

Supplementary Figure S1. Comparison of protein sequences of JAKs between golden pompano, large yellow croaker, zebrafish and human, and their Gene accession numbers are listed in Figure 5. The protein domains are predicted by Simple Modular Architecture Research Tool (SMART) (<http://smart.emble-heidelberg.de>). The FERM domain is marked in green. The STYKc domain of human is marked in red and the Tyrkc domain is marked in blue.

trJAK2a	--MACILLTMDPPTS	GPTANHNDLCPDLNTAAGCDPKQ--	VIDATQ	LT	THLYNLGKDG	GGGGRAKSS	ESVLTFFP	PEYVAE	ETCIAAAKAC	87																																																																				
LatJAK2a	--MACILLTMDPPTS	GPTPHQNGLCPLHDPAGTDPKQE	ATDATQ	LT	THLYNLGKDG	GGGGAAGKSS	ESVLTFFP	PEYVAE	ETCIAAAKAC	88																																																																				
DanJAK2a	-----	-----	-----	-----	-----	-----	-----	-----	-----	52																																																																				
HomJAK2	MGMACLTMT	TEG	STSTSIYQN	-----	GD	ISGNANSMQ	IDP-VLQ	VYLYHSLG	KSE-----ADYLTFFP	SEYVAE	ETCIAAAKAC	75																																																																		
trJAK3	-----	MD	SEESAPLVIR	-----	DR	GSQRSSST	GP	SLQVHI	YFFPTTKEE-----	AT	YISSGQ	ISAENV	CIQAGKKC	66																																																																
LatJAK3	-----	MD	SEESAPLVIR	-----	DR	GSQRSSST	GP	SLQVHI	YFFPTTKEE-----	TT	QISCGQ	IAEN	VCIOAGKKC	66																																																																
DanJAK3	-----	MS	EEEVPLMKS	-----	ER	AGSQRSS	CD	S-----ALQ	HLIYSP	SLNSE-----	TT	FSIPTGH	VT	ABSCVCLAAKAS	62																																																															
HomJAK3	-----	MA	PPSEETPLIP	-----	QR	SCSL	STEAG	-----	ALH	LLPAR	-GPGPP-----	QR	LSFS	FGD	HLAEDLCVQAAKAS	61																																																														
trJAK1	--MPTLWVME	SRQLCGKMRRS	-----	NK	RAQLSS	PTT	TLGL	ETHFY	SPD-----	IH	QLEYL	KGCY	TABE	LCVDAAKKC	68																																																															
LatJAK1	--MTTLWVME	SRQLCGKMRRS	-----	SK	RTQLSC	SP	TT	TLGL	ETHFY	TPD-----	VH	QLEYF	FKGCY	TABE	LCVDAAKKC	68																																																														
DanJAK1	--MPELAVMD	GRQLCVKMKK	-----	QR	KAEM	TIP	TAMK	GL	ETHFY	LAD-----	TH	QLEFF	KAC	Y	TABDLCVEAAKRC	66																																																														
