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RESEARCH ARTICLE

Structural Analysis and Molecular Mechanics of Pxr1 Gene which is Responsible For Zellweger Syndrome

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Abstract

Zellweger syndrome is an autosomal recessive disorder caused by mutations in genes that encode peroxins, proteins required for the normal assembly of peroxisomes. It causes a defect is the perioxisomes, which affects the body severally. It affects both males and females and is present at birth. The target gene coding protein in zellweger syndrome had been identified. Blast P is used for the similarities identification of pxr1 protein and the Functional identification of pxr1 is viewed through AMIGO. Secondary structural analyses of pxr1 protein were carried through tools like, TARGET P, GLOBPROT, and DOMAIN LINKER PREDICTION. From the molecular mechanics study, the electrostatic properties have been identified.

INTRODUCTION

Zellweger syndrome, also called cerebrohepatorenal syndrome, is a rare congenital disorder, characterized by the reduction or absence of functional peroxisomes in the cells of an individual[1]. IT is one of a group of four related diseases called peroxisome biogenesis disorders (PBD), which are part of a larger group of diseases known as the leukodystrophies[2]. These are inherited conditions that damage the white matter of the brain and also affect how the body metabolizes particular substances in the blood and organ tissues. They are caused by defects in any one of 12 genes, termed PEX genes that are required for the normal formation and function of peroxisomes (cell structures that break down toxic substances in the liver, kidneys, eyes, and brain, and synthesize fatty materials that are necessary for cell function). Peroxisomes are required for normal brain development and the function and formation of myelin, the whitish material that coats nerve fibers[3].

Zellweger syndrome is an inherited peroxisomal metabolic disorder. Peroxisomes are found in almost all body cells and are responsible for many important cellular processes. Zellweger syndrome causes a defect in the peroxisomes, which affects the body severely (Fig – 1). Zellweger syndrome is estimated to occur in 1 of every 50,000 to 100,000 births. It affects both males and females and is present at birth[4]. Peroxisomes are usually abundant in a person's kidney and liver.

Peroxisomes are cell structures that break down toxic substances and synthesize lipids (fatty acids. Oils, and waxes) that are necessary for cell function. Peroxisomes are required for normal brain development and function and the formation of myelin, the whitish substance that coats nerve fibers[5]. They are also required for normal eye, liver, kidney, and bone functions. Zellweger spectrum disorders result from dysfunctional lipid metabolism, including the over-accumulation of very long-chain fatty acids and phytanic acid, and defects of bile acids and plasmalogens--specialized lipids found in cell membranes and myelin sheaths of nerve fibers. Symptoms of these disorders include an enlarged liver; characteristic facial features such as a high forehead, underdeveloped eyebrow ridges, and wide-set eyes; and neurological abnormalities such as mental retardation and seizures[6]. Infants will Zellweger syndrome also lack muscle tone, sometimes to the point of being unable to move, and may not be able to suck or swallow. Some babies will be born with glaucoma, retinal degeneration, and impaired hearing. Jaundice and gastrointestinal bleeding also may occur.

AIM AND OBJECTIVES

To find out the mutational genes involved in Zellweger syndrome. To predict 3D Structure of the Protein. To visualize molecular mechanics of the protein.

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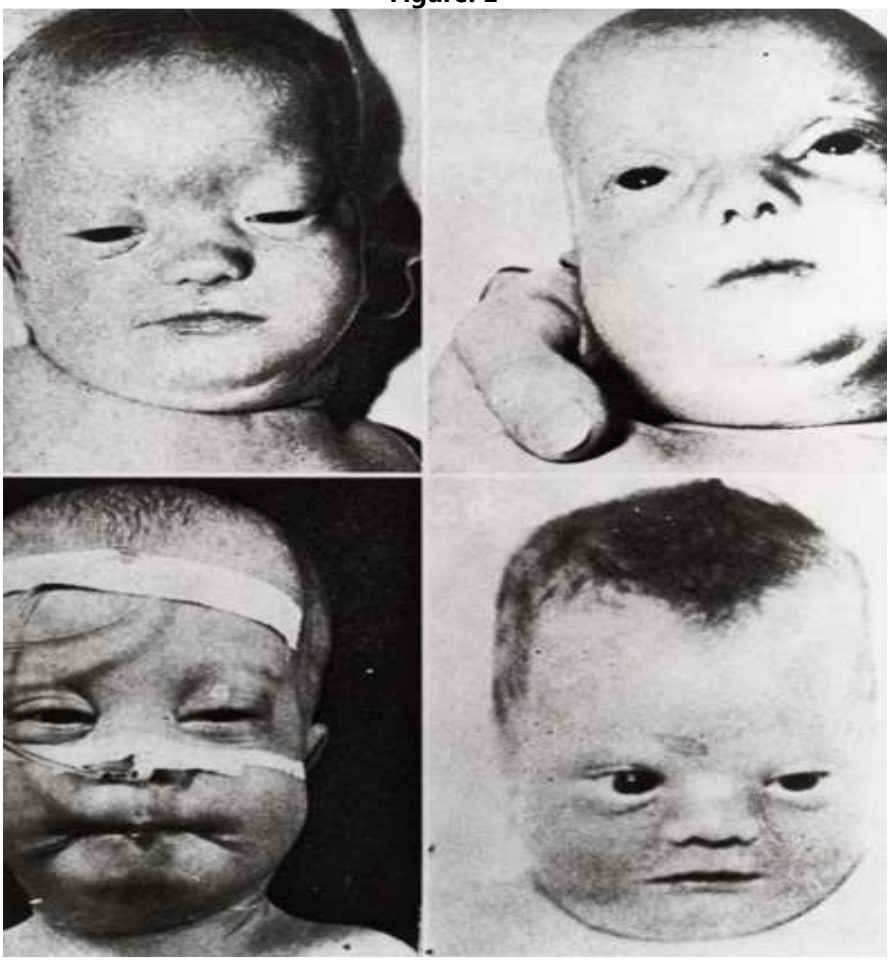
METHODOLOGY

