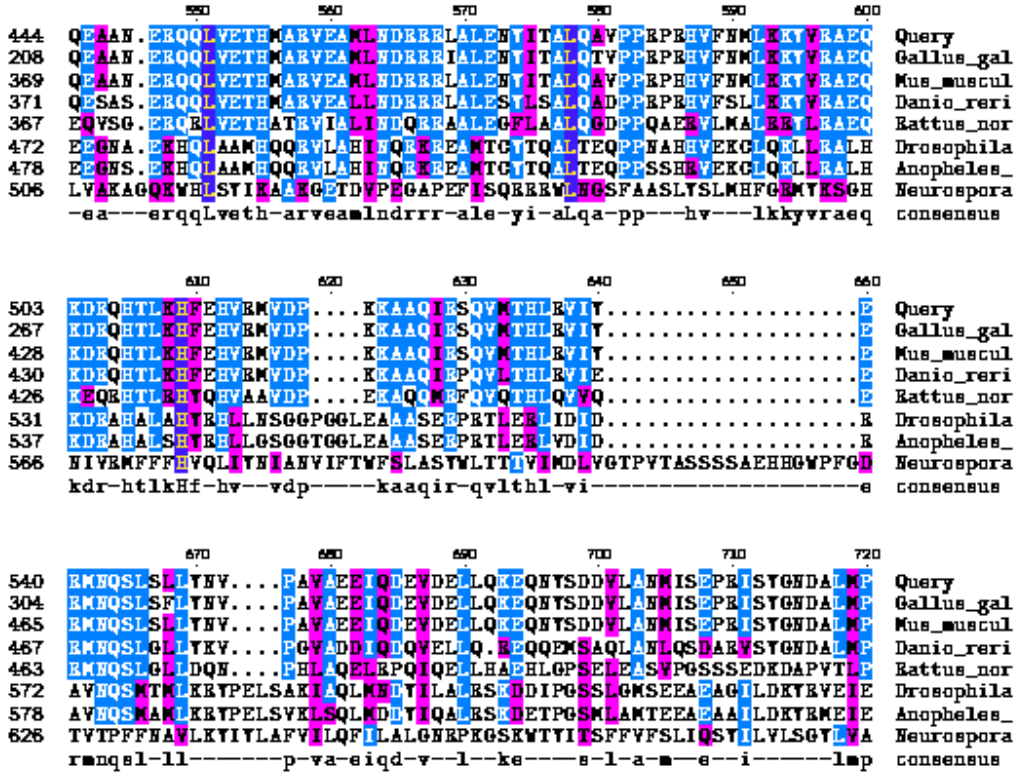
MICROORGANISMS:
chitin synthase 1 [Neurospora crassa]
Organism: Neurospora crassa
Blosum 45
Expect threshold:50

Score = 28.6 bits (82),
Expect = 7.1,
Method: Compositional matrix adjust.
Identities = 21/70 (30%),
Positives = 32/70 (45%),
Gaps = 1/70 (1%)

Sequence:
>gi|164426762|ref|XP_961338.2| chitin synthase 1 [Neurospora crassa OR74A]
MAYHGRGDGYDGHQLQDLPGGHNQGDQHDDAQAPFLSENPMPYDNDRLGTDTPPVR
PVSAYSLTESYAPG
AGTTRAGVAVNPTPPPHGGYGGGGVSSGVDQGYNYGGDYATDPAYRMSAIDEDDSWL
RRQQPNAAPTGGL
KRYATRKVKLVQGSVLSLDYPVPSAIRNAVQPKYRDEEGNNEEFFKMRYTAATCDPND
FTLKNGYDLRPR
MYNRHTELLIAITYYNEDKVLLSRTLHSVMTNIRDIVNLKKSSFWNRGGPAWQKIVVCL
VFDGLDKTDKN
VLDVLATIGVYQDGVIKKDVDGKETVAHIFEYTSQLSVTPNQALIRPVDDGPQTLPPVQF
IFCLKQKNTK
KINSHRWLFNAFGRILNPEVCILLDAGTKPSPRSLLALWEGFYNDKDLGGACGEIHAML
GKGGKKLLNPL
VAVQNFEYKISNILDKPLESAFGYVSVLPGAFSAYRFRAIMGRPLEQYFHGDHTLSKLLG
KKGIEGMNIF
KKNMFLAEDRILCFELVAKAGQKWHLSYIKAAKGETDVPEGAPEFISQRRRWLNGSFA
ASLYSLMHFGRM
YKSGHNIVRMFFFHVQLIYNIANVIFTWFSLASYWLTTTVIMDLVGTPVTASSSSAEHHG
WPFGDTVTPF
FNAVLKYIYLAFVILQFILALGNRPKGSKWTYITSFFVFSLIQSYILVLSGYLVARAFSVPL
DQQLQLDN
AKDAMASLFGGSGSAGVILVALVTIYGLYFLASFMYLDPWHMFHSFPYYMLLMSTYINI
LMIYAFNNWHD
VSWGTKGSDKAEALPSANVSKGEKDEAVVEEIEKPQEDIDQQFEATVRRALAPYKEDET
PEPKDLEDSYK
SFRTMLVVSWLFSNCLLAVVITSDNFNTFGIGQTASARTAWFFKFLLFATGALSVIRFIGF
CWFLGRTGI
MCCFARR

Function:
Glycosyltransferase family A (GT-A) includes diverse families of glycosyl transferases with a common GT-A type structural fold.