HomJAK1	-----	MA	FAKMR	-----	SK	TEVN	LEA	PE	GP	VE	IF	Y	LSD-----	RE	PL	LGSGEY	TABE	LCIRAQAC	56																																																											
trTYK2	-----	MS	RNWSKRSR	-----	TG	AFPSQ	SE	PPK	GGQ	GH	LLFW	TK--	DG-----	EK	Y	SHT	SGK	VTABE	LCISAAEAV	61																																																										
LatTYK2	-----	MS	PTM	PRIGMSKRSR	-----	PG	SFLN	QIE	PP	QD	Q	GH	LLFW	TK--	EG-----	ER	Y	SHT	SGK	VTABE	LCISAAEAV	65																																																								
DanTYK2	-----	MY	RRGRSRRSKK	-----	AG	TSK	Q	SE	GP--	--GV	H	LLFW	TK--	DG-----	ER	CL	SY	K	GE	VTABE	LCISAAEAV	60																																																								
HomTYK2	-----	MP	L	RHWGMARGSKP	-----	VG	DGA	Q	MAAM	G--	GL	K	LLH	WAG	PGGG-----	EP	W	T	F	SE	SS	TABE	LCISAAEAV	64																																																						
trJAK2a	GIAPVYCN	LFG	MRES	DR	IE	PP	NHIF	KL	DQ	SASE	T	LF	RIRY	YP	PG	WYNN	NTNS	SFY-AH	RY	GV	SK	GM-----	ESP	V	IDD	DC	VM	YQ	166																																																	
LatJAK2a	GIAPVYCN	LFG	MRES	DR	IE	PP	NHIF	KL	DQ	SASE	T	LF	RIRY	YP	PG	WYNN	NTNS	SFY-AH	RY	GV	SK	GM-----	ESP	V	IDD	DC	VM	YQ	167																																																	
DanJAK2a	GVSPVHCAL	FGL	MRES	DR	IE	PP	NHIF	KL	DQ	SASE	T	LF	RIRY	YP	PG	WYNN	NTNS	SFY-AH	RY	GV	SK	GM-----	ESP	V	IDD	DC	VM	YQ	130																																																	
HomJAK2	GITP	VYHNL	FA	L	ASE	DL	S	Y	W	PP	NH	L	E	K	SEEP--	VK	Y	Y	R	F	R	F	FP	SS	MF	Q	ES	R	A--	SY	F	S	L	S	K	G	R-----	I	F	A	V	L	D	Y	153																																	
trJAK3	GILP	VYLS	L	F	G	A	S	S	D	S	F	W	Y	P	P	S	H	V	E	N	T	D	E	N--	LQ	H	R	F	R	F	F	P	G	N	W	Y	G	E	G	P	R	Q--	S	Y	R	Y	S	L	T	R	D	R-----	I	S	P	V	L	D	Y	142																		
LatJAK3	GILP	VYLS	L	F	G	A	S	S	D	S	F	W	Y	P	P	S	H	V	E	N	T	D	E	N--	LQ	H	R	F	R	F	F	P	G	N	W	Y	G	E	G	P	R	Q--	S	Y	R	Y	S	L	T	R	D	R-----	I	S	P	V	L	D	Y	142																		
DanJAK3	GILP	VYHNL	FA	L	ASE	DL	S	Y	W	PP	NH	L	E	K	SEEP--	VK	Y	Y	R	F	R	F	FP	SS	MF	Q	ES	R	A--	SY	F	S	L	S	K	G	R-----	I	F	A	V	L	D	Y	138																																	
HomJAK3	GILP	VYHNL	FA	L	ASE	DL	S	Y	W	PP	NH	L	E	K	SEEP--	VK	Y	Y	R	F	R	F	FP	SS	MF	Q	ES	R	A--	SY	F	S	L	S	K	G	R-----	I	F	A	V	L	D	Y	137																																	
trJAK1	SISPLCHNL	FA	L	Y	N	E	T	T	D	T	W	Y	P	P	N	H	E	F	K	I	T	D	E	T	S	I	K	H	Y	R	M	R	F	Y	R	N	W	H	G	T	T	E	G	E	S	P	V	W	R	H	C	I	S	K	L	R	G	G	L	S	P	Q	K	T	P	E	G	T	P	L	D	A	A	S	L	D	Y	158