Zellweger syndrome is the most severe of three PBD disorders that have overlapping features; the other disorders being neonatal adrenoleukodystropsy and Infantile Refsum Disease, the mildest disorder[7]. The National Center for Biotechnology Information (NCBI) provides a comprehensive website for biologists that includes biology-related databases, and tools for viewing and analyzing the data inherent in the databases. Basic Local Alignment Search Tool, or BLAST, is an algorithm for comparing primary biological sequence information, such as the amino-acid sequences of different proteins or the nucleotides of DNA sequences. . AmiGO is the official web-based set tools for searching and browsing the Gene Ontology database, which consists of a controlled vocabulary of terms covering biological concepts, and a large number of genes or gene products whose attributes have been annotated using Gene Ontology terms. ClustalW starts by finding the score of the Multiple alignment between each pair of sequences, using a scoring function that is appropriate for proteins. Target to predict the subcellular location of eukaryotic proteins. GlobPlot is a web service that allows the user to plot the tendency within the query protein for order/globularity and disorder. Domain Linker Prediction-SVM is a domaininker predictor. It is composed of three loops-length dependent SVM predictors of domain linkers (SVM-All, SVM-Long and SVM-Short), and SVM-Joint, which combines the results of SVM-Short and SVM-Long into a single consolidated prediction. DIPOLE MOMENT SERVER used to predict Electrostatic properties of the target proteins.

Figure: 1



RESULTS AND DISCUSSION

1. NCBI-SEQUENCE RETREIVAL

PROTEIN

>gi|223590138|sp|A5DRH5.2|PXR1_PICGU RecName: Full=Protein PXR1; AltName: Full=PinX1-related protein 1

MGLAGTKVKQRFGLDPRNTSWSNDKSRFGHRYLESMGWAPGKGLGLVEHATTTHVKVSVKDDTVGLGL

AKRSGTDDLETDSSGLDDFQRILGRLNGRGREVDEALEQKRKDNIINGKWGMHFIKGEVLCSTWDRKSKS
HMLKTALEDESEVNFKSSKKRRQSGSEPSRDSTSHAKRMRGDESKKSTRDQSKQERKEKKIKTEKKEKKE
KKEKKEKKEKKEKKEKKEKKERDYGNRASPVEPRKHDQISNVGRLSARAKYIKQKRASVMDAKAK

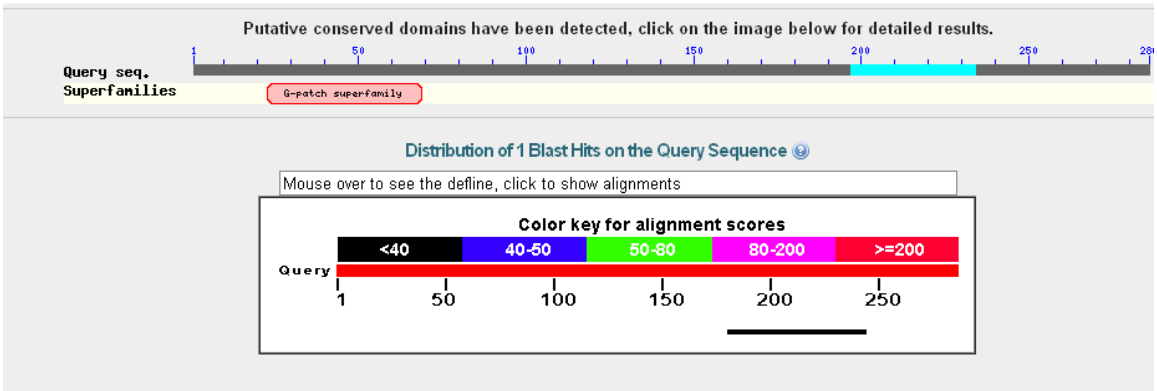
NUCLEOTIDE

>gi|359750250:9857-12145 Torulaspora delbrueckii CBS 1146 chromosome 7, complete genome

