Ein kleines Jubiläums-Paper zur Visualisierung des 4000-sten Gens im Metasystem iGene.

CD276 CD276 molecule [Homo sapiens]

Also known as B7H3; B7-H3

GeneID: 80381 updated 04-Aug-2007

Official Full Name

CD276 moleculeprovided by HGNC

Primary source HGNC:19137

See related Ensembl:ENSG00000103855; HPRD:05756; MIM:605715

Gene type: protein coding

RefSeq status: Validated

Organism: Homo sapiens

Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

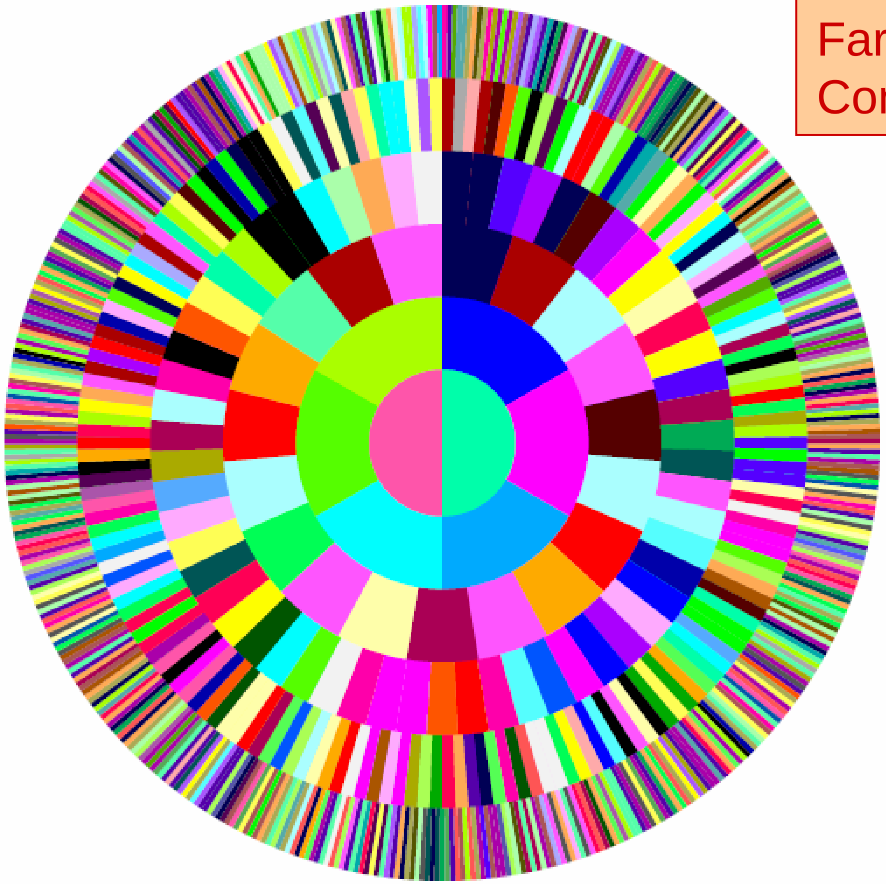
Metasystemischer Befund zu CD276_B7-H3

First biomarker discovered that predicts prostate cancer outcome

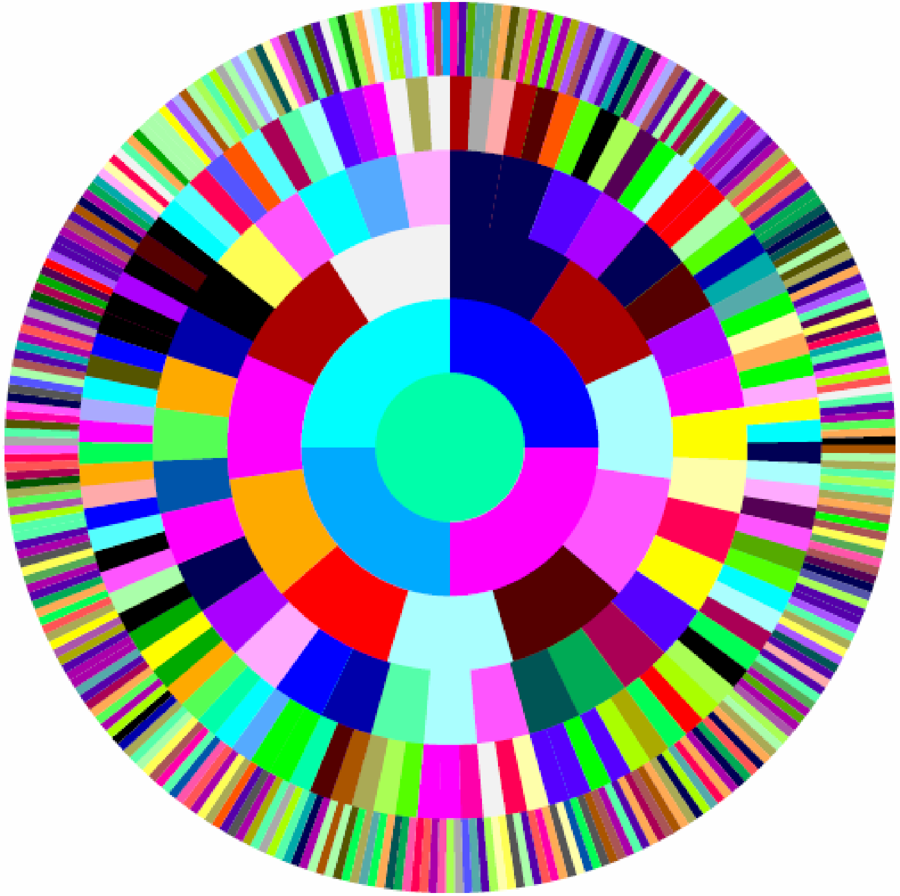
Mayo Clinic researchers have identified the first immune molecule that appears to play a role in prostate cancer development and in predicting cancer recurrence and progression after surgery. The report on the B7-H3 molecule by Mayo Clinic Cancer Center appears today in Cancer Research.