LatJAK1	SISPLCHNL	FA	L	Y	N	E	T	T	D	T	W	Y	P	P	N	H	E	F	K	I	T	D	E	T	S	I	K	H	Y	R	M	R	F	Y	R	N	W	H	G	T	T	E	G	E	S	P	V	W	R	H	C	I	S	K	L	R	G	G	L	S	P	Q	K	T	P	E	G	T	P	L	D	A	A	S	L	D	Y	158
DanJAK1	RILP	CHNL	FA	L	Y	E	S	D	L	A	P	N	H	V	E	K	I	T	D	E	T	S	I	K	H	Y	R	M	R	F	Y	R	N	W	H	G	T	T	E	G	E	S	P	V	W	R	H	C	I	S	K	L	R	G	G	L	S	P	Q	K	T	P	E	G	T	P	L	D	A	A	S	L	D	Y	156			
HomJAK1	RISPLCHNL	FA	L	Y	N	E	T	T	D	T	W	Y	P	P	N	H	E	F	K	I	T	D	E	T	S	I	K	H	Y	R	M	R	F	Y	R	N	W	H	G	T	T	E	G	E	S	P	V	W	R	H	C	I	S	K	L	R	G	G	L	S	P	Q	K	T	P	E	G	T	P	L	D	A	A	S	L	D	Y	146
trTYK2	GITP	CHNL	FA	L	Y	N	P	L	S	R	C	W	N	S	P	N	H	I	F	S	P	E	N	T	S	L	V	H	Y	C	M	R	F	Y	R	N	W	H	G	L	N	E	K	E	P	T	V	S	R	Y	L	R	S--	GT	N	Q	G	S	S	P--	LT	E	I	T	S	L	E	Y	L	144								
LatTYK2	GITP	CHNL	FA	L	Y	N	P	L	S	R	C	W	N	S	P	N	H	I	F	S	P	E	N	T	S	L	V	H	Y	C	M	R	F	Y	R	N	W	H	G	L	N	E	K	E	P	T	V	S	R	Y	L	R	S--	GT	N	Q	G	S	S	P--	LT	E	I	T	S	L	E	Y	L	148								
DanTYK2	GITP	CHNL	FA	L	Y	N	P	L	S	R	C	W	N	S	P	N	H	I	F	S	P	E	N	T	S	L	V	H	Y	C	M	R	F	Y	R	N	W	H	G	L	N	E	K	E	P	T	V	S	R	Y	L	R	S--	GT	N	Q	G	S	S	P--	LT	E	I	T	S	L	E	Y	L	145								
HomTYK2	GITP	CHNL	FA	L	Y	N	P	L	S	R	C	W	N	S	P	N	H	I	F	S	P	E	N	T	S	L	V	H	Y	C	M	R	F	Y	R	N	W	H	G	L	N	E	K	E	P	T	V	S	R	Y	L	R	S--	GT	N	Q	G	S	S	P--	LT	E	I	T	S	L	E	Y	L	152								
trJAK2a	FFQWRSD	FL	D	G	W	V	Q	I	P	V	S	H	E	C	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	R	C	M	Q	S	R	I	Q	E	Y	N	I	L	R	K	R	I	R	F	R	F	K	R	F	250							
LatJAK2a	FFQWRSD	FL	D	G	W	V	Q	I	P	V	S	H	E	C	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	R	C	M	Q	S	R	I	Q	E	Y	N	I	L	R	K	R	I	R	F	R	F	K	R	F	251							
DanJAK2a	CAQWRSD	FL	D	G	W	V	Q	I	P	V	S	H	E	C	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	N	M	R	E	H	T	Q	N	Q	H	L	R	K	R	I	R	F	R	F	K	R	F	214								
HomJAK2	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E	T	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	C	I	R	A	K	I	Q	D	Y	H	I	L	R	K	R	I	R	F	R	F	K	R	F	237						
trJAK3	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E	T	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	C	I	R	A	K	I	Q	D	Y	H	I	L	R	K	R	I	R	F	R	F	K	R	F	226						
LatJAK3	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E	T	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	C	I	R	A	K	I	Q	D	Y	H	I	L	R	K	R	I	R	F	R	F	K	R	F	226						
DanJAK3	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E	T	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	C	I	R	A	K	I	Q	D	Y	H	I	L	R	K	R	I	R	F	R	F	K	R	F	222						