TTAAAAGAGACAAACGAGGGACAACAACAGAACTGACAGTGATGATCTCACACGTGCCGCAGAGCCCTCG
TAGGACGTTAGGCTTGCCTGAGTATGAATAGATGCGAAACCAGTCGAAGAAGGCTCGCTTTTTGGAATAC
TTGATGTTGAAGCGGGTGCCTGACTGATCGTAGTCATAGTACTTTGCAACCCACTAACAACTTCAGATTG
GCCAGAAAGTTGTTGATTAGTCGTTGCAGAAGCATGAGTTGAACTTGGATTCGAGGATAAAGTCTCACCA
TAGTTTATGGTCGAGGCCACAGAGCTTAGGGATTCTGTAGGAGCTATGTGGCTTCCGGGTATCGAAAGGG
TGGTAGTTCGATGGGATCTAACTTTTGTAACCGTAGCAGTAGTGCCTTCTGAGGAAGATGTTACCGAAAC
ACCTGTGTCAGTTGACGTCTCGGGTAATTGTGATACCTCACTGCTTTGAGCACAAGCTTCACACTCTACC
TGACTTTGAATCCCTATAGATCCACTAGAGGCTGGAGATGGGGTCAACGTTACTGGGCTTCTTGGAACGA
AGGTAGCGGAATTTTGTGTGGAGTCCGTGCTATCAGACCTTGAGCAGGTTACGAAAGGTGCAGAATCAGA
TGATACCAAAGGCGTAGAATTAGGTGGTACCAATGTGCAACTAGATAGTCCGGAGCAGCTACGGATAGAA
ACTACCACCGTAGAAGTAGTTTCCATAACGGATGTATAGCTGGGTAGTACCGATGTAGAAGTACTTGCCA
CTAAAAATGTAGAACCAGATGCAATCGAAGTAGAAGGTACTGAAGTGGTCGAGCTAGATGCAGAACCAGA
TAGTGCTGAAGAAGCGGAGCTAGATGGTGCTGAAGACGCAGAGCTAGATGGTGCAGATGATATCCATGAA
GCTGGTTGCTTTGTGGTGCTAGCTGGCACTGAAGTAGTTGAGCTAGATGCAGAGCTAGATGGTGCTGAAG
ACGCAGAACTAGATGGTGGTGATGATGTCCATGAAGCTGGTTGCTTTGTGGTGCTAGCTGGCACTGAAGT
GGTCGAGCTAGATGCAGAGCTAGATGGTGTTGAAGACGCAGAGCTAGATGGTGCAGATGATATCCATGAA
GCTGGTTGCTTTGTGGTGCTAGCTGGCACTGAAGTGGTCGAGCTAGATGCAGGGTTAGATGGTGCCGAAG
ACGTAGAACTAGATGGTGCGGACAATGTCGAACTAGATGATGTGGAGGATGCAGCGCTAGATCTAGAGTT
AGATGAAACCAAAGACTTGGAGCTAGTTGGTTGTAATGTTTTTGTAGTAGAACCAGGAACAGATGACGAT
GAAGAAGCGGAGCTATGCGCAGAGCTAATAGAAGCGGAGTTAGATGGCACTGACGATATCCAACTGGCTG
GTTCCCTTGTAGTGCTAGCTGGCACTGAAGTAGTTGAGCTAGATGCTGAGCTAGAAGATGTCGAACTAGG
ACTGCTTGTGCTTATTGGGACTGATGTGGCAGAGCTAGAAGCTGACGGTACCGAAGAAGTAGATTTAGAT
GGTGCTGAAGTCGTCAAAATAGAAACAGAGCTAGCTGGCTCCTTTGTGGTACTAGCTGGCACTGAAGACG
TGGAGCTTGTGGAGCTGGTAGAGCTTGTGGAGCTGGTAGAGCTTGTGGAGCTGGTAGAGCACTTAGCATT
ATCCCAGTACCATAGCGGAAAGTCAGCATTAGAATTGCCATTGTTGTCTGCGTTACAACCAGTCATCAAA
TCAAAAGCAGTTGCACCCCATTTCCAAGTTTGCCAGTACTGAGCGGCATCACCTTGCAGATACTCGTATT
GAATTTGGAATGATGGCATAGCAACTTTACATTCATCGCCATTATACTTTTGACCATAAACTTGAATTTT
CGTCGTGAAATCTGTCGGGTTATCAATTATATAGGTATTCTCATTCTTACCCCAAAGTTGTTTAGTACCC
ATTGGACCATTGATGCCAATGATTTTTAAGGAATAGAGATACTTCATATCAATCTGTTGATCACCCTTGA
CATTTATTGAAAGTTCATAAGTATTGTCACCGACCCAATCGACTGACAATAGATCCATGTAATATGGCAT
GGTGTTGGTATTTTTTGCGTGCCATTTGAAGTTCAAATTTGGACACATATTAGTAACTCCAGACACAGCT
GACGATGTGCGGCGAACTAACGCTGAATCACCATTATTAGAATAAAAATCAGTCTCGTAAGTATTATCGG
AGGCTGCTGAAGCAACCCCTAACAAACATAAGAGCAGATAGGAAAGCAT