Until now there were no strongly-predictive molecules for prostate cancer. The most notable other prostate biomarkers, prostate-specific antigen (PSA), and prostate-specific membrane antigen (PSMA) are useful to diagnose prostate cancer. However, PSA tends to leave prostate cancer cells and migrate throughout the body, making it a poor target for therapy.

Farbkreise PerZan
Condensed Values:



CD 276 iso b
leveln-1
TAGA
TAG 56 Suche (stop) AGA 10
leveln-2
TTAATATGATAa
TTA 20 ..ATA 61 ..TGA 12 Stockung (stop)
TAA 33 Rueckzug (stop)



CD 276 iso a
leveln-1
TAGACGa
TAG 56 Suche (stop)…. ACG 26
leveln-2
TTAATATGATAACATGATAa
TTA 20 …ATA 61… TGA 12 Stockung (stop)
TAA 33 Rueckzug (stop)….CAT 55 …. GAT 32

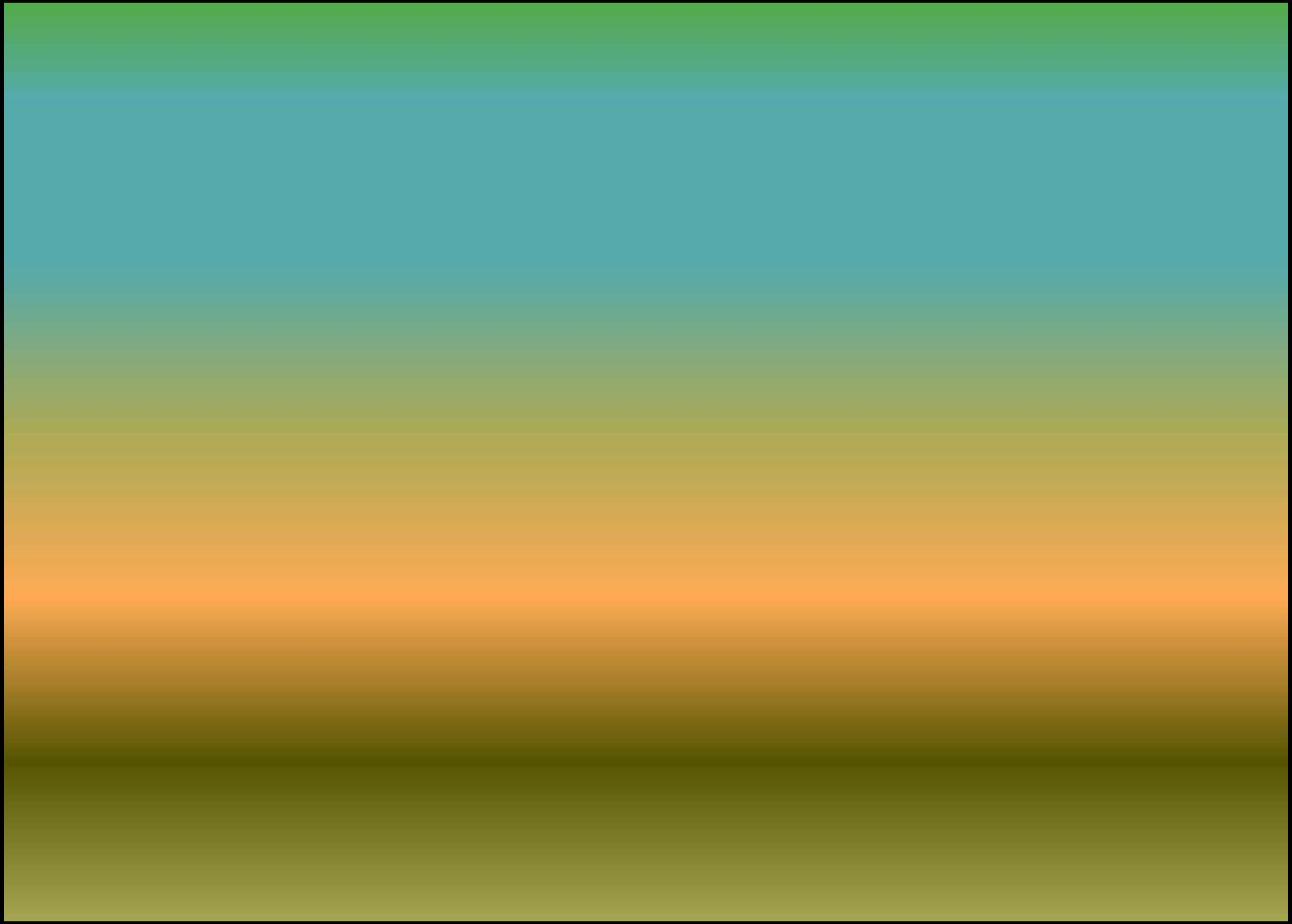
Ergebnis:

Die beiden Farbkreise von B7-H3/CD 276 in den Isoformen a und b zeigen auf engstem Raum im Kern levn-1 und dem Kern folgenden Radius n-2 sämtliche metasystemischen Krebs-Marker:

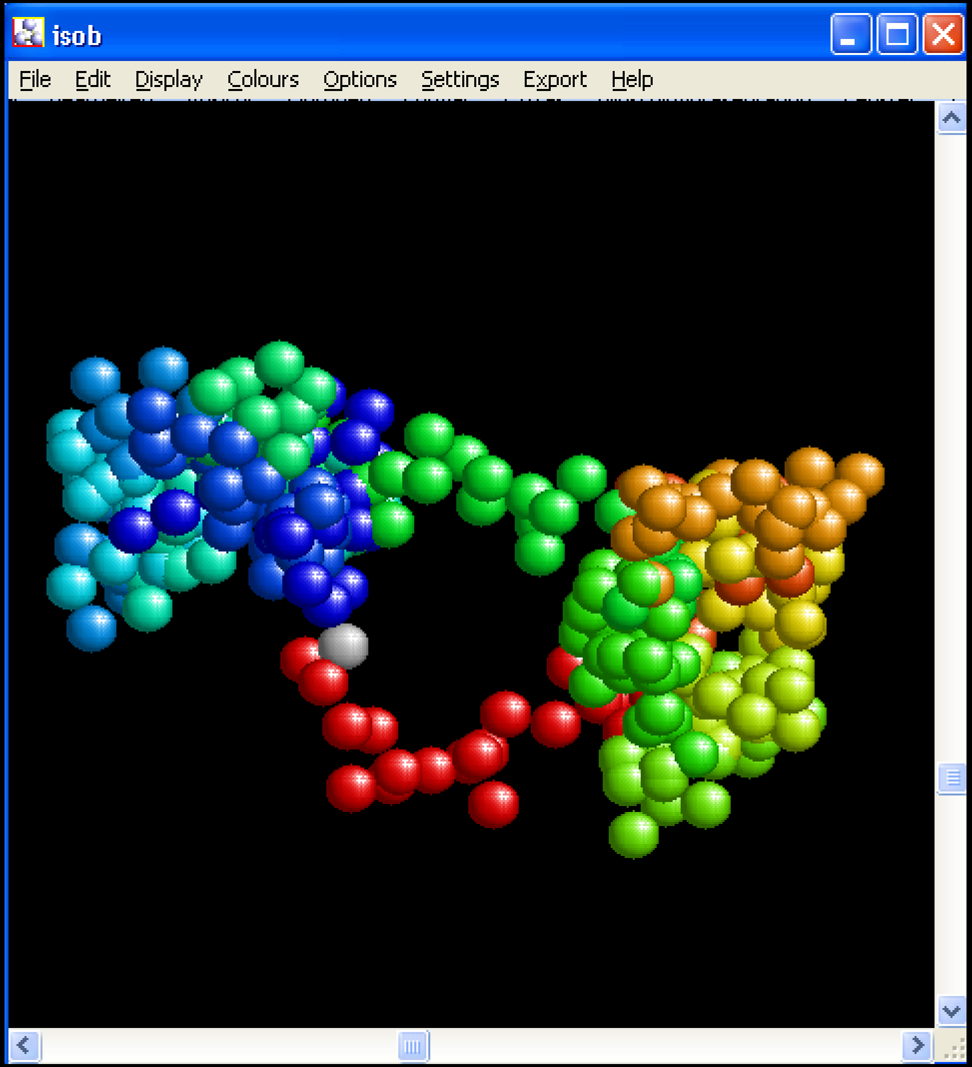
TAA-33 , TAG-56 und TGA-12
sowie den Co-Faktor
(>Entzündungs-/ Immunsystem-Marker)
ATA-61

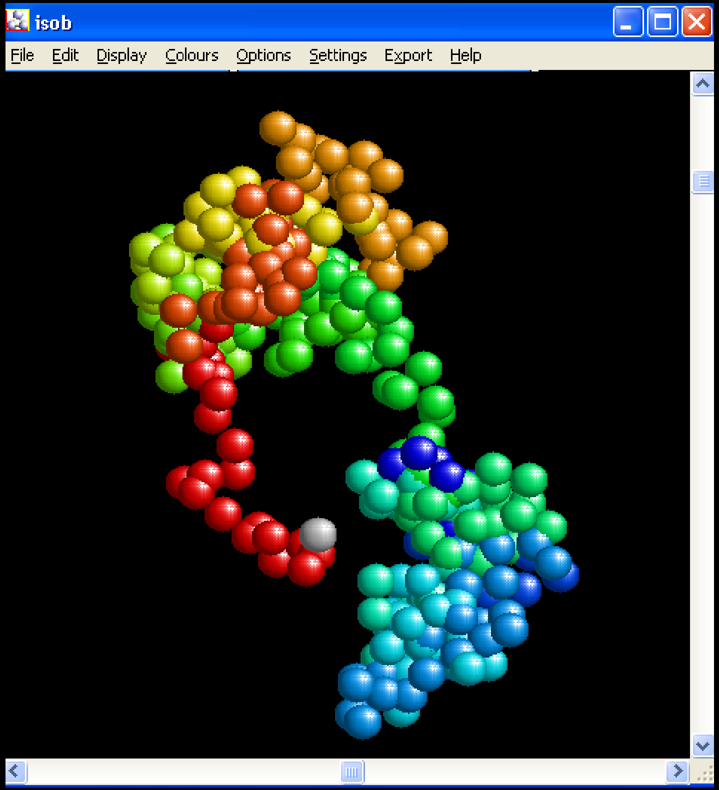
Eine solche Dichte der metasystemischen Krebs-Marker konnte bisher bei keiner der untersuchten 4000 Strukturen festgestellt werden.

