

Sequence logo for the P-T motif. The logo shows the conservation of amino acids at each position, with a color scale from 0 (blue) to 100 (red). The motif is P-T, with positions 100 and 120 marked. The sequence is: P K K A E E S E S G I V T S T P E A P F T Q K Y A V P E D L D K Y S S Q K T N S Y A F E T V A R K A P A T S E R N V S T K L D K V L Q T T A R A P V T L E R R V N P N L D D E L E T V A R Q A P V T Y E R R V R T D L D D K M Q T V A A Q A P V T A E R R V R E D M E E Y L D R A A P F A P V T F H R P V R D D L E T T M A T V A P Y A P V T Y H R R A R V D L D D R. The motif is P-T.

Sequence logo for the P-T motif. The logo displays the conservation of amino acids across 140 positions. The y-axis represents information content in bits, ranging from 0 to 1.0. Key motifs include 'PIE' at the start, 'VTST' and 'GAS' around position 100, and 'FT' at the end. A 'P' is conserved at position 135 and a 'T' at position 136.

[illegible]

Glycine		Proline knot	
G	A K S Y L P	-	D P F F
-	S D S W W P T T	-	-
-	S D S W W P T T	-	-
Q	D S K L P	-	N P T
-	D S K L P	-	N P L
-	D S K L P	-	N P T
Q	D S K L P	-	N P L
Q	D S K L P	-	N P L
-	S P S W L P	-	D P M
-	L K S W L P	-	D P R L
-	A P G L L	-	D P R L
-	Y D G W L P	-	D P R F
-	L P G W L P	-	S L F
-	L P G W L P	-	S P W
-	L P G W L P	-	S P F F
R	P G K W L P	-	S P L
-	L P G W L P	-	S P F
-	L P G W L P	-	S P F F
W	G T W L P	-	D P F F
M	G S W L P	-	D P L
R	L A Y S W L P	-	D L W F
R	L A Y S W L P	-	D P W F
-	L K S Y L P	-	D P F F
Q	K S W L P L L	G N P L	-
-	Q D S W L P	-	D P R F
-	L D S W L P	-	H P F
-	S D S W L P	-	D P F F
W	D S F Y F	-	D P F M
-	D S W L P	-	D P F F

260

280

RLLVPSMH	-	KAKHGS	DSA	TFD	-	NEGRFL	PSKFFED	FTK		
TVHLKNH	-	RMMHGS	DSG	VYERN	SGRLN	HQRLDK	LFQG			
TVHLKNH	-	RMMHGS	DSG	VYERN	SGRLN	HQRLDK	LFQG			
PIYIKNI	-	-	KGKHTSDSE	TYN	-	PDGTIN	PKKFNQ	-	FQE	
PIYIKNI	-	-	RGKHTSDSD	TYN	-	TDGTIN	PKKFNQ	-	FQK	
PIYIKNI	-	-	KGKHTSDSE	TYN	-	PDGTIN	PKKFNQ	-	FQE	
PIYIKNI	-	-	RGKHTSDSD	TYN	-	TDGTIN	PKKFEQ	-	FQK	
PIYIKNI	-	-	RGKHTSDSD	TYD	-	TDGTIN	PKKFEQ	-	FQK	
RHVSRRRLQ	GR	TKHGS	DSE	TYD	-	TEGRFV	PQKFEEL	-	FSK	
PIYLDRH	-	-	RTKHGS	DSE	YYD	-	NEGRFV	PQKFEEL	-	FSK
PIYQRLH	-	-	KAKHGS	DSE	YYD	-	TEGRFV	PEKFEEL	-	FTK
PIYLEKH	-	-	RTKHGS	DTE	YYD	-	TEGRFV	PEKFEEL	-	FTK
PIHNRH	-	-	KAKHGS	DSE	YYD	-	TEGRFV	PSKFEEL	-	FTK
PIYLNRH	-	-	KAKHGS	DTE	YYD	-	SEGRFL	PANFEN	-	FSK
PIYVHNH	-	-	KVKHGS	DSG	TYD	-	TEGRFV	PANFEN	-	FSK
PIYIKNI	-	-	KGKHGS	DSG	YYD	-	SEGRFV	PEKFEQ	-	FKK
PIYIRNH	-	-	KAKHGS	DSG	TYD	-	TEGRYM	PVNLN	-	FSK
PIYIHNH	-	-	KSXKHS	DSK	TYD	-	NEGRFM	PVNLN	-	FSK
RKVRNMH	-	-	KAKHGS	DTE	SYT	-	TTGEFD	EKRNFY	-	FNM
...LPSED	-	-	QAKHGS	DSE	YYT	-	GLGEYD	DNRNFY	-	MDM
RYYVRSVH	-	-	KAKHGS	DSG	TYD	-	PEGRFL	QLFEN	-	FAK
RYYVRSVH	-	-	KAKHGS	DSG	TYD	-	PEGRFL	QLFEN	-	FAK
RINLNDH	-	-	KAKHGS	DSN	TYD	-	TEGRFS	PQKFEED	-	FSK
NVYVDTLS	-	-	KAKHGS	DSE	TFD	-	TEGRFV	PEKFEEL	-	FSK
RYYVKNH	-	-	KAKHGS	DSE	SYD	-	TEGRFV	PEKFEEL	-	MWT
PIYIKNI	-	-	RCKHGS	DTG	TYD	-	TEGRFV	PQRFEEL	-	FTK
GITYVANS	-	-	RCKR	GSHCG	YYD	-	SDGRID	VNFVEEL	-	QKQFGR
GVLVNRH	-	-	SKKHGS	DSE	YYD	-	TEGRFV	PQKFEEL	-	FSK
PIYIKNI	-	-	XAKHGS	DSE	TYD	-	TEGRFV	PQKFEEL	-	FSK