The above results show the FASTA format sequence of PXR1.

2. BLAST P

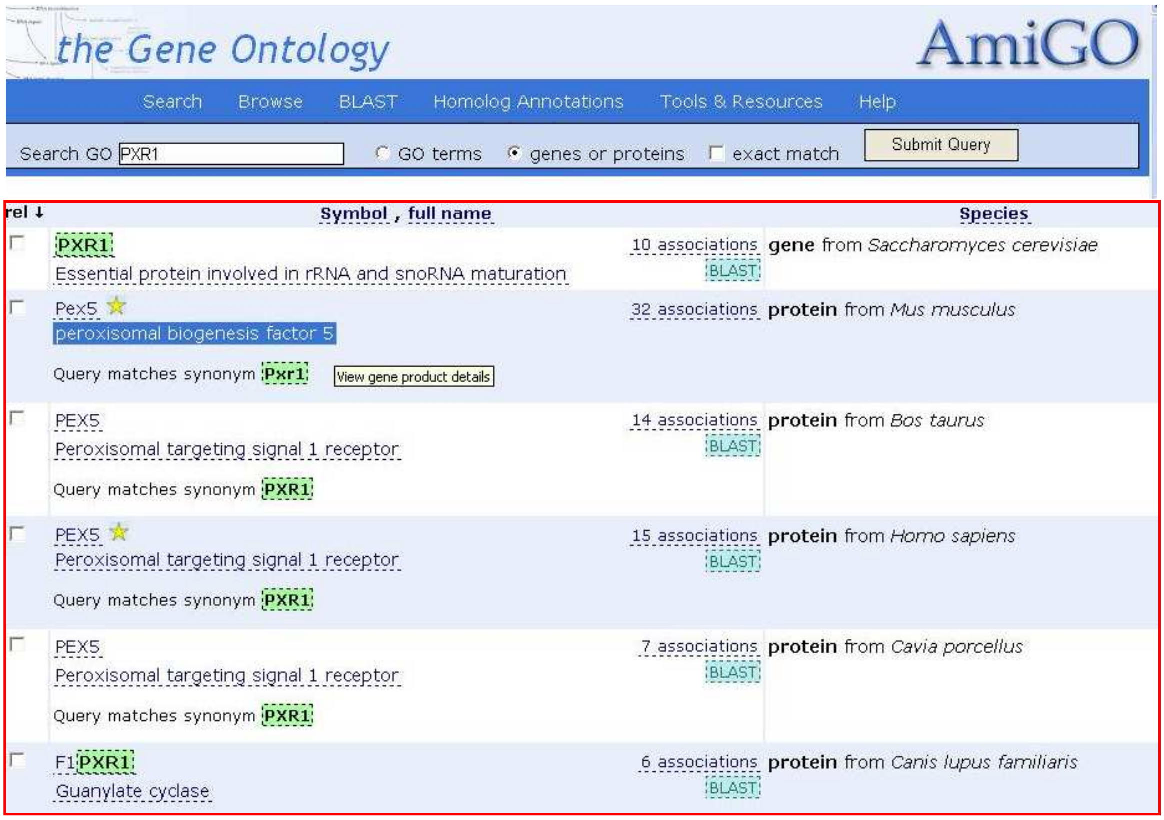


Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
3KZ4_A	Chain A, Crystal Structure Of The Rotavirus Double Layerec	33.5	33.5	22%	0.16	34%

The above result shows the similarity search of PXR1.

3. FUNCTIONAL IDENTIFICATION-AMIGO



The above result shows the functional identification of PXR1.