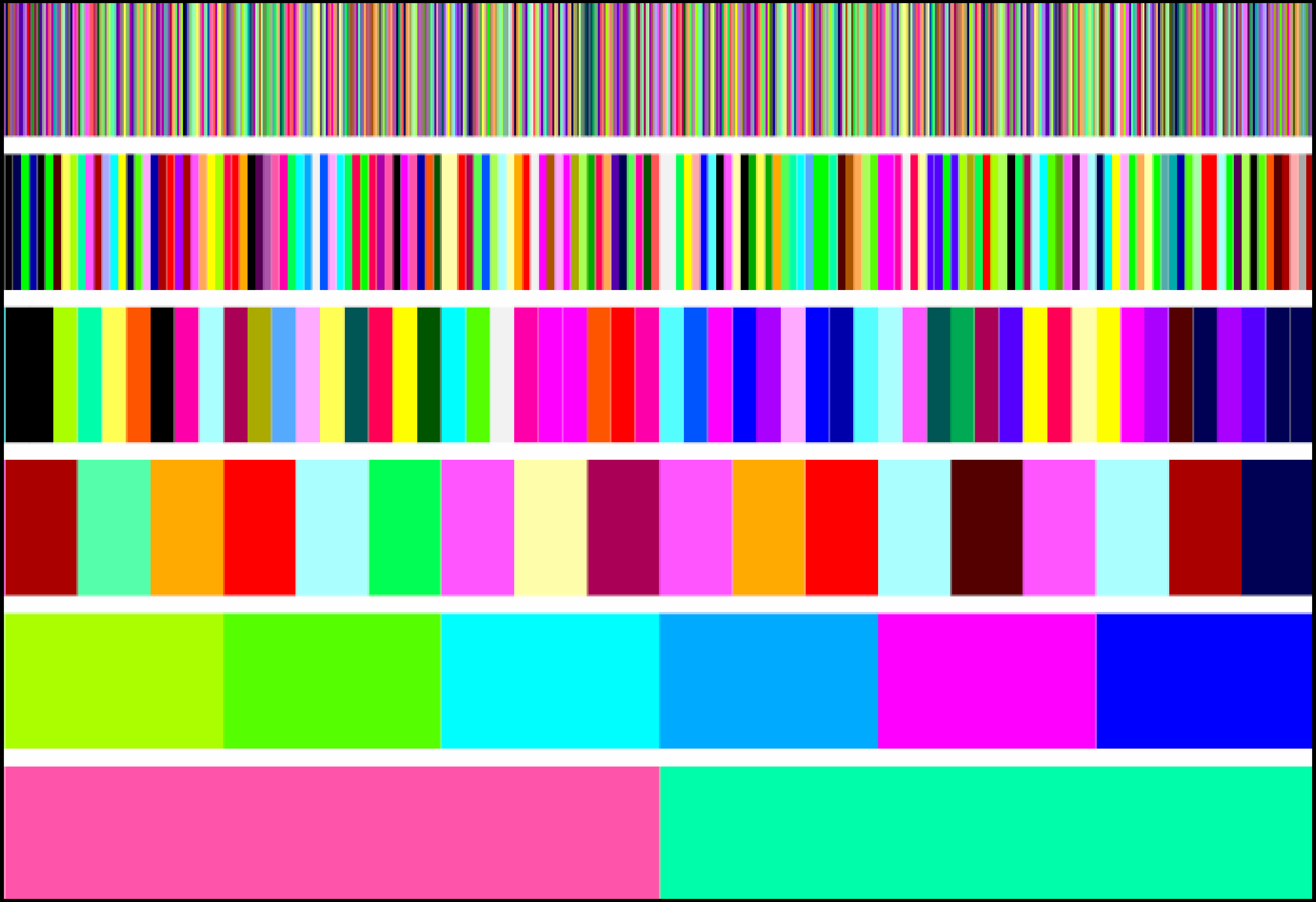
Das metasystemische Ergebnis entspricht mithin vollumfänglich der molekularbiologischen Funktion.