TEXSHADE

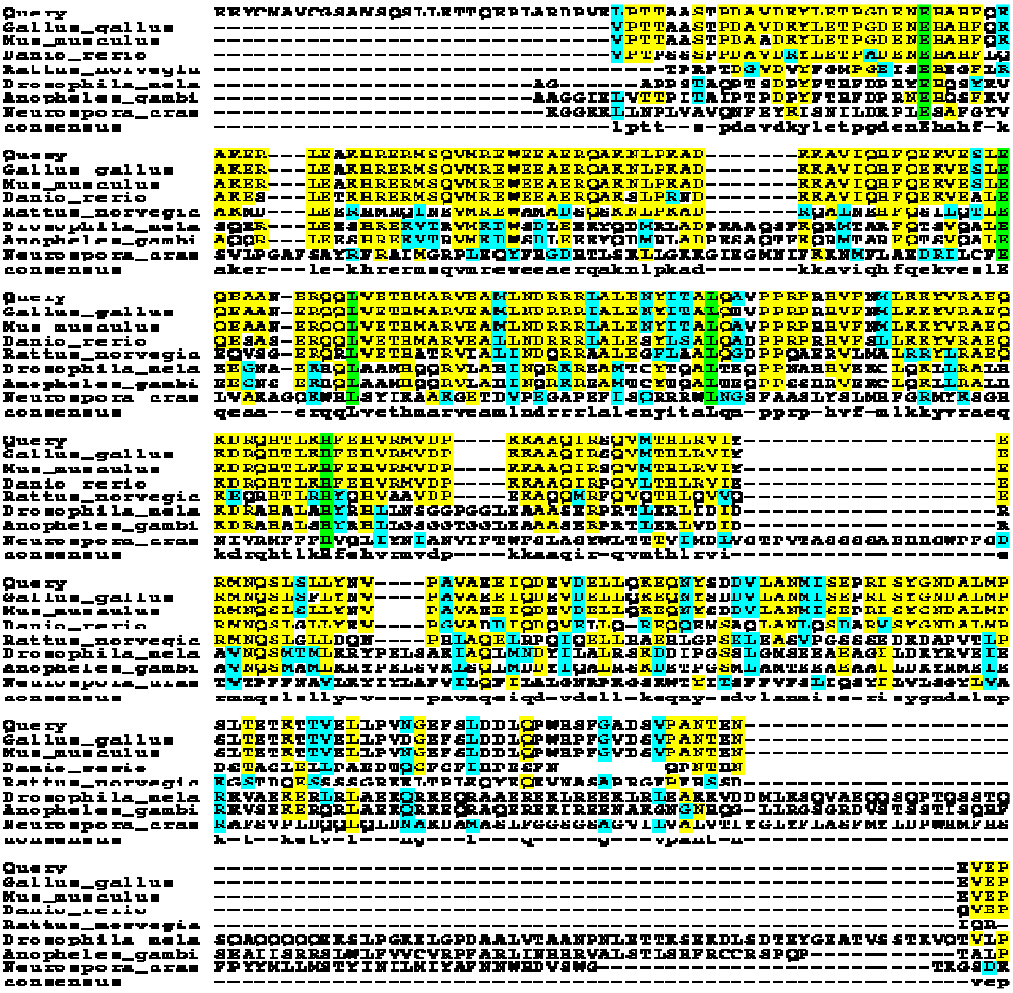


Glycosyltransferases (GTs) are enzymes that synthesize oligosaccharides, polysaccharides, and glycoconjugates by transferring the sugar moiety from an activated nucleotide-sugar donor to an acceptor molecule, which may be a growing oligosaccharide, a lipid, or a protein. Based on the stereochemistry of the donor and acceptor molecules, GTs are classified as either retaining or inverting enzymes. To date, all GT structures adopt one of two possible folds, termed GT-A fold and GT-B fold. This hierarchy includes diverse families of glycosyl transferases with a common GT-A type structural fold, which has two tightly associated beta/alpha/beta domains that tend to form a continuous central sheet of at least eight beta-strands. The majority of the proteins in this superfamily are Glycosyltransferase family 2 (GT-2) proteins. But it also includes families GT-43, GT-6, GT-8, GT13 and GT-7; which are evolutionarily related to GT-2 and share structure similarities.

BOXSHADE
Yellow-conserved
Green-identical
Cyan-similar
Clustal Distance Matrix

		(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Query	**(1)**	**0.000**	**0.069**	**0.029**	**0.328**	**0.620**	**0.742**	**0.737**	**0.908**
Gallus_gallus	(2)	0.069	0.000	0.081	0.359	0.624	0.750	0.729	0.910
Mus_musculus	(3)	0.029	0.081	0.000	0.326	0.622	0.726	0.723	0.909

Danio_rerio (4) 0.328 0.359 0.326 0.000 0.618 0.739 0.739 0.932
Rattus_norvegicus (5) 0.620 0.624 0.622 0.618 0.000 0.743 0.757 0.927
Drosophila_melanogas (6) 0.742 0.750 0.726 0.739 0.743 0.000 0.380 0.909
Anopheles_gambiae (7) 0.737 0.729 0.723 0.739 0.757 0.380 0.000 0.898
Neurospora_crassa (8) 0.908 0.910 0.909 0.932 0.927 0.909 0.898 0.000



CONCLUSION

Using NCBI I have done the data mining of beta amyloid and from phylogenetic analysis I can infer that Mus musculus is closely related to beta amyloid .From Texshade and Box shade alignments I have observed that more conserved regions are present when compared different model organisms .The energy range before docking is Energy range: Emin = -132.04, Emax = -82.92 and after docking is Energy range: Emin = -134.00, Emax = -68.35.

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