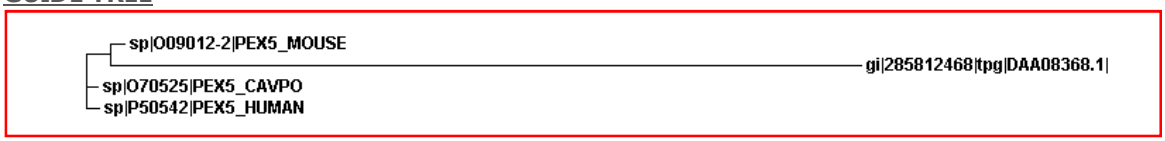
4. PHYLOGENETIC ANALYSIS

CLUSTAL 2.1 multiple sequence alignment

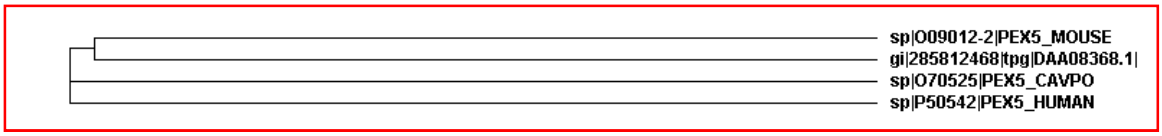
```
sp|O70525|PEX5_CAVPO       MAMRELVEGECGGANPLMKLAGHFTQDKALRQEGLRPGPWPPGAPASETV 50
sp|P50542|PEX5_HUMAN       MAMRELVEAECGGANPLMKLAGHFTQDKALRQEGLRPGPWPPGAPASEAA 50
sp|O09012-2|PEX5_MOUSE     MRELVEGECGGANPLMKLATHFTQDKALRQEGLRPGPWPPGASAAETV 50
gi|285812468|tpg|DAA08368.1|MGLAATRTKQRFGLDP--RNTAWSNDTSRFGHQFLEKFGWKPGMGLGLSP 48
                             *:     : * :*  : :   .: . : :: *.   * **    . :

sp|O70525|PEX5_CAVPO       SKPLGVASEDELVAEFLQDQNAPLVSRAPQTFKMDDLLAEMQEIEQSNFR 100
sp|P50542|PEX5_HUMAN       SKPLGVASEDELVAEFLQDQNAPLVSRAPQTFKMDDLLAEMQQIEQSNFR 100
sp|O09012-2|PEX5_MOUSE     SKPLGVGTEDELVSEFLQDQNATLVSRAPQTFKMDDLLAEMQEIEQSNFR 100
gi|285812468|tpg|DAA08368.1|     MN-----SNTSHIKVSIKDDNVGLGAKLKRKDKKDEFD------------ 81
                              :    :: . :  ::*:*. * ::  :. * *::

sp|O70525|PEX5_CAVPO       APQRAPGVADLALSENWAQEFLAAGDAVDVTQDYNETDWSQEFIAEVTD 150
sp|P50542|PEX5_HUMAN       QAPQRAPGVADLALSENWAQEFLAAGDAVDVTQDYNETDWSQEFISEVTD 150
sp|O09012-2|PEX5_MOUSE     QAPQRAPGVADLALSENWAQEFLAAGDAVDVAQDYNETDWSQEFIAEVTD 150
gi|285812468|tpg|DAA08368.1|     ----------------------------------NGECAGLDVFQRILG 96
```

```
                                            *    . :.: .: .
sp|O70525|PEX5_CAVPO       PLSVSPARWAEEYLEQSEEKLWLGEPEGAATTDRWYDEYHPEEDLQHTAS 200
sp|P50542|PEX5_HUMAN       PLSVSPARWAEEYLEQSEEKLWLGEPEGTAT-DRWYDEYHPEEDLQHTAS 199
sp|O09012-2|PEX5_MOUSE     PLSVSPARWAEEYLEQSEEKLWLGDQEGSSTADRWYDEYHPEEDLQHTAS 200
gi|285812468|tpg|DAA08368.1|    RLNGKESKISEELDTQRKQKIIDG---------KWGIHFVKGEVLASTWD 137
                      *. . :: .** * .:*: *     :*  .:   * *  * .
sp|O70525|PEX5_CAVPO       DFVAKVDDPKLANSEFLKFVRQIGEGQVSLESVAGSGRAQAEQWAAEFIQ 250
sp|P50542|PEX5_HUMAN       DFVAKVDDPKLANSEFLKFVRQIGEGQVSLESGAGSGRAQAEQWAAEFIQ 249
sp|O09012-2|PEX5_MOUSE     DFVSKVDDPKLANSE---------------------------------- 215
gi|285812468|tpg|DAA08368.1|    PKTHKLRN----------------------------------------- 145
                       . *: :
sp|O70525|PEX5_CAVPO      QQGTSDAWVDQFTRPVN-TSALDMEFERAKSAIESDVDFWDKLQAELEEM 299
sp|P50542|PEX5_HUMAN      QQGTSDAWVDQFTRPVN-TSALDMEFERAKSAIESDVDFWDKLQAELEEM 298
sp|O09012-2|PEX5_MOUSE    --GTSEAWVDQFTRPGNKIAALQVEFERAKSAIESDVDFWDKLQAELEEM 263
gi|285812468|tpg|DAA08368.1|    ------------------------YSNAK-----------KRKREGDDS 159
                                :..**          * : * ::
sp|O70525|PEX5_CAVPO      AKRDAEAHPWLSDYDDLTSASYDKGYQFEEENPLRDHPQPFEEGLLRLEE 349