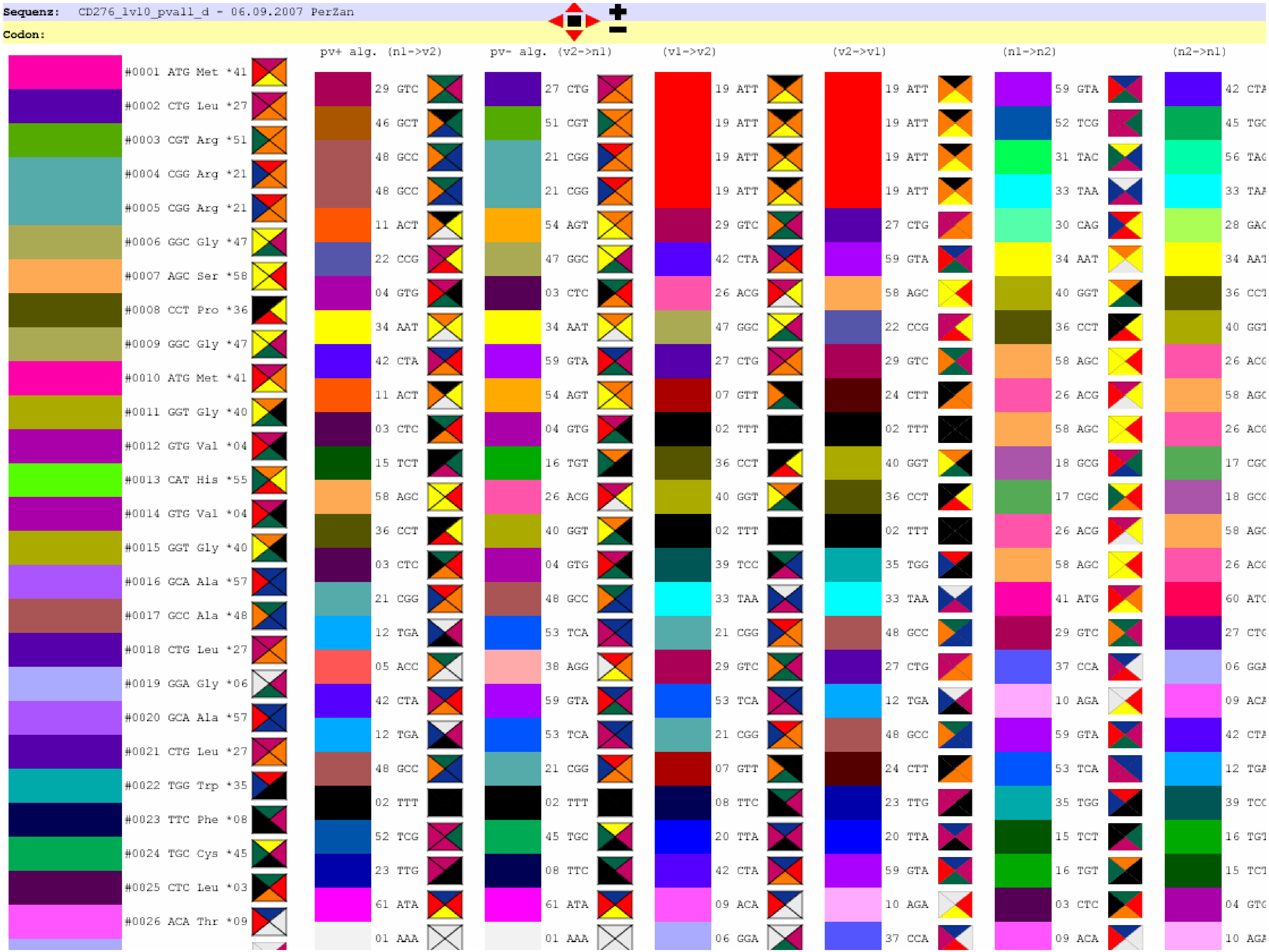
de novo Strukturprognose iGene







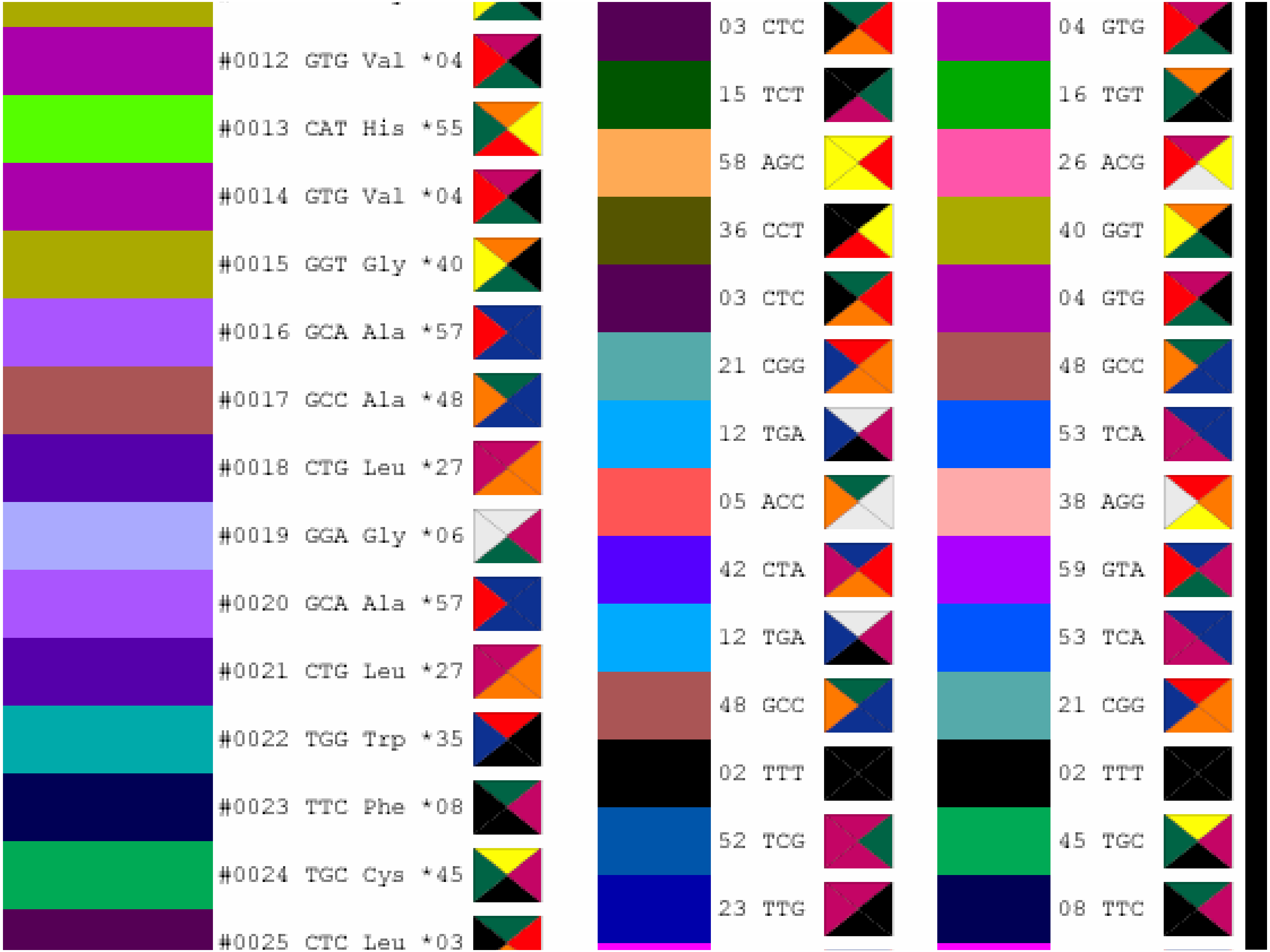
CD276_all_d.svg



Sequenz: CD276_lv10_pvall_d - 06.09.2007 PerZan

Codon:

	pv+ alg. (n1->v2)	pv- alg. (v2->n1)	(v1->v2)	(v2->v1)	(n1->n2)	(n2->n1)
#0001 ATG Met *41	29 GTC	27 CTG	19 ATT	19 ATT	59 GTA	42 CT
#0002 CTG Leu *27	46 GCT	51 CGT	19 ATT	19 ATT	52 TCG	45 TG
#0003 CGT Arg *51	48 GCC	21 CGG	19 ATT	19 ATT	31 TAC	56 TA
#0004 CGG Arg *21	48 GCC	21 CGG	19 ATT	19 ATT	33 TAA	33 TA
#0005 CGG Arg *21	11 ACT	54 AGT	29 GTC	27 CTG	30 CAG	28 GA
#0006 GGC Gly *47	22 CCG	47 GGC	42 CTA	59 GTA	34 AAT	34 AA
#0007 AGC Ser *58	04 GTG	03 CTC	26 ACG	58 AGC	40 GGT	36 CC
#0008 CCT Pro *36	34 AAT	34 AAT	47 GGC	22 CCG	36 CCT	40 GG
#0009 GGC Gly *47	42 CTA	59 GTA	27 CTG	29 GTC	58 AGC	26 AC
#0010 ATG Met *41	11 ACT	54 AGT	07 GTT	24 CTT	26 ACG	58 AG
#0011 GGT Gly *40	03 CTC	04 GTG	02 TTT	02 TTT	58 AGC	26 AC
#0012 GTG Val *04	15 TCT	16 TGT	36 CCT	40 GGT	18 GCG	17 CG
#0013 CAT His *55	58 AGC	26 ACG	40 GGT	36 CCT	17 CGC	18 GC
#0014 GTG Val *04	36 CCT	40 GGT	02 TTT	02 TTT	26 ACG	58 AG
#0015 GGT Gly *40	03 CTC	04 GTG	39 TCC	35 TGG	58 AGC	26 AC
#0016 GCA Ala *57	21 CGG	48 GCC	33 TAA	33 TAA	41 ATG	60 AT
#0017 GCC Ala *48	12 TGA	53 TCA	21 CGG	48 GCC	29 GTC	27 CT
#0018 CTG Leu *27	05 ACC	38 AGG	29 GTC	27 CTG	37 CCA	06 GG
#0019 GGA Gly *06	42 CTA	59 GTA	53 TCA	12 TGA	10 AGA	09 AC
#0020 GCA Ala *57	12 TGA	53 TCA	21 CGG	48 GCC	59 GTA	42 CT
#0021 CTG Leu *27	48 GCC	21 CGG	07 GTT	24 CTT	53 TCA	12 TG
#0022 TGG Trp *35	02 TTT	02 TTT	08 TTC	23 TTG	35 TGG	39 TC
#0023 TTC Phe *08	52 TCG	45 TGC	20 TTA	20 TTA	15 TCT	16 TG
#0024 TGC Cys *45	23 TTG	08 TTC	42 CTA	59 GTA	16 TGT	15 TC
#0025 CTC Leu *03	61 ATA	61 ATA	09 ACA	10 AGA	03 CTC	04 GT
#0026 ACA Thr *09	01 AAA	01 AAA	06 GGA	37 CCA	09 ACA	10 AG



#0012 GTG Val *04
#0013 CAT His *55
#0014 GTG Val *04
#0015 GGT Gly *40
#0016 GCA Ala *57
#0017 GCC Ala *48
#0018 CTG Leu *27
#0019 GGA Gly *06
#0020 GCA Ala *57
#0021 CTG Leu *27
#0022 TGG Trp *35
#0023 TTC Phe *08
#0024 TGC Cys *45
#0025 CTC Leu *03

03 CTC
15 TCT
58 AGC
36 CCT
03 CTC
21 CGG
12 TGA
05 ACC
42 CTA
12 TGA
48 GCC
02 TTT
52 TCG
23 TTG

04 GTG
16 TGT
26 ACG
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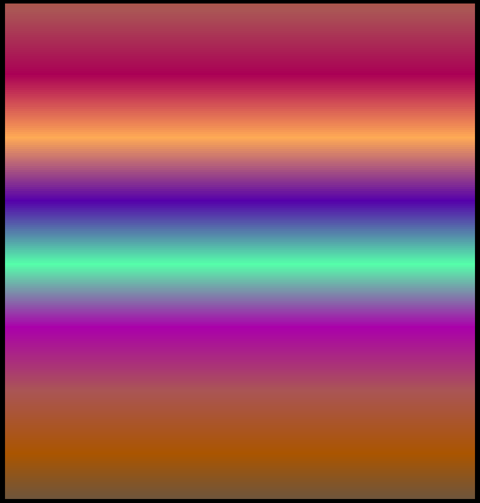
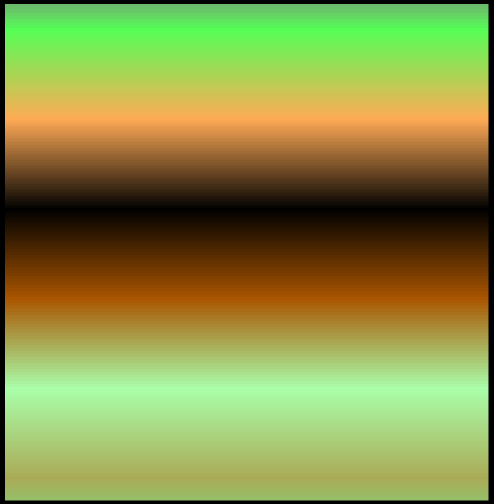
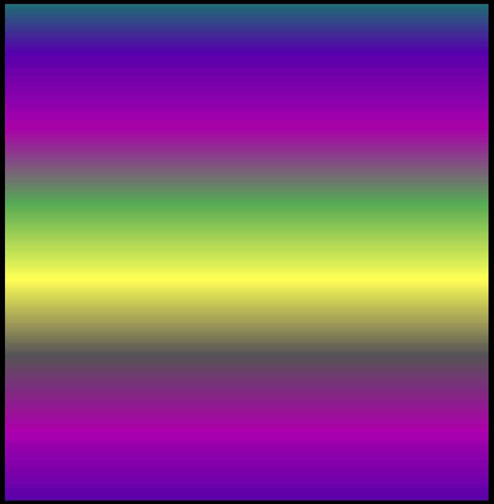
04 GTG
48 GCC
53 TCA
38 AGG
59 GTA
53 TCA
21 CGG
02 TTT
45 TGC
08 TTC

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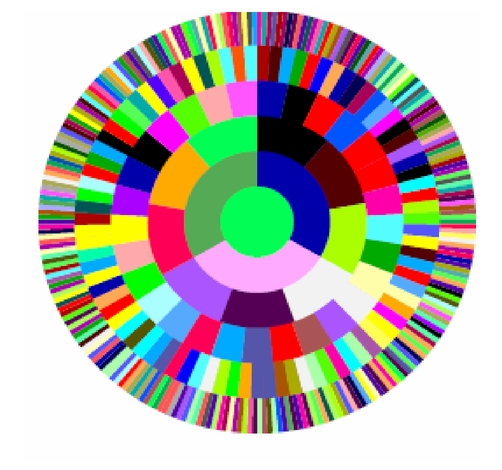
interacting 1

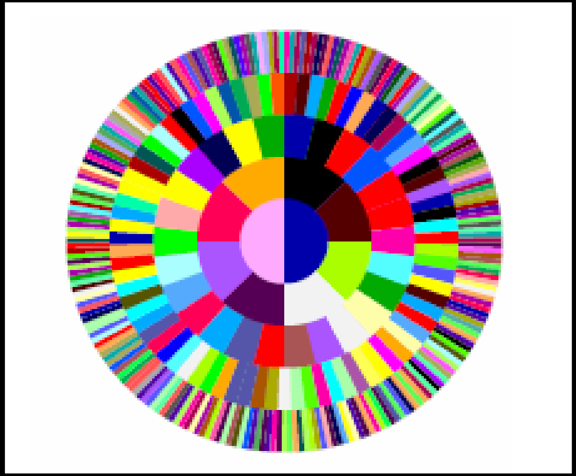
PROSTATA ANTI-CANCER GEN (PSA)