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GT	TYLLCR	---	-DQGWVEKE	DMRKV	
WLP	FFLNWRHYG	TLS	---ISRK	TIEQM	
WLP	FFLNWRHYG	TLS	---ISRK	TIEQM	
WTF	WLA	---	--NGYKLNAK	DIQAS	
WTF	WLA	---	--NDYKDAK	DIQAS	
WTF	WLA	---	--NGYKLNAK	DIQAS	
WVF	WLA	---	--NDYKDAK	DIQAS	
WVF	WLA	---	--NDYKDAK	DIQAS	
WNT	SFYLA-AKDT	PQGR	-MLDK	DARAL	
WIA	GGLLA-RDH	-KG	-LVSK	KIRGV	
WIA	TWLLA-KEVA	PDGRE	MLTRE	AIRGV	
WGF	TYWL	V-K	---	DEEGFASKE	AIRGV
WGF	LYLLA-K	---	DDGGFLPKE	AVRRG	
WGL	LYLLA-R	---	DEHGF	LPKE	AMRAT
WGL	LYLLA-R	---	DEHGF	LSKE	AIRRC
WKL	FTLCK	---	-DKDG	HKD	TTRAV
WGL	LYLLA-R	---	DEEGFLSKE	AVRRG	
WGL	LYLLA-R	---	DEEGFLSKE	AIRRC	
WVA	SYLLW	---	-PKDGYVSKA	DYRAL	
WTA	TYIMLW	---	-PADGKMGRE	DJKGV	
WGT	TWLLQ	---	-KDGKVYKE	DLRAV	
WGT	TWLLQ	---	-KDGKVYKE	DLRAV	
WGV	TYIMLW	---	-PEDGR	LKKE	DYRRV
WGT	LYLLCE	---	-KDGIVYKE	DYRSK	
WGT	LMVLGERHP	ATKQ	LYLTRD	HLRGQ	
WNT	WLCL-K	---	-DEHGVYKKE	QLRRV	
WTL	LAWL	---	-ENNS	SKS	SLDLC
---	---	-RQAR	MXEKG	RKKK	DIRSQ
WGT	LYLLA	---	-DEDGKLSKE	DIRAV	

Sequence logo for the 1000 Genomes Project. The logo displays nucleotide conservation across a 500 bp region from position 380 to 460. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows genomic positions. A vertical purple line marks the position of the rs1121513 variant (GTTGTTGTTG). The logo shows high conservation in the 380-400 bp region, with a notable peak at position 380 (G). The 400-420 bp region shows moderate conservation, and the 420-440 bp region shows low conservation. The 440-460 bp region shows moderate conservation, with a notable peak at position 440 (G). The 460-480 bp region shows low conservation.