sp|P50542|PEX5_HUMAN      AKRDAEAHPWLSDYDDLTSATYDKGYQFEEENPLRDHPQPFEEGLRRLQE 348
sp|O09012-2|PEX5_MOUSE    AKRDAEAHPWLSDYDDLTSASYDKGYQFEEENPLRDHPQPFEEGLHRLEE 313
gi|285812468|tpg|DAA08368.1|EDEDDDDK-----EDKDSDKKKHKKHKKHKKDKKKDKKDKKEHKKHKKEE 204
                      ..* : :     *. :. . .* :: .::: :*: :  *.   : :*
sp|O70525|PEX5_CAVPO       GDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLEL 399
sp|P50542|PEX5_HUMAN       GDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLEL 398
sp|O09012-2|PEX5_MOUSE     GDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLEL 363
gi|285812468|tpg|DAA08368.1|    KRLK----------------------------KEKRAEKTKETKKTSKL 225
                        *                 :*:.    .  ::  :*
sp|O70525|PEX5_CAVPO       KPDNRTALMALAVSFTNESLQRQACETLRDWLRCTPAYAHLVTPAEEGAG 449
sp|P50542|PEX5_HUMAN       KPDNQTALMALAVSFTNESLQRQACETLRDWLRYTPAYAHLVTPAEEGAG 448
sp|O09012-2|PEX5_MOUSE     KPDNRTALMALAVSFTNESLQRQACETLRDWLRYSPAYAHLVAPGEEGAT 413
gi|285812468|tpg|DAA08368.1|    KSSESASNIPDAVNTR--------LSVRSKWIKQK--------------- 252
                      *.:: :: :. **.          .. .*:. .
sp|O70525|PEX5_CAVPO          GAGLGSSKRILGSLLSDSLFLEVKELFLAAVRLDPTSIDPDVQCGLGVLF 499
sp|P50542|PEX5_HUMAN           GAGLGPSKRILGSLLSDSLFLEVKELFLAAVRLDPTSIDPDVQCGLGVLF 498
sp|O09012-2|PEX5_MOUSE          GA--GPSKRILGSLLSDSLFLEVKDLFLAAVRLDPTSIDPDVQCGLGVLF 461
gi|285812468|tpg|DAA08368.1|    ------RAALMDSKALNEIFMITND------------------------ 271
                           ::*   .:*: .::
sp|O70525|PEX5_CAVPO      NLSGEYDKAVDCFTAALSVRPNDYLLWNKLGATLANGNQSEEAVAAYRRA 549
sp|P50542|PEX5_HUMAN      NLSGEYDKAVDCFTAALSVRPNDYLLWNKLGATLANGNQSEEAVAAYRRA 548
sp|O09012-2|PEX5_MOUSE NLSGEYDKAVDCFTAALSVRPNDYLMWNKLGATLANGNQSEEAVAAYRRA 511
gi|285812468|tpg|DAA08368.1|    --------------------------------------------------

sp|O70525|PEX5_CAVPO        LELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGA 599
sp|P50542|PEX5_HUMAN        LELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGA 598
sp|O09012-2|PEX5_MOUSE      LELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGA 561
gi|285812468|tpg|DAA08368.1|    --------------------------------------------------

sp|O70525|PEX5_CAVPO          MSENIWSTLRLALSMLGQSDAYRAADARDLSALLALFGLSQ 640
sp|P50542|PEX5_HUMAN          MSENIWSTLRLALSMLGQSDAYGAADARDLSTLLTMFGLPQ 639
sp|O09012-2|PEX5_MOUSE        MSENIWSTLRLALSMLGQSDAYGAADARDLSALLAMFGLPQ 602
gi|285812468|tpg|DAA08368.1|    -----------------------------------------
```

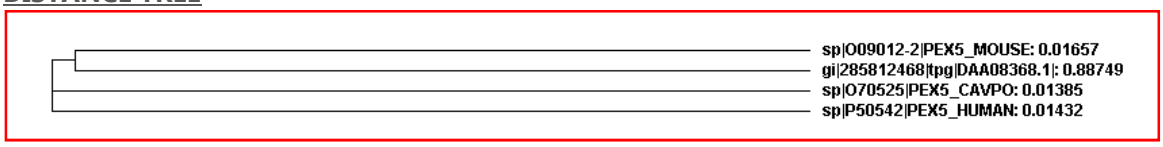
GUIDE TREE



CLADOGRAM TREE



DISTANCE TREE



The above result shows the phylogenetic analysis of PXR1.

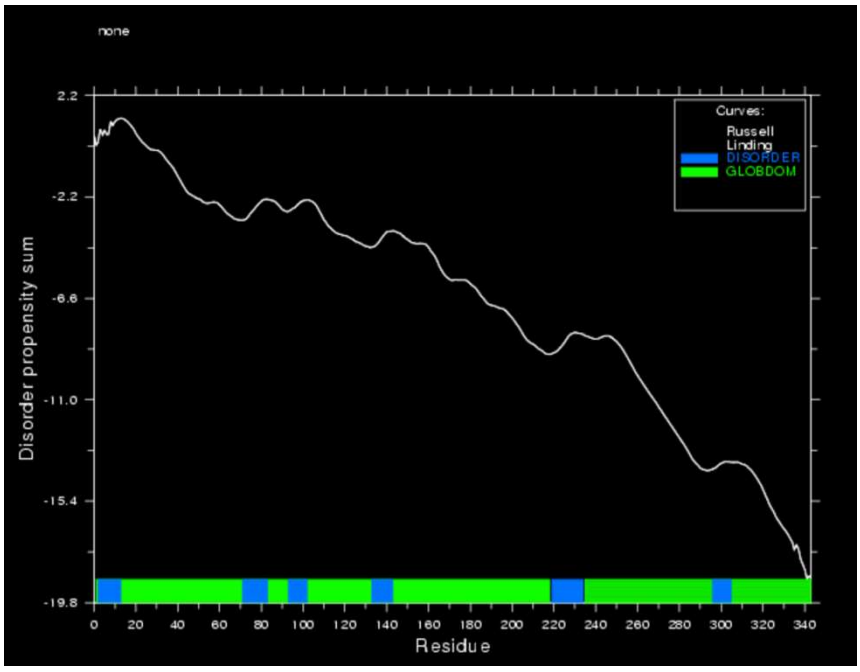
5.STRUCTURAL ANALYSIS

A.TARGETP

```
### targetp v1.1 prediction results ###################################
Number of query sequences:  1
Cleavage site predictions not included.
Using NON-PLANT networks.

Name                 Len          mTP     SP  other  Loc  RC
----------------------------------------------------------------------
gi_223590138_sp_A5DR  286         0.440  0.038  0.614  _    5
----------------------------------------------------------------------
cutoff                           0.000  0.000  0.000
```

The above result shows the transmembrane reigns in the PXR1.

B.GLOBPLOT



Disordered by Russell/Linding definition

```
>none_Disorder 2-13, 71-83, 93-102, 133-143, 219-234, 296-305
gISPADRHPR PICgrecnam efllprtein praltnamef llpinrelat edprteinmg lagtkvkqrf GLDPRNTSWS
NDKsrfghry leSMGWAPGK GLglvehatt thvkvsvkdd tvglgaklak rsGTDDLETD SSGlddfqri lgrlngrgre
vdealeqkrk dniingkwgm hfikgevlcs twdrksksnm lktaledese vnfksskkRR QSGSEPSRDS TSHAkrmrgd
eskkstrdqs kqerkekkik tekkekkekk ekkekkekke kkekkekkek kerdyGNRAS PVEPRkhdqi snvgrlsara
kyikqkrasv mdakalneif misk
```

Potential globular domains (GlobDoms) by Russell/Linding definition

```
>none_GlobDoms 1-218, 235-344
GISPADRHPR PICGRECNAM EFLLPRTEIN PRALTNAMEF LLPINRELAT EDPRTEINMG LAGTKVKQRF GLDPRNTSWS
NDKSRFGHRY LESMGWAPGK GLGLVEHATT THVKVSVKDD TVGLGAKLAK RSGTDDLETD SSGLDDFQRI LGRLNGRGRE
VDEALEQKRK DNIINGKWGM HFIKGEVLCS TWDRKSKSHM LKTALEDESE VNFKSSKKrr qsgsepsrds tshaKRMRGD
ESKKSTRDQS KQERKEKKIK TEKKEKKEKK EKKEKKEKKE KKEKKEKKEK KERDYGNRAS PVEPRKHDQI SNVGRLSARA
KYIKQKRASV MDAKALNEIF MISK
```

JOB-ID:	none_121427BWYRtgoLCBQAADgiisEAAAAL
Paramters:	propensities=Russell/Linding smooth=10 dy/dx_smooth=10
Disorder frames:	peak-frame=5 join-frame=4
Globularity frames:	peak-frame=74 join-frame=15
Name:	None
Description:	None
Plot title/ID:	None
Sequence length:	344
Download Results	smoothed raw dydx

The above result shows the disorders regions of PXR1 protein.

C.DOMAIN LINKER PREDICTION

Candidate Region:

SVM-All

Rank	Peak Value	Peak Position	Region	Sequence
1	2.009	165	148 - 247	EDESEVNFKSSKKRRQSGSEPSRDSTSHAKRMRGDE SKKSTRDQSKQERKEKKIKTEKKEKKEKKEKKEKKEKKE KKEKKEKKEKKERDYGNRASPVEPR
2	0.305	75	73 - 79	RSGTDDL

SVM-Long

Rank	Peak Value	Peak Position	Region	Sequence
1	1.406	245	205 - 247	KKEKKEKKEKKEKKEKKEKKEKKEKKEKKERDYGNR ASPVEPR
2	1.192	167	156 - 190	KSSKKRRQSGSEPSRDSTSHAKRMRGDESKKSTRD

SVM-Short

Rank	Peak Value	Peak Position	Region	Sequence
1	1.494	191	178 - 200	RMRGDESKKSTRDQSKQERKEKK
2	1.148	110	107 - 112	LEQKRK

SVM-Joint

Rank	Peak Value	Peak Position	Region	Sequence
1	1.406	245	205 - 247	KKEKKEKKEKKEKKEKKEKKEKKEKKEKKERDYGNRASPV EPR
2	1.192	167	156 - 190	KSSKKRRQSGSEPSRDSTSHAKRMRGDESKKSTRD

The above result shows the domain regions in the pxr1.

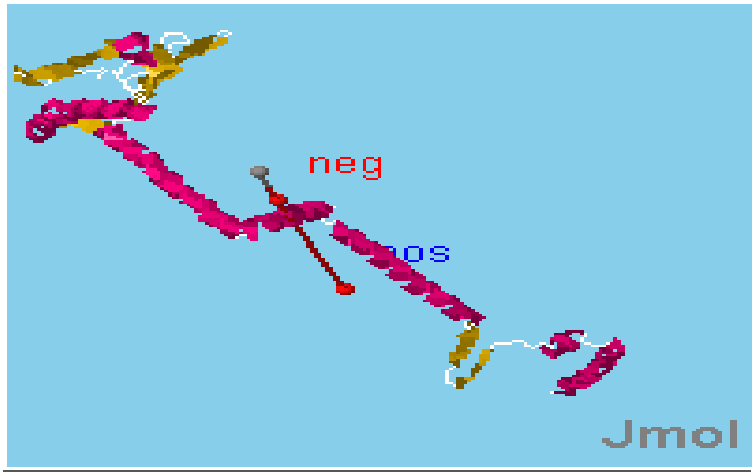
6. MOLECULAR MECHANICS –Dipole moment server

Dipole moment for

	No. of Chains=1		Elongated							
	No.Atoms	No.Res.	R_M	Pos.Res.	Neg.Res.	Charge	Dipole	Quadrapole	Crg./Nat.	Dip./Nat.
Value	1860.	230.	844.91	67.	42.	25.	2685.	73779.	0.0134	1.4437
No.Dev.Units	0.08	0.03	3.87	2.53	0.71	3.69	5.13	21.36	2.60	3.80

Dipole vector (in atomic units): -147.08 -122.68 -525.23

Mass Moments vector: 604.34 732.18 2350.23



The above results show the dipole interaction of the PXR1 protein

CONCLUSION

Zellweger spectrum disorders are a group of rare, genetic, multisystem disorders that were once thought to be separate entities. These disorders are now classified as different expressions (variants) of one disease process [8]. Collectively, they form a spectrum or continuum of disease. Zellweger syndrome is the most severe form; neonatal adrenoleukodystrophy is the intermediate form; and infantile Refsum [9]. NCBI is used for the gene and protein sequence retrieval which is responsible for Zellweger syndrome. Functional unit of PXR1 is identified using AMIGO. From the clustal w, evolutionary relationship of PXR1 protein is viewed. Through the dipole movement server, the molecular mechanics properties of PXR1 protein are revealed. A comprehensive study of gene may be further used in research for discovering a drug to prevent the molecular cause of Disease [10].

REFERENCES

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