HomJAK3	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E	T	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	C	I	R	A	K	I	Q	D	Y	H	I	L	R	K	R	I	R	F	R	F	K	R	F	221						
trJAK1	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E	T	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	C	I	R	A	K	I	Q	D	Y	H	I	L	R	K	R	I	R	F	R	F	K	R	F	246						
LatJAK1	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E	T	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	C	I	R	A	K	I	Q	D	Y	H	I	L	R	K	R	I	R	F	R	F	K	R	F	248						
DanJAK1	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E	T	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	C	I	R	A	K	I	Q	D	Y	H	I	L	R	K	R	I	R	F	R	F	K	R	F	246						
HomJAK1	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E	T	Q	E-----	EC	L	MA	V	L	D	M	R	L	A	K	E	S	G	S	P	V	D	I	Y	N	D	T	S	Y	K	S	F	L	P	K	C	I	R	A	K	I	Q	D	Y	H	I	L	R	K	R	I	R	F	R	F	K	R	F	236						
trTYK2	FAQWRH	D	F	V	H	G	W	I	K	V	P	T	H	E																																																																

HomJAK3	T-----QGEQE-----VLQPFCDFFPFIIVDLSIQAPRVGGPAGEHRLVTVIRTDNQILE	329
trJAK1	R-----KKPATMSLVSKKEGK---SKNKLDGKQKNDNRKEAN-EGWVVFCDFFHFIHTHTVIKEAT-----VTIIFKQDDKRM	404
LatJAK1	R-----KKPAATSVISKEGK---SRKNKLDGKQKNDRKKEAN-EGWVVFCDFFHFIHTHTVIKEAM-----VTIIFKQDNKRM	406
DanJAK1	R-----RKPAPNQLILKDKPK---SKIKIGD-KQWNDKMKDS---GWTLESCDFHFIHTHTVIKDCC-----VTIIFKQDNKTM	389
HomJAK1	R-----HKPNVVSVE-KEKNK---LKRKLENKHKHKDEEKNKIREEWNNSYFFPFIHTHTVIESV-----VSINQDNKKME	381
trTYK2	R-----KVSQGKAQANSYLNRNDYLS---KTKQQSSHPKTANTPNK-----LTAFCDFDFPFIHTHTAITGAN-----VCISTQDNCRME	388
LatTYK2	R-----KVSQGKAQANSYLNRDYMYSMRKTKHQSNQPNNGNTPDE-----WTVFCDFDFPFIHTHTAITSGAN-----VCISTLDNHCME	395
DanTYK2	R-----KFSAQRSQSDDYSHS-----QNKETAALNEEED-----WNIFCDFDFPFIHTHTAIQGIN-----VCISTQDNMSMD	381
HomTYK2	WPVEEEVKNKEEGSSGSSSGRN PQAS---LFGKKAKAHKAVGPQADRPREPRLWAYFCDFDFPFIHTHTVLEHC-----VSIHFQDNKCLE	404

trJAK2a	LEFHSLSHALSFVSLVDGYRYRLVADAHHYLCKEVAPERLLECTQSYHHGVPVSMFETDKLRRSGNHQCLVILRGSPRDYDKYFMSFVVGY	447
LatJAK2a	LEFHSLSHALSFVSLVDGYRYRLVADAHHYLCKEVAPERLLECTQSYHHGVPVSMFETDKLRRSGNHQCLVILRGSPRDYDKYFMSFVVGY	448
DanJAK2a	LEFQSLSHALSFVSLIDGYRYRLTDAHHYLCKEVAPERLLEATQINCHGPISTEFASRLRRCCEGQPGVILRGSPKDYDRYFLSMFVEA	409
HomJAK2	IELSSLRREALSFVSLIDGYRYRLTDAHHYLCKEVAPAVLENTQSNCHGPISMDFAVSKLKKAGNQTGLVILRGSPKDFNKYFLTFAVER	443