TAC 31

TTG 23
AGA 10

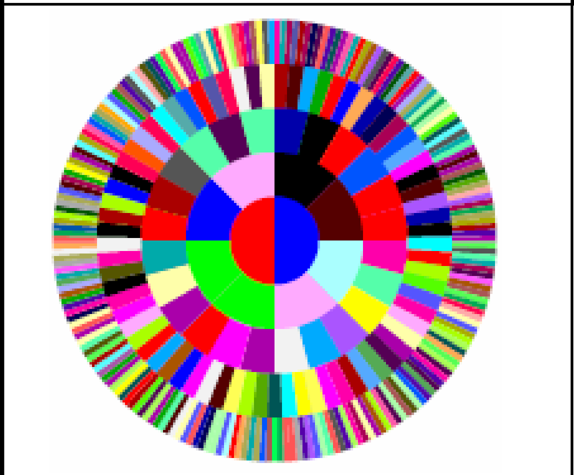
Isoformen 1,3,4,5,6

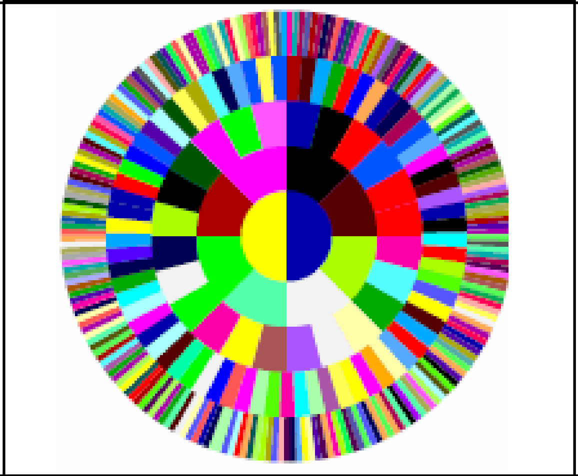


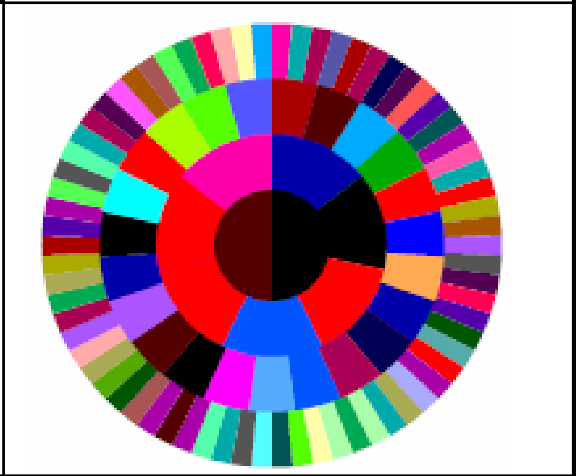
TTA 20
ATT 19

TTG 23
AAT 34

TTT 2
CTT 24

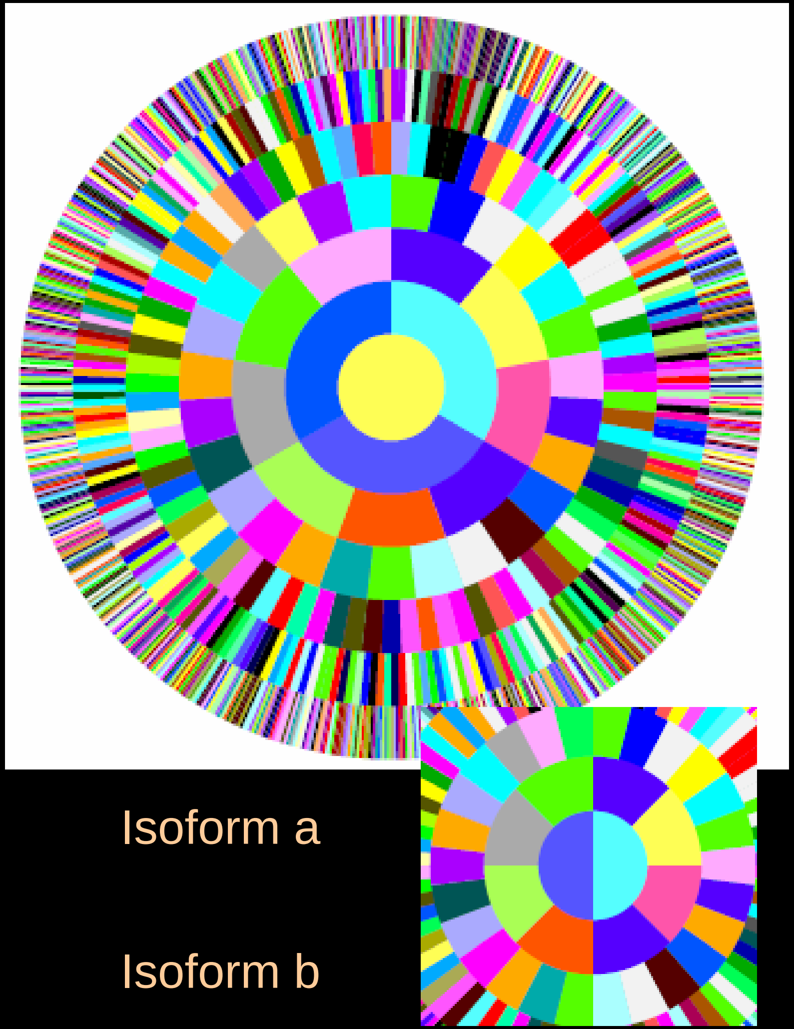






interacting 2:
FOLH1 folate hydrolase (prostate-specific membrane antigen) 1 [Homo sapiens]

"…until now there were no strongly-predictive molecules for prostate cancer. The most notable other prostate biomarkers, prostate-specific antigen **PSA**, and prostate-specific membrane antigen **PSMA / FOLH1** are useful to diagnose prostate cancer. However, PSA tends to leave prostate cancer cells and migrate throughout the body, making it a poor target for therapy"



Isoform a

Isoform b