A DNA-binding protein GATA1 with a biological unit FOG1 Zinc finger Protein molecule is synergistic to the region of the X chromosome which occurred at a 'exome' splice site X-linked involving the GATA-type zinc finger domain.

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The human ERYF1 gene (summary) NF-E1 DNA-binding protein GATA1, locus Xp11.23 [§§; †] containing 2 'finger' motifs referred to as ERYF1 of an erythroid-specific gene. The cDNA for the human ERYF1 gene is almost identical to that of chicken and mouse GATA1 gene consisting of 2 zinc finger' type motifs its activator domain contains the binding sites for protein GATA1 and the CACCC (HS2)^ region. FOG is specific to this complex corresponding cDNA and interacts with element in the beta-globin IVS2 promoter from hemoglobin protein subunit promoters (alpha-chain gene‡, gamma, epsilon^ and (embryonic), a switch from fetal to adult haemoglobin -or- relative to the T to C substitution of fetal hemoglobin (HPFH), implications for fetal hemoglobin - HbF``) distinct for erythroid (INHBA) and megakaryocyte differentiation, in vertabrate though, the N- and C-terminal thirds of the human protein. Friend of GATA-1, FOG1; ZFPM1, zinc finger protein region a coregulator of the GATA1 associations facilitates a chromatin locus control region-(LCR) modifying proximity fetal to adult (gamma) to beta globin including the erythroid (EKLF krüpple-like) factor DNAse1^ histone hypersensative site (HS)^ locus (LCR) GATA1 establishes, facilitates interactions with immunoprecipitation, cross-regulatory roles reduced histone, acetylation and antagonism (EKLF-FlI-1) mechanisms. PU.1 - of the Ets family is 'synergistic' to the major basic protein, (MBP) handles bistability in the erythroid-'myeloid switch « directed by PU.1,' influenced DNA binding and is involved with MZF-1 (myeloid zinc finger 1), it interacts with the 'C-terminal zinc finger « (CF)' of GATA1. A bipotential function in multiple contexts (erythroid versus megakaryocytic myeloid cells, GATA1 switches myeloid cell fate into eosinophils)° as two multi-protein complexes when segregated into two types (factor P-TEFb) one of the characteristics of (TAL-1, T-cell acute-) leukemic (SCL) stem cells is both types in circulating blood, for both the downregulation of GATA-1 and with the upregulation of GATA-2 (3q21)° that CD34^{5_P} has the transcription capacity observed in immature hematopoietic progenitor stem cells, specific regions of each (Sequencing of FOG1 with GATA1 and GATA2), requires intact DNA-binding domains. The C-terminal zinc finger (CF) basic tail shares, in an antagonistic fashion 'mutations' in exon 2‡ (-GATA1s is a shorter GATA1 isoform (sf) found in DS (Down syndrome) a transient leukemia (TL)-AMKL) that lacks the transactivation'" domain, in cis-acting GATA element, identification requires intact long forms (lf) of NF-E1 DNA-binding domain. Two novel zinc-finger domains demonstrate that the NFE1 gene cDNA-binding protein is assigned the human locus located in Xp11.23, required for normal megakaryocytic and erythroid development. A mutation in the FOG1-GATA1 N-terminal zinc finger (N-finger of leukemic cell (Igs)-immunoglobulins) or lacking the N-terminal activation the binding of Fog1 and the N-finger in the DNA face of Fog1, with non X-linked associations (16q22-24) if different clinical entities linking to X-linked (X is any amino acid, substitution in the DNA-binding (Nf) region) thrombocytopenia in males-(XLTT*'-GATA1) with anemia low platelet levels traces discernable steps as embryos with a *defect* in forming erythroid burst-forming units *BFU-E* ☞ (*summary - of all DNA that is transcribed which occurred at a exome splice site*), to Minimal residual disease MRD - (cancer, "preleukemia" - myeloproliferative disorder (TMD), myeloid leukaemia-AML, SCL° and megakaryocytic AMKL) the GATA1-HS2-modified vector allowed remission in blood component and heme (Protoporphyrinogen) at the seventh GATA site in exon 1*'/intron-7° as a cofactor involving 6 non-coding exons and transactivation by USF1 and GATA1. A DNA Cytosine mechanism ara-c (Arabinofuranosylcytosine) short (sf) and (lf) long forms is used to kill these megakaryocytic cancer cells; clarifies that GATA-1

controls genes that manipulate the cell cycle and apoptotic cell death underlying normal (PI3K) and pathologic (PU.1) erythropoiesis - 'differentiation' is (FKBP12) lacking basal expression'" in contrast to Bcl when Bcl-X(L) is cleaved by caspases. Anti-apoptotic Hsp70 protects GATA-1 during the switching[a] of the erythroleukemia[sp] cells that fail to complete maturation, proteolysis undergoing cell death in both the megakaryocytic and erythroid cells, established that phospholipase C (PLC)[a] is involved in the signalling pathway (PI3K)/Akt equally expressed 'as' a probable negative FOG regulator, interacts with the PU.1 related Ets domain of glycoprotein (GP)(1) VI*' by expressing thrombopoietin activation of platelets in megakaryocytic cell lines, expressing both Fli-1 and GATA-1. A weak loss of aspartate in the amino-N-terminal zinc finger (Nf) loop GATA1's three base substitution mutations results in incomplete megakaryocyte/platelet maturation as assessed by the DNA demethylating agent 5-azacytidine, activity in the presence of ara-c which occurred at a *exome* splice site. GATA1 appears to interact with RNA-mediated basal expression against these pathways, associated protein or mammalian targets clarified that the basal transcription apparatus with transcription factors`` appears to interact with an HS2 region mutated in its GATA motif -GATA1s a shorter GATA1 isoform.

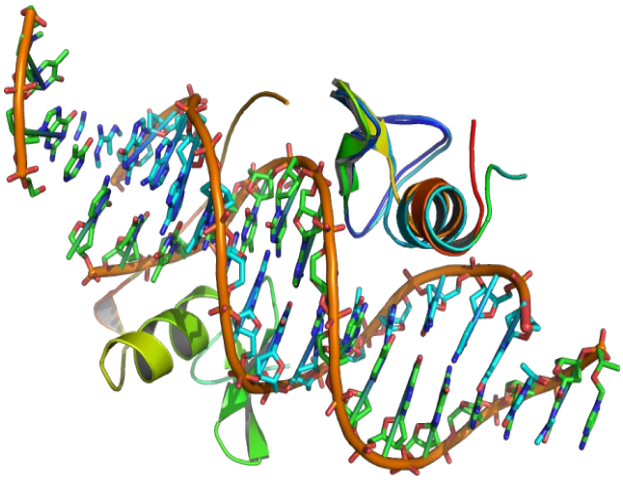


Figure 1: PDB 1y0j-a (MMDB ID: 31470; Mus musculus A). superimposed on -3vd6 4 Angstrons ogf DNA, six finger Znf DNA potential ('X is any amino acid, substitution') to co-ordinate C2H2 znf-1y0j-B (Protein chain B, MMDB ID: 31470), and the original structure of DNA_GATA1_HUMAN PDB: 1Y0J_uniprot/P15976 ProteinModelPortal P15976. / PDB: _3vd6; Names: GATA1 :ERYF1, GF1 with the consensus seqence [AT]GATA[AG] upper left DNA fragment seen in SPNA1 DNA binding an essential determinant of specific GATA 1 Fig.2 binding, wraps around into the minor groove seen as the lower RNA representing PDB 1GAT in this single PDB 3VD6 rendering with PDB: 1YOJ- element-A DNA-binding protein GATA1 RNA Mus musculus eg. the red tail is the assumed Adjacent GATA DNA binding of PDB: 3DFV (Structure|id=PIRSF003027)

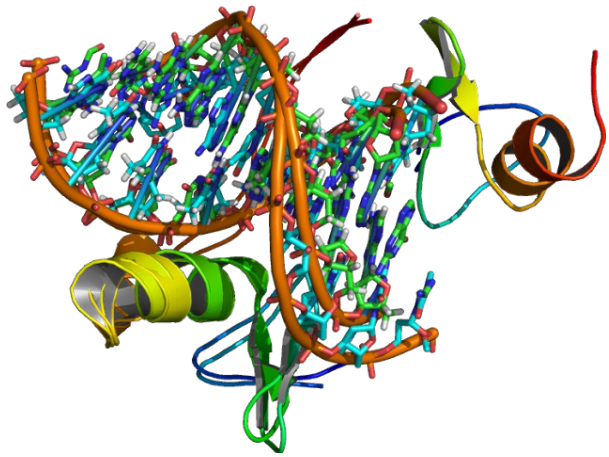


Figure 2: 4 Angstroms of PDB 1GAT in this 4 Angstrom PDB 3VD6 rendering of 1YOJ-A RNA, modifyed to complete Fig.1. both are manually defined selected to provide The two zinc fingers functionality that contains 2 GATA-type zinc fingers (See; Figure 3: FOG1_B Zinc finger Protein (MMDB ID: 31470) has an absence of the PDB: 1YOJ- element- A DNA-binding protein GATA1 RNA thereby The two (Znf) fingers are functionally distinct bridging two separate DNA fragments (Structure|ids=PIRSF003027).

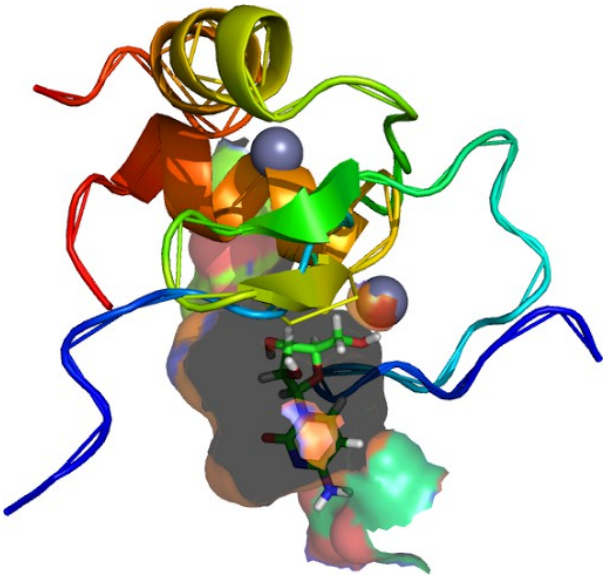
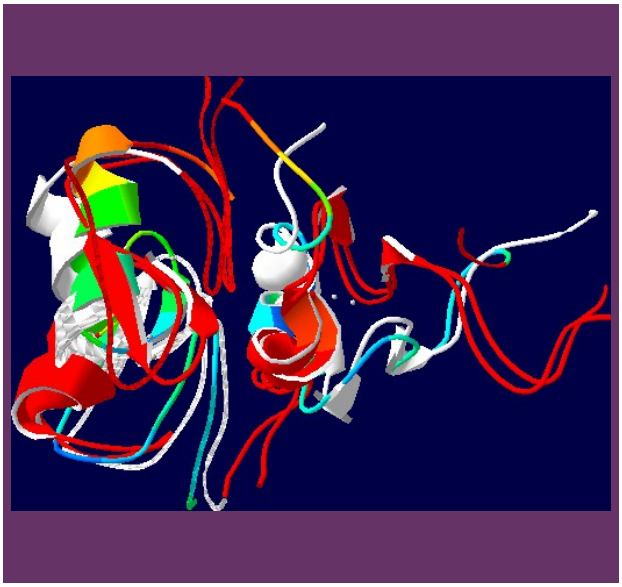


Figure 3: This incorporates PDB 1YOJ_A_B the Sructural basis of GATA1_A erythroid trascription factor and FOG1_B Zinc finger Protein (MMDB ID: 31470; Mus musculus A- Drosophila melanogaster-B) interactions with Human components of Complexed With a molecue biological unit ara-C (Arabinofuranosylcytosine) Cytarabine (CID_6253; SDF File (.sdf)) = ara-c (MMDB ID: 23600 PDB ID: 1P5Z) short (sf) and (lf) long forms 2 'finger' motifs of GATA 1 (lf) and FOG (sf) with (FKBP12) basal expression PDB 2FAP_component A represented as the ligand surface partially framing the FOG heterodimer prevents formation of DNA component PDB: 1GAT-cDNA when lacking basal expression. This apparatus appears to interact with an HS2 region mutated in its GATA motif.



Zinc fingers as protein recognition motifs: structural basis for the GATA-1/Friend of GATA interaction

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