trJAK3	AMFQGLKHALSFVSLVDGYFRLTIDSSHYFCQDIAPESILEGKKNHCHGPITSEFAVHKLKKSFGKGGTILRGSPKNYDSFLLTVCVQT	427
LatJAK3	AKFQSLKHALSFVSLVDGYFRLTIDSSHYFCQDIAPESILEGKKNHCHGPITSEFAVHKLKKSFGKGGTILRGSPKNYDNFLLTVCVQT	427
DanJAK3	AEFQTLTDAHSFVSLVDGYFRLTIDSTHYFCQDVAPERLLEDTQNYCHGPITSEFAVHKLKKGAGKNMILLRHSPKEADKYFLTVCIQIT	422
HomJAK3	AEFFGLPHALSFVSLVDGYFRLTIDSCHEFFCKEVAPERLLEEVAEQCHGPITLDFAVHKLKTGGSRPGSVILRGSPQDNDSFLLTVCVQN	419
trJAK1	MQMAARVHALSFAALVDGYFRLTIDAHHYLSKEVAPASVVHNNNGCHGPICTEYAVHKLRODGNEECAMILRWSTCTDYQYIIITAVVCTE	494
LatJAK1	MLMASRPHALSFAALVDGYFRLTIDAHHYLCKEVAPASVVHNNNGCHGPICTEYAVHKLROEGNEECTVILRWSTCTDYFYIIITVTVCTE	496
DanJAK1	LDLFYRDAALSFAALVDGYFRLTIDAHHYLCCTDVAPSSVVQNNENGCHGPICTEYAVHKLROEGNEECTVILRWSTCTEYFIIMTVVCIE	479
HomJAK1	LKLSHSEHALSFVSLVDGYFRLTIDAHHYLCCTDVAPILVHNTQNGCHGPICTEYAVHKLROEGSEECMSVLRWSTCTDFDNILMTVTCFE	471
trTYK2	VQMNSSQARSFISLLDGYRYRLTIDAHHYLCHEVAPERVVLSEANGLHGPMHDDFVILKLKKEAAEDCALVLRWSALDYHRIILAVLNTN	478
LatTYK2	AQMNSSQARSFISLLDGYRYRLTIDAHHYLCHEVAPERVVLSEANGLHGPMHDDFVILKLKKEAAEECALVLRWSALDYHRIILAVLNKN	485
DanTYK2	ISLDSISARSFISLLDGYFRLTIDAHHYLCHEVAPERVVLSEANGLHGPMHDDFVILKLKREVEERG-AALVLRWSALDYHRIILASLSRS	470
HomTYK2	LSLPSRAAALSFSVSLVDGYFRLTIDSGHYLCHEVAPERLVMSTRDGIHGPLLEFFVQAKLR--PEDCLLIHWSSTSHPYRLILTVAQRS	491

SH2 domain

trJAK2a	-----ETMVDYKHCCIMKTESGEYILSKAKRSFGSLRELLHCYQKEALRTDGYTFOITRCPPSPKDKSNLIVCRNNQGADVPLSPYLQ	531
LatJAK2a	-----ETMVDYKHCCIMKTESGEYILSKAKRSFGSLRELLHCYQKEALRTDGYTFOITRCPPSPKDKSNLIVCRNNQGAEVPLSPSLH	532
DanJAK2a	-----EGQLELKHCLVLRSLSGEFVLSKARCSFSSISELLARYQKEALRSDTHVFOITRCPPSPKDKSNLIVCRTHQGSEVCAPSSEH	493
HomJAK2	-----ENVIEYKHCLITKNENEEYNLSCTKKNFSSLRDLNLCYQMETVRSNIIIFQFTKCCPPKPKDKSNLIVFRTNGVDSFLLTVCVQLQ	527
trJAK3	-----PLGLDYKDCCLIKNEH--YSLPQVQKSFSSLRKLTSSYYQHTKILLAEVPVMIGCCPPPRPEELTNLIIRNNNTVTGTHGSPTLE	509
LatJAK3	-----PLGLDYKDCCLIKNEH--YSLPQVQKTFSSLRRELTSHYQHTKILLAEVPVMIGHCLPPRPKEFTNLTIIRSSNSVDTCQSSPTPE	509
DanJAK3	-----PLGMDYKDCCLIEKNEK--ESLAGIHNSFINLQDLDFYQLSTVYSDIIPVTIGKCCPPRAKELTNMIIRNSSMTLIPSSPTLQ	504
HomJAK3	-----PLGPDYKGCILRRSPTGTLELLVCLSRPHSSLRELLATCWDGGLHVDGVAVTTSCCIPRPKEKSNLIVVQRGHSPPTSSLVQPQ	503
trJAK1	IDLRESRPVRKYNFOIEVASDG-YRLYCTDTLRLPILRELEHLEHGQSRLTDNLHFQILRCPPQPREVSNLIVVTKD-----RAPVPQ	577
LatJAK1	IDLKESRPVKQYNFOIEVASDG-YRLYCTDTLRLPILRELEHLEHGQSRLTDNLHFQILRCPPQPREVSNLIVVTKD-----RAPAPQ	579
DanJAK1	LDLCESRPVPQYNFOIETS PQG-YRLYCTDTRFRPLKELLEHLQQLLRTDNLRFQILRCPPQPREISNLIIVMTTD-----REBPVPQ	562
HomJAK1	KSEQVQGAQKQYNFOIEVQKGR-YSLHESDRSFPSIGDLMSHLKKQILRTDNLISFMIKKCCQPKPREISNLIIVATK-----KAQEWQ	553
trTYK2	KNES----TQSHKQFRITQYKGSV-ECLEGLDQEFSSVKELTDSLKTFFVLKSGSDNFSIKKCCQFPRQAEISNLIIVMRQGV-----RSVHND	560
LatTYK2	ENGL----TPSHKQFRITQHRGSM-ECLEGLDQEFSSVKELTDSLKTFFVLKSGSDSFTIKKCCQFPRQAEISNLIIVMRKGVG-----RNNNTS	567
DanTYK2	KEGE----NPVYKQFRITRONGSL-FHLEGLDQDFSSIKELTSSLKTFFVLKSGSDSFTIKKCOLPKPGELSNLIIVRKGAKE-----SSIKSAS	552
HomTYK2	QAPDGMQ-SLRLRKFPITREQDGA-FVLEGLWGRSFPSVRELGAALQGCLIRAGDDCFSLRCCQLPQGETSNLIIVIMRG-----ARASP	571

trJAK2a	K--HISQMVFHKIKRKEDLVINSLCGGTFTKIFCG-----VRKELGDYGEIHQIDVVIKILHKAENYSESFEEBAASM	602
LatJAK2a	K--HINQMVFHKIQKEDLIINSLCGGTFTKIFCG-----VRKELGDYGEIHQIDVVIKILHKAENYSESFEEBAASM	603
DanJAK2a	R--LVNQMVFHKIHRREDLQTTGSLCGGTFTCQVRG-----LRREVGDYGEVHKMEVVMKILDKSHNYTESFEEBAASM	564
HomJAK2	RPTHMNMV FHKIARNEDLIFNESLCGGTFTKIFKG-----VRREVGDYQQLHETEVLKLVLDKAHNYSESFEEBAASM	600
trJAK3	-RNKFSHHCFFNMIKYKDLKWEBSLCGGSTTRIFKG-----YKTDIHD-GEKHVTEVLLKELDVARNCWESFEEBAASL	580
LatJAK3	-RSKFSHHCFFNMIKYEDLTSGBSLCGGSTTRIFKG-----CTDIRD-GEKHLTEVLLKELDVARNCWESFEEBAASL	580
DanJAK3	-RHKPSHHCFFNMIKHEDLIWSBSLCGGSTTRIFRG-----SKIDQRD-GGTHSTEVLLKVLNDANHCWESLFEBAASL	575
HomJAK3	SQYQLSQMVFHKIIPADSLEWHENLHGSGSTTKIFRG-----CRHEVVD-GEARKTEVLLKLVMDAKHNCMESLFEBAASL	575
trJAK1	TPMQBSQLSFHRILKEBIEQEHLGLGTRTNIYSGTLRVK-----SEEEEDAG-YSSFQEVKVVLLKULGSGHDIISLAFFETASM	656
LatJAK1	TPMQBSQLSFHRILKEBIEQEHLGLGTRTNIYSGTLRVK-----SEEEEDAG-YSSFQEVKVVLLKULGSGHDIISLAFFETASM	658
DanJAK1	KKTQVSQLSFDRILKEBIEVQGHGLGRGTRTNIYAGILKPK-----SDDEDDLGGYS--QEVKVVLLKULGSGHDIISLAFFETASM	640
HomJAK1	PVYPMSQLSFDRILKKDLVQGEHLGRGTRTHIYSGTLM DY-----KDDEGTSE---EKKIKVILKVLDPSSHRIISLAFFETASM	629
trTYK2	FSRNMSSQRFHFHVKEKEIVQGBHLGRGTRTNIYSGRYLVQGRGN-----SEDDDEFNNNSDRKGRVVLKLDQSHEDIALAFETASL	644
LatTYK2	LSLNLTLQRFHOKDREIVQGBHLGRGTRTNIYAGRLRVRSRGD-----DDDDCCNNNFSAGKGRVVLKLEQSHEDIALAFETASL	651
DanTYK2	ETPDLSQLSFNPTKDBEITKEGBHLGRGTRTNIYSGWLKIRGSL-----DEDDSNNNHCKTKGRVVLKLEBQSQHEDKALAFETASL	636
HomTYK2	RTLNLSQLSFHRVDQKEITQLSHLCGGTRTNIYVEGRRLRVEGSGDPPEGKMDDEDPLVPGDRGQELRVVLKVLDPSSHRIISLAFFETASL	661

trJAK2a	MSLSYKHLLLLNYGVVCGDENIMVVEYKGFSGSLDTYLRANKSCVNITWKLEVAQQLAWAMHFLLEDNKLHGVVCAKVLILREEDRKTG	692
LatJAK2a	MSLSYKHLLLLNYGVVCGDENIMVVEYKGFSGSLDTYLRANKSCVNITWKLEVAQQLAWAMHFLLEDNKLHGVVCAKVLILREEDRKTG	693
DanJAK2a	MSLSYKHLLLLNYGVVCGDENIMVVEYKGFSGSLDTYLRANKSCVