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Protein Designing Studies and Biophysical Characterization of Gaucher Disease

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Abstract
Gaucher disease a series of disorders that is due to deficient activity of the enzyme glucocerebrosidase, which leads to accumulation of glucocerebroside in tissues of the body. The five types of Gaucher disease encompass a continuum of clinical findings from a lethal form that occurs before or just after birth to a form so mild that it may not be diagnosed until old age. All types of Gaucher disease are inherited in an autosomal recessive manner. The *GBA* gene provides instructions for making an enzyme called beta-glucocerebrosidase. This enzyme is active in lysosomes, which are structures inside cells that act as recycling centers. Lysosomes use digestive enzymes to break down toxic substances, digest bacteria that invade the cell, and recycle worn-out cell components. Glucocerebroside is a component of the membrane that surrounds cells. It gets broken down by beta-glucocerebrosidase when cells die, and the components are reused as new cells are formed. The sequence of glucosidase beta acid (GBA) retrieved from National Centre for Biotechnology Information in fasta format. The sequence analysis of glucosidase beta acid (GBA) were carried out by using bioinformatics tools like Protparam, Radar, Smart tools and structural designing of glucosidase beta acid were carried out by using CPH server. Further studies are required to investigate the glucosidase beta acid (GBA) of for potential pharmacological properties.

Keywords
Gaucher disease, *GBA* gene, Protparam, Radar, Smart, CPH server.

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INTRODUCTION
Gaucher disease (GD) encompasses a continuum of clinical findings from a perinatal lethal disorder to an asymptomatic type. The identification of three major clinical types (1, 2, and 3) and two other subtypes (perinatal-lethal and cardiovascular) is useful in determining prognosis and management.

GD type 1 is characterized by the presence of clinical or radiographic evidence of bone disease (osteopenia, focal lytic or sclerotic lesions, and osteonecrosis), hepatosplenomegaly, anemia and thrombocytopenia, lung disease, and the absence of primary central nervous system disease.

GD types 2 and 3 are characterized by the presence of primary neurologic disease; in the past, they were distinguished by age of onset and rate of disease progression, but these distinctions are not absolute.

- Disease with onset before age two years, limited psychomotor development, and a rapidly progressive course with death by age two to four years is classified as GD type 2.
- Individuals with GD type 3 may have onset before age two years, but often have a more slowly progressive course, with survival into the third or fourth decade.

The *perinatal-lethal form* is associated with ichthyosiform or collodion skin abnormalities or with

nonimmune hydrops fetalis. The *cardiovascular form* is characterized by calcification of the aortic and mitral valves, mild splenomegaly, corneal opacities, and supranuclear ophthalmoplegia. Cardiopulmonary complications have been described with all the clinical subtypes, although varying in frequency and severity.

METHODOLOGY

Target Protein of Glucosidase Beta Acid (GBA) sequence were retrieved from NCBI data base.The retrieved sequences is submitted to tha following server and tools,for protein prolifing and functional annotation.The retrieved sequence is submitted to the protparam tool and radar tool,for the identification of primary sequence analysis in glucosidase beta acid (GBA).The retrieved sequence is submitted to thesopma , Smart, and scan prosite tool for the identification of secondary structural analysis in glucosidase beta acid (GBA).The retrieved protein sequence was applied into CPH server in order to predict 3D dimensional structure of glucosidase beta acid (GBA).The modeled protein 3D structure was viewed with the help of advanced visualization molecular software called Jmol in order to identify the structural region and classify the entire structure of 3D element. The retrived sequence is submitted to dipole movement server tool, for tha biophysical characterization of glucosidase beta acid (GBA).The retrived sequence is submitted to the ANNIE tool,for the identification of motif in glucosidase beta acid(GBA).The retrieved sequence is submitted to the CAST-P server,for the identifications of functional units in glucosidase beta acid (GBA).

RESULTS AND DISCUSSION

1. GENE SELECTION:

NCBI:

The gene sequences are collected from using NCBI data base. Among the collected gene sequence.DNA polymerase subunit gamma-1 [Homo sapiens] were selected for further analysis.

A. PROTEIN SEQUENCE:

>NP_001119603.1 DNA polymerase subunit gamma-1 [Homo sapiens]

MSRLLWRKVAGATVGPGPVPAPGRWVSSSVPASDPSDG
QRRRQQQQQQQQQQQQPQQPQVLSSEGGQLR
HNPLDIQMLSRGLHEQIFGQGGEMPGEAAVRRSVEHLQK
HGLWGQPAVPLPDVELRLPPLYGDNLDQHFR
LLAQKQSLPYLEAANLLLQAQLPPKPPAWAWAEGWTRYG
PEGEAVPVAIPEERALVFDVEVCLAEGTCPT
LAVAISPSAWYSWCSQRLVEERYSWTSQLSPADLIPLEVPT
GASSPTQRDWQEQLVVGHNVSFDRAHIRE
QYLIQGSRMRFLDTMSMHMAISGLSSFQRSLWIAAKQGK
HKVQPPTKQGQKSQRKARRGPAISSWDWLDI
SSVNSLAEVHRLYVGGPPLEKEPRELFVKGTMKDIRENFQD
LMQYCAQDVWATHEVFQQQLPLFLERCPH
PVTLAGMLEMGVSYLPVNQNWERYLAEAQGTYEELQREM
KKSLMDLANDACQLLSGERYKEDPWLWDLEW
DLQEFKQKKAKKVKKEPATASKLPIEGAGAPGDPMDQEDL
GPCSEEEEFQQDVMARACLQKLKGTTELLP
KRPQHLPGHPGWYRKLCPRLDDPAWTPGPSLLSLQMRVT
PKLMALTWDGFPLHYSERHGWGYLVPGRRDN
LAKLPTGTTLESAGVVCPYRAIESLYRKHCLEQGKQQLMPQ
EAGLAEEFLLTDNSAIWQTVEELDYLEVE
AEAKMENLRAAVPGQPLALTARGGPKDTQPSYHHGNGPY
NDVDIPGCWFFKLPHKDGNSCNVGSPFAKDF
LPKMEDGTLQAGPGGASGPRALEINKMISFWRNAHKRISS
QMVVWLPRSALPRAVIRHPDYDEEGLYGAI
LPQVVTAGTITRRAVEPTWLTASNARPDRVGSELKAMVQA
PPGYTLVGADVDSQELWIAAVLGDAHFAGM
HGCTAFGWMTLQGRKSRGTDLHSKTATTVGISREHAKIFN
YGRIYGAGQPFAERLLMQFNHRLTQQEAAE
KAQQMYAATKGLRWYRLSDEGEWLVRELNLPVDRTEGG
WISLQDLRKVQRETARKSQWKKWEVVAERAWK
GGTESEMFNKLESIATSDIPRTPVLGCCISRALEPSAVQEEF
MTSRVNWVVQSSAVDYLHLMLVAMKWLF
EEFAIDGRFCISIHDEVRYLVREEDRYRAALALQITNLLTRCM
FAYKLGLNDLPQSVAFFSAVDIDRCLR
KEVTMDCKTPSNPTGMERRYGIPQGEALDIYQIIELTKGSLE
KRSQPGP

B. NUCLEOTIDE SEQUENCE:

>NM_001126131.1:271-3990 Homo sapiens DNA polymerase gamma, catalytic subunit (POLG), transcript variant 2, mRNA

ATGAGCCGCCTGCTCTGGAGGAAGGTGGCCGGCGCCAC
CGTCGGGCCAGGGCCGGTTCCAGCTCCGGGGC
GCTGGGTCTCCAGCTCCGTCCCCGCGTCCGACCCCAGCG
ACGGGCAGCGGCGGCGGCAGCAGCAGCAGCA
GCAGCAGCAGCAGCAGCAACAGCAGCCTCAGCAGCCGC
AAGTGCTATCCTCGGAGGGCGGGCAGCTGCGG
CACAACCCATTGGACATCCAGATGCTCTCGAGAGGGCTG
CACGAGCAAATCTTCGGGCAAGGAGGGGAGA
TGCCTGGCGAGGCCGCGGTGCGCCGCAGCGTCGAGCAC
CTGCAGAAGCACGGGCTCTGGGGGCAGCCAGC
CGTGCCCTTGCCCGACGTGGAGCTGCGCCTGCCGCCCCT
CTACGGGGACAACCTGGACCAGCACTTCCGC
CTCCTGGCCCAGAAGCAGAGCCTGCCCTACCTGGAGGCG
GCCAACTTGCTGTTGCAGGCCCAGCTGCCCC
CGAAGCCCCCGGCTTGGGCCTGGGCGGAGGGCTGGACC
CGGTACGGCCCCGAGGGGGAGGCCGTACCCGT
GGCCATCCCCGAGGAGCGGGCCCTGGTGTTCGACGTGG
AGGTCTGCTTGGCAGAGGGAACTTGCCCCACA
TTGGCGGTGGCCATATCCCCCTCGGCCTGGTATTCCTGGT
GCAGCCAGCGGCTGGTGGAAGAGCGTTACT
CTTGGACCAGCCAGCTGTCGCCGGCTGACCTCATCCCCCT
GGAGGTCCCTACTGGTGCCAGCAGCCCCAC
CCAGAGAGACTGGCAGGAGCAGTTAGTGGTGGGGCACA
ATGTTTCCTTTGACCGAGCTCATATCAGGGAG
CAGTACCTGATCCAGGGTTCCCGCATGCGTTTCCTGGACA
CCATGAGCATGCACATGGCCATCTCAGGGC
TAAGCAGCTTCCAGCGCAGTCTGTGGATAGCAGCCAAGC
AGGGCAAACACAAGGTCCAGCCCCCCACAAA

GCAAGGCCAGAAGTCCCAGAGGAAAGCCAGAAGAGGCC
CAGCGATCTCATCCTGGGACTGGCTGGACATC
AGCAGTGTCAACAGTCTGGCAGAGGTGCACAGACTTTAT
GTAGGGGGGCCTCCCTTAGAGAAGGAGCCTC
GAGAACTGTTTGTGAAGGGCACCATGAAGGACATTCGTG
AGAACTTCCAGGACCTGATGCAGTACTGTGC
CCAGGACGTGTGGGCCACCCATGAGGTTTTCCAGCAGCA
GCTACCGCTCTTCTTGGAGAGGTGTCCCCAC
CCAGTGACTCTGGCCGGCATGCTGGAGATGGGTGTCTCC
TACCTGCCTGTCAACCAGAACTGGGAGCGTT
ACCTGGCAGAGGCACAGGGCACTTATGAGGAGCTCCAG
CGGGAGATGAAGAAGTCGTTGATGGATCTGGC
CAATGATGCCTGCCAGCTGCTCTCAGGAGAGAGGTACAA
AGAAGACCCCTGGCTCTGGGACCTGGAGTGG
GACCTGCAAGAATTTAAGCAGAAGAAAGCTAAGAAGGT
GAAGAAGGAACCAGCCACAGCCAGCAAGTTGC
CCATCGAGGGGGCTGGGGCCCCTGGTGATCCCATGGATC
AGGAAGACCTCGGCCCCTGCAGTGAGGAGGA
GGAGTTTCAACAAGATGTCATGGCCCGCGCCTGCTTGCA
GAAGCTGAAGGGGACCACAGAGCTCCTGCCC
AAGCGGCCCCAGCACCTTCCTGGACACCCTGGATGGTAC
CGGAAGCTCTGCCCCCGGCTAGACGACCCTG
CATGGACCCCGGGCCCCAGCCTCCTCAGCCTGCAGATGC
GGGTCACACCTAAACTCATGGCACTTACCTG
GGATGGCTTCCCTCTGCACTACTCAGAGCGTCATGGCTG
GGGCTACTTGGTGCCTGGGCGGCGGGACAAC
CTGGCCAAGCTGCCGACAGGTACCACCCTGGAGTCAGCT
GGGGTGGTCTGCCCCTACAGAGCCATCGAGT
CCCTGTACAGGAAGCACTGTCTCGAACAGGGGAAGCAG
CAGCTGATGCCCCAGGAGGCCGGCCTGGCGGA
GGAGTTCCTGCTCACTGACAATAGTGCCATATGGCAAAC
GGTAGAAGAACTGGATTACTTAGAAGTGGAG
GCTGAGGCCAAGATGGAGAACTTGCGAGCTGCAGTGCC
AGGTCAACCCCTAGCTCTGACTGCCCGTGGTG
GCCCCAAGGACACCCAGCCCAGCTATCACCATGGCAATG
GACCTTACAACGACGTGGACATCCCTGGCTG
CTGGTTTTTCAAGCTGCCTCACAAGGATGGTAATAGCTGT
AATGTGGGAAGCCCCTTTGCCAAGGACTTC
CTGCCCAAGATGGAGGATGGCACCCTGCAGGCTGGCCC
AGGAGGTGCCAGTGGGCCCCGTGCTCTGGAAA
TCAACAAAATGATTTCTTTCTGGAGGAACGCCCATAAAC
GTATCAGCTCCCAGATGGTGGTGTGGCTGCC
CAGGTCAGCTCTGCCCCGTGCTGTGATCAGGCACCCCGA
CTATGATGAGGAAGGCCTCTATGGGGCCATC
CTGCCCCAAGTGGTGACTGCCGGCACCATCACTCGCCGG
GCTGTGGAGCCCACATGGCTCACCGCCAGCA
ATGCCCGGCCTGACCGAGTAGGCAGTGAGTTGAAAGCC
ATGGTGCAGGCCCCACCTGGCTACACCCTTGT
GGGTGCTGATGTGGACTCCCAAGAGCTGTGGATTGCAGC
TGTGCTTGGAGACGCCCACTTTGCCGGCATG
CATGGCTGCACAGCCTTTGGGTGGATGACACTGCAGGGC
AGGAAGAGCAGGGGCACTGATCTACACAGTA
AGACAGCCACTACTGTGGGCATCAGCCGTGAGCATGCCA
AAATCTTCAACTACGGCCGCATCTATGGTGC
TGGGCAGCCCTTTGCTGAGCGCTTACTAATGCAGTTTAAC
CACCGGCTCACACAGCAGGAGGCAGCTGAG
AAGGCCCAGCAGATGTACGCTGCCACCAAGGGCCTCCGC
TGGTATCGGCTGTCGGATGAGGGCGAGTGGC
TGGTGAGGGAGTTGAACCTCCCAGTGGACAGGACTGAG
GGTGGCTGGATTTCCCTGCAGGATCTGCGCAA
GGTCCAGAGAGAAACTGCAAGGAAGTCACAGTGGAAGA
AGTGGGAGGTGGTTGCTGAACGGGCATGGAAG
GGGGGCACAGAGTCAGAAATGTTCAATAAGCTTGAGAG
CATTGCTACGTCTGACATACCACGTACCCCGG
TGCTGGGCTGCTGCATCAGCCGAGCCCTGGAGCCCTCGG
CTGTCCAGGAAGAGTTTATGACCAGCCGTGT
GAATTGGGTGGTACAGAGCTCTGCTGTTGACTACTTACA
CCTCATGCTTGTGGCCATGAAGTGGCTGTTT
GAAGAGTTTGCCATAGATGGGCGCTTCTGCATCAGCATC
CATGACGAGGTTCGCTACCTGGTGCGGGAGG
AGGACCGCTACCGCGCTGCCCTGGCCTTGCAGATCACCA
ACCTCTTGACCAGGTGCATGTTTGCCTACAA
GCTGGGTCTGAATGACTTGCCCCAGTCAGTCGCCTTTTTC
AGTGCAGTCGATATTGACCGGTGCCTCAGG
AAGGAAGTGACCATGGATTGTAAAACCCCTTCCAACCCA
ACTGGGATGGAAAGGAGATACGGGATTCCCC
AGGGTGAAGCGCTGGATATTTACCAGATAATTGAACTCA
CCAAAGGCTCCTTGGAAAAACGAAGCCAGCC
TGGACCATAG

The above results show the protein sequence of glucosidase beta acid (GBA).

2. PRIMARY ANALYSIS:

A. PROTPARAM:

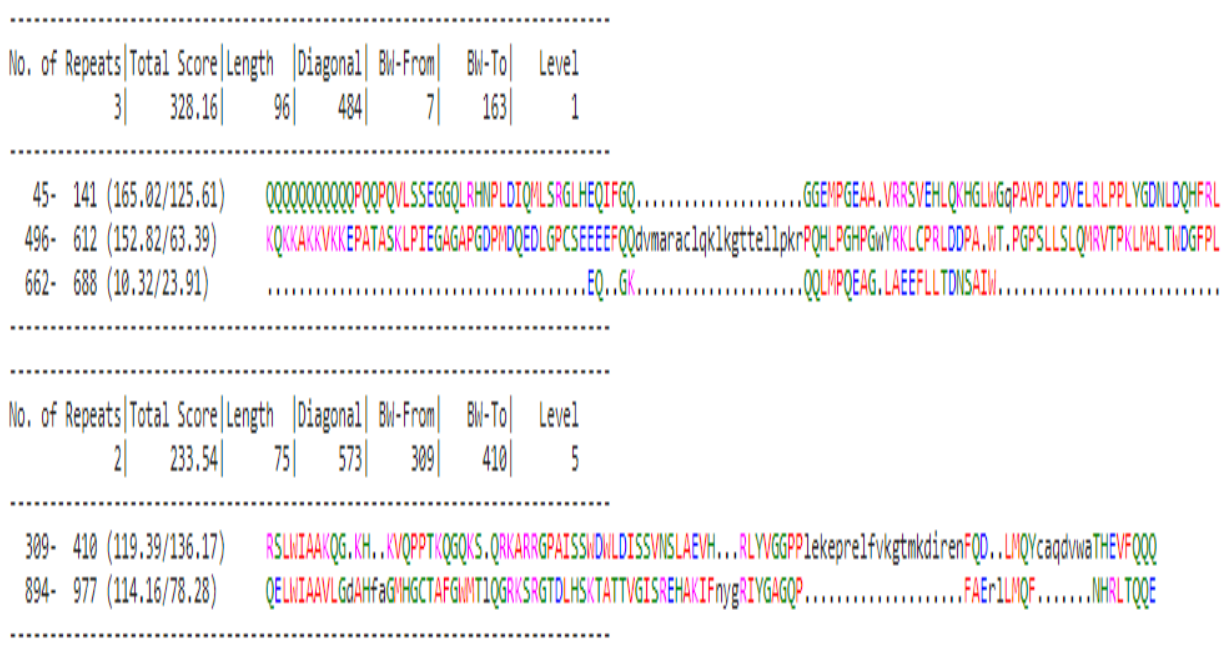
10	20	30	40	50	60
MSRLLWRKVA	GATVGPGPVP	APGRWVSSSV	PASDPSDGQR	RRQQQQQQQQ	QQQQQPQQPQ
70	80	90	100	110	120
VLSSEGGQLR	HNPLDIQMLS	RGLHEQIFGQ	GGEMPGEAAV	RRSVEHLQKH	GLWGQPAVPL
130	140	150	160	170	180
PDVELRLPPL	YGDNLDQHFR	LLAQKQSLPY	LEAANLLLQA	QLPPKPPAWA	WAEGWTRYGP
190	200	210	220	230	240
EGEAVPVAIP	EERALVFDVE	VCLAEGTCPT	LAVAISPSAW	YSWCSQRLVE	ERYSWTSQLS

250	260	270	280	290	300
PADLIPLEVP	TGASSPTQRD	WQEQLVVGHN	VSFDRAHIRE	QYLIQGSRMR	FLDTMSMHMA
310	320	330	340	350	360
ISGLSSFQRS	LWIAAKQGKH	KVQPPTKQGQ	KSQRKARRGP	AISSWDWLDI	SSVNSLAEVH
370	380	390	400	410	420
RLYVGGPPLE	KEPRELFVKG	TMKDIRENFQ	DLMQYCAQDV	WATHEVFQQQ	LPLFLERCPH
430	440	450	460	470	480
PVTLAGMLEM	GVSYLPVNQN	WERYLAEAQG	TYEELQREMK	KSLMDLANDA	CQLLSGERYK
490	500	510	520	530	540
EDPWLWDLEW	DLQEFKQKKA	KKVKKEPATA	SKLPIEGAGA	PGDPMDQEDL	GPCSEEEEFQ
550	560	570	580	590	600
QDVMARACLQ	KLKGTTELLP	KRPQHLPGHP	GWYRKLCPRL	DDPAWTPGPS	LLSLQMRVTP
610	620	630	640	650	660
KLMALTWDGF	PLHYSERHGW	GYLVPGRRDN	LAKLPTGTTL	ESAGVVCPYR	AIESLYRKHC
670	680	690	700	710	720
LEQGKQQLMP	QEAGLAEEFL	LTDNSAIWQT	VEELDYLEVE	AEAKMENLRA	AVPGQPLALT
730	740	750	760	770	780
ARGGPKDTQP	SYHHGNGPYN	DVDIPGCWFF	KLPHKDGNSC	NVGSPFAKDF	LPKMEDGTLQ
790	800	810	820	830	840
AGPGGASGPR	ALEINKMISF	WRNAHKRISS	QMVVWLPRSA	LPRAVIRHPD	YDEEGLYGAI
850	860	870	880	890	900
LPQVVTAGTI	TRRAVEPTWL	TASNARPDRV	GSELKAMVQA	PPGYTLVGAD	VDSQELWIAA
910	920	930	940	950	960
VLGDAHFAGM	HGCTAFGWMT	LQGRKSRGTD	LHSKTATTVG	ISREHAKIFN	YGRIYGAGQP
970	980	990	1000	1010	1020
FAERLLMQFN	HRLTQQEAAE	KAQQMYAATK	GLRWYRLSDE	GEWLVRELNL	PVDRTEGGWI
1030	1040	1050	1060	1070	1080
SLQDLRKVQR	ETARKSQWKK	WEVVAERAWK	GGTESEMFNK	LESIATSDIP	RTPVLGCCIS
1090	1100	1110	1120	1130	1140
RALEPSAVQE	EFMTSRVNWV	VQSSAVDYLH	LMLVAMKWLF	EEFAIDGRFC	ISIHDEVRYL
1150	1160	1170	1180	1190	1200
VREEDRYRAA	LALQITNLLT	RCMFAYKLGL	NDLPQSVAFF	SAVDIDRCLR	KEVTMDCKTP

1210 1220 1230
SNPTGMERRY GIPQGEALDI YQIIELTKGS LEKRSQPGP

The above results shows the primary sequence analysis of glucosidase beta acid(GBA).

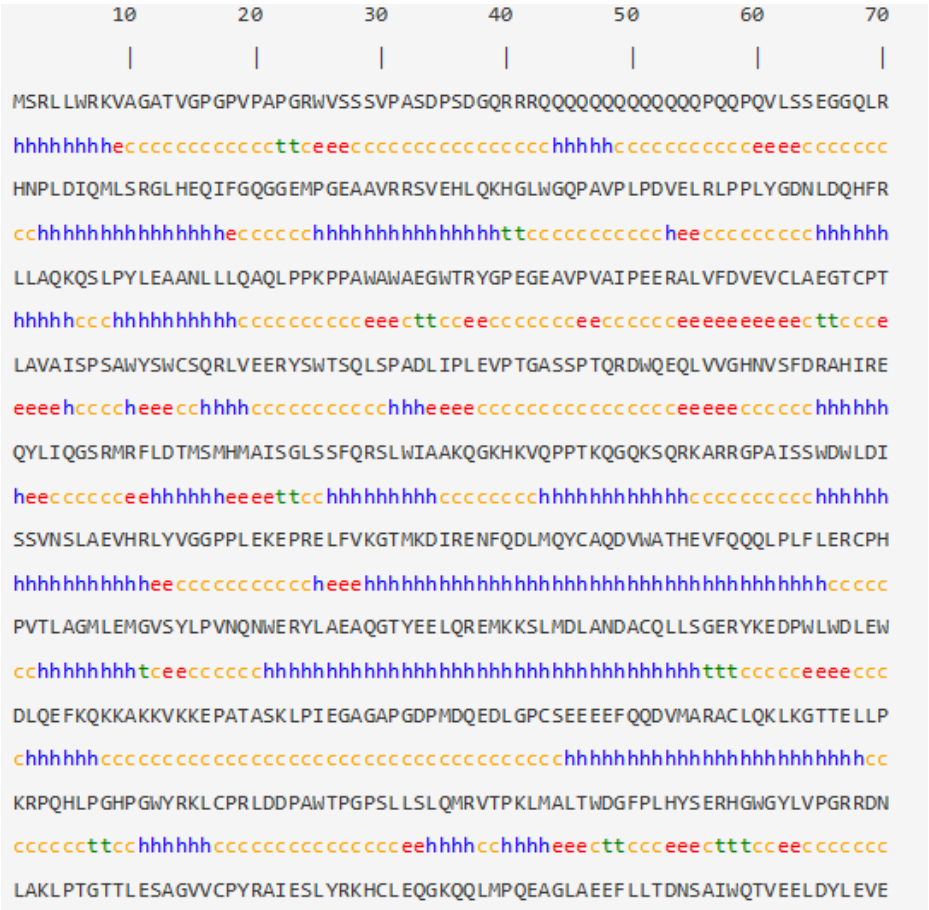
B. RADAR :



The above results show the motif region in glucosidase beta acid (GBA) here hydrophobicity of the amino acids is indicating in different colour.

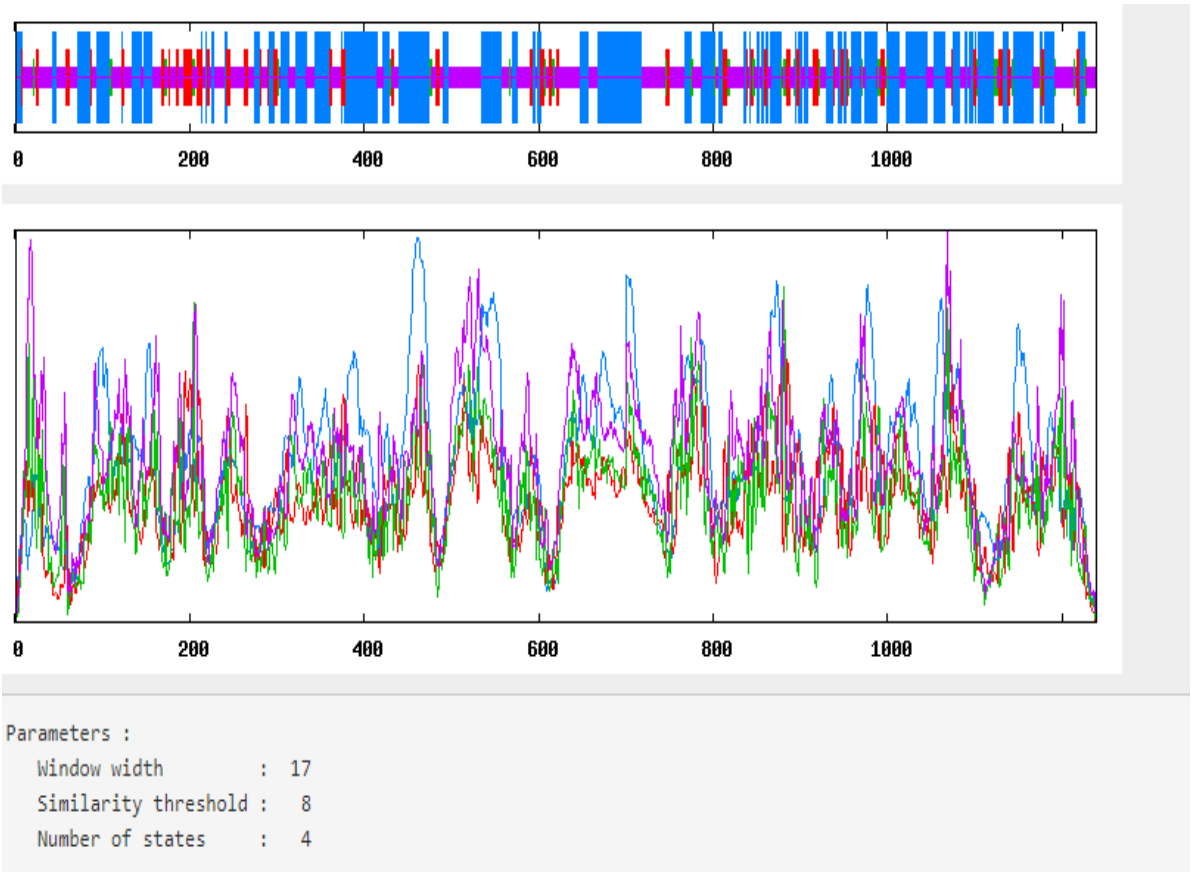
3. SECONDARY ANALYSIS:

A. SOPMA



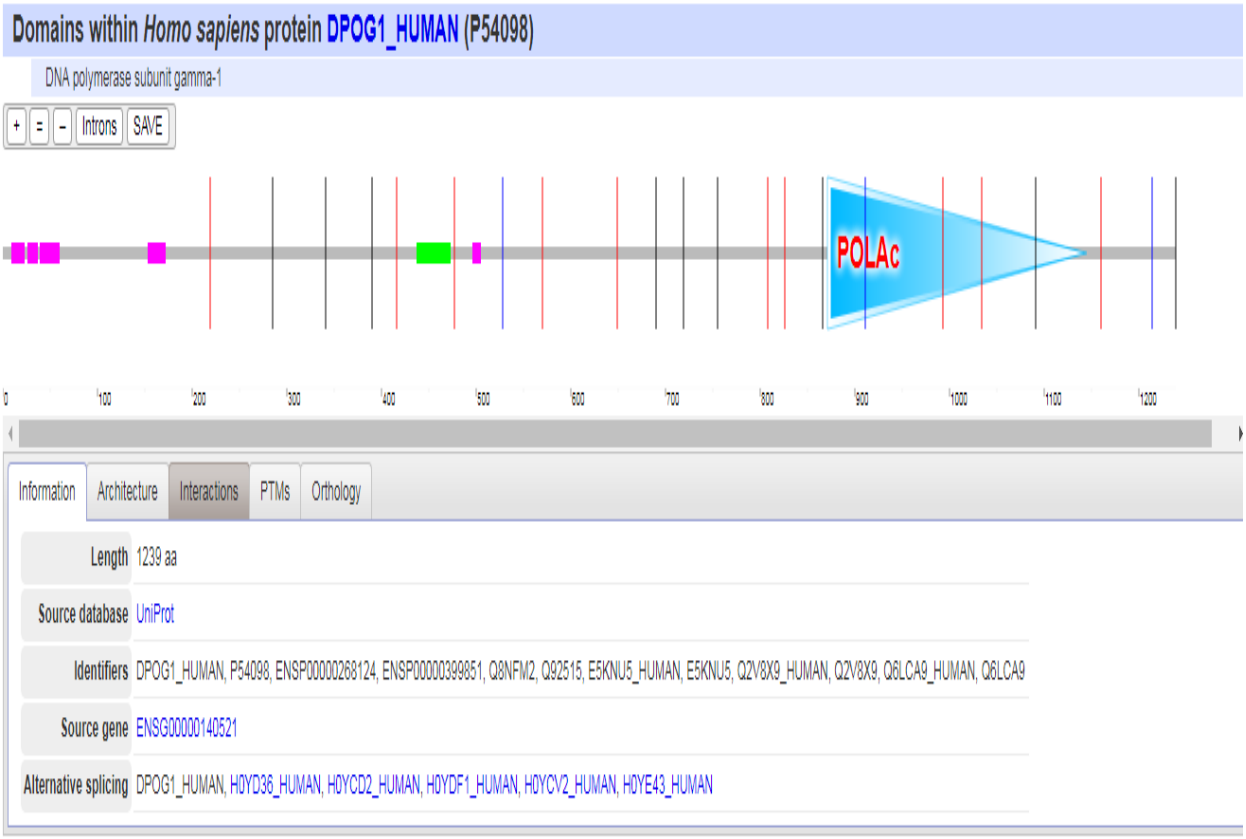
```
ccccccccccccccccchhhhhhhhhhcccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
AEAKMENLRAAVPGQPLALTARGGPKDTQPSYHHGNGPYNDVDIPGCWFFKLPHKDGNSCNVGSPFAKDF
hhhhhhhhhhhhhhhhhhccccccccccccccccccccccccccteeeeeccccccccccccccchhh
LPKMEDGTLQAGPGGASGPRALEINKMISFWRNAHKRISSQMVVWLPRSALPRAVIRHPDYDEEGLYGAI
hhhhhttccccccccchhhhhhhhhhhhhhhhtcccchhhhheeeeeecttcccccccccccccccchhee
LPQVVTAGTITRRAVEPTWLTASNARPDRVGSELKAMVQAPPGYTLVGADVDSQELWIAAVLGDAHFAGM
ccheeettcccchhhcchhheehhcccchhhhhhhhhhhhhtccttceeeeccccchheehhhhcccchhhhc
HGCTAFGWMTLQGRKSRGTDLHSKTATTVGISREHAKIFNYGRIYGAGQPFAERLLMQFNHRLTQQEAAE
ccccceeeeeettcccccchhhhhhhheecccchhheeehhheettcchhhhhhhhhcttcchhhhhh
KAQQMYAATKGLRWYRLSDEGEWLVRELNLPVDRTEGGWISLQDLRKVQRETARKSQWKKWEVVAERAWK
hhhhhhhhcttcceeeecchhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhhhhhhcccccc
GGTESEMFNKLESIATSDIPRTPVLGCCISRALEPSAVQEEFMTSRVNWVVQSSAVDYLHLMLVAMKWLF
cccchhhhhhhhhhhhhcccccccceehhhhhhhhhccccccchhhcchhhheeehcthhhhhhhhhhhhhhhh
EEFAIDGRFCISIHDEVRYLVREEDRYRAALALQITNLLTRCMFAYKLGLNDLPQSVAFFSAVDIDRCLR
hhttttcceeeehhhhhheeecttthhhhhhhhhhhhhhhhhhhhhhhcccccccthheeehhhhhhhhhh
KEVTMDCKTPSNPTGMERRYGIPQGEALDIYQIIELTKGSLEKRSQPGP
Htccccccccccccccccccccttcceehhhhhhhttcccccccccc
```

```
Sequence length :  1239
SOPMA :
   Alpha helix     (Hh) :   543 is  43.83%
   3₁₀ helix       (Gg) :     0 is   0.00%
   Pi helix        (Ii) :     0 is   0.00%
   Beta bridge     (Bb) :     0 is   0.00%
   Extended strand (Ee) :   131 is  10.57%
   Beta turn       (Tt) :    55 is   4.44%
   Bend region     (Ss) :     0 is   0.00%
   Random coil     (Cc) :   510 is  41.16%
   Ambiguous states (?)  :     0 is   0.00%
   Other states         :     0 is   0.00%
```



The above results shows the secondary sequence analysis of glucosidase beta acid(GBA).

B.SMART:



Confidently predicted domains, repeats, motifs and features:

Name	Start ▲	End	E-value
low complexity	9	23	N/A
low complexity	26	37	N/A
low complexity	39	60	N/A
low complexity	153	172	N/A
coiled coil	437	473	N/A
low complexity	496	505	N/A
POLAc	871	1145	1.72e-113

Click on a row to highlight the feature in the diagram above. Click the feature name for more information.

The above results show the identification and annotation of genetically mobile domains and the analysis of domain architectures in glucosidase beta acid (GBA). protein.

4.MOTIF SEARCH:

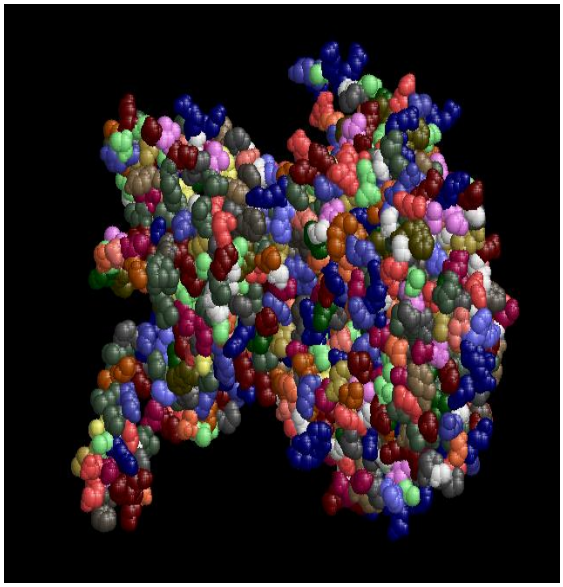
A. SCANEPROSITE:

MSRLLWRKVAGATVGPGPVPAPGRWVSSSVPASDPSDGQRRRQQQQQQQQQQQQPQQPQVLSSEG
GQLRHNPLDIQMLSRGLHEQIFGQGGEMPGEAAVRRSVEHLQKHGLWGQPAVPLPDVELRLPPLYG
DNLDQHFRLLAQKQSLPYLEAANLLLQAQLPPKPPAWAWAEGWTRYGPEGEAVPVAIPEERALVFD
VEVCLAEGTCPTLAVAISPSAWYSWCSQRLVEERYSWTSQLSPADLIPLEVPTGASSPTQRDWQEQ
LVVGHNVSFDRAHIREQYLIQGSRMRFLDTMSMHMAISGLSSFQRSLWIAAKQGKHKVQPPTKQGQ
KSQRKARRGPAISSWDWLDISSVNSLAEVHRLYVGGPPLEKEPRELFVKGTMKDIRENFQDLMQYC
AQDVWATHEVFQQQLPLFLERCPHPVTLAGMLEMGVSYLPVNQNWERYLAEAQGTYEELQREMKKS
LMDLANDACQLLSGERYKEDPWLWDLEWDLQEFKQKKAKKVKKEPATASKLPIEGAGAPGDPMDQE
DLGPCSEEEEFQQDVMARACLQKLKGTTELLPKRPQHLPGHPGWYRKLCPRLDDPAWTPGPSLLSL
QMRVTPKLMALTWDGFPLHYSERHGWGYLVPGRRDNLAKLPTGTTLESAGVVCPYRAIESLYRKHC
LEQGKQQLMPQEAGLAEEFLLTDNSAIWQTVEELDYLEVEAEAKMENLRAAVPGQPLALTARGGPK
DTQPSYHHGNGPYNDVDIPGCWFFKLPHKDGNSCNVGSPFAKDFLPKMEDGTLQAGPGGASGPRAL
EINKMISFWRNAHKRISSQMVVWLPRSALPRAVIRHPDYDEEGLYGAILPQVVTAGTITRRAVEPT
WLTASNARPDRVGSELKAMVQAPPGYTLVGADVDSQELWIAAVLGDAHFAGMHGCTAFGWMTLQGR
KSRGTDLHSKTATTVGISREHAKIFNYGRIYGAGQPFAERLLMQFNHRLTQQEAAEKAQQMYAATK
GLRWYRLSDEGEWLVRELNLPVDRTEGGWISLQDLRKVQRETARKSQWKKWEVVAERAWKGGTESE
MFNKLESIATSDIPRTPVLGCCISRALEPSAVQEEFMTSRVNWVVQSSAVDYLHLMLVAMKWLFEE
FAIDGRFCISIHDEVRYLVREEDRYRAALALQITNLLTRCMFAYKLGLNDLPQSVAFFSAVDIDRC
LRKEVTMDCKTPSNPTGMERRYGIPQGEALDIYQIIELTKGSLEKRSQPGP

The above Results the shows the motif region present in the GBA protein, yellow colour indicates motif region and green colour indicates domain regions and the position start 143 ends with 162.

5.HOMOLOGUS MODELING:

CPH MODELING



The above results show the CPH modeling server:

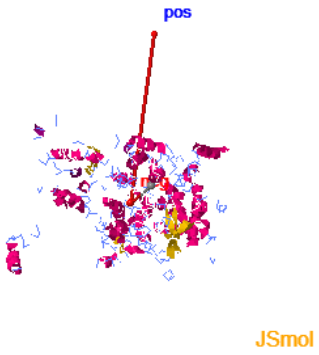
- Pink colour indicates helix.
- Yellow colour indicates sheets.
- Blue colour indicates turns.
- White colour indicates coil regin in glucosidase beta acid (GBA).

6.BIOPHYSICAL CHARACTERISATION:
DIPOLE MOVEMENT SERVER

Dipole moment for

	No. of Chains=1		Spherical							
	No.Atoms	No.Res.	R_M	Pos.Res.	Neg.Res.	Charge	Dipole	Quadrapole	Crg./Nat.	Dip./Nat.
Value	9293.	1170.	1137.33	132.	145.	-12.	2804.	11272.	-0.0013	0.3018
No.Dev.Units	6.41	6.33	5.81	6.40	5.93	-1.14	5.41	2.64	0.02	-0.24

Dipole vector (in atomic units): 61.54 434.93 -384.64
Mass Moments vector: 2321.97 1797.00 1738.08
Open a larger Jmol window.



The above results shows the dipole and mass moment vectors in, here red and grey-green line shows biophysical nature of proteins, respectively.

CONCLUSION

Gaucher disease is a rare, inherited disorder. It is a type of lipid metabolism disorder. If you have it, you do not have enough of an enzyme called glucocerebrosidase. This causes too much of a fatty substance to build up in your spleen, liver, lungs, bones and, sometimes, your brain. This prevents these organs from working properly.Glucocerebrosidase enzyme activity is stimulated by interaction with the lipid phospatidylserine and the protein saposin C. Structural predictions (based on hydrophobic cluster analysis) indicate that the glutamine residues 235 and 340 play key roles in the active site of human glucocerebrosidase. Glucocerebrosidase is a lysosomal membrane-associated glycoprotein. Abnormal gene product. *GBA* pathogenic variants result in mRNA instability and/or loss of protein, or in an enzyme with altered activity and/or conformation. The protein sequence of glucosidase beta acid was retrieved from NCBI data base. The protein modeling and characterization of were analyzed using in silico bioinformatics tools. The present's studies revealed a number of interesting facts findings. Hence, we conclude that in future. The results should be used in drug designing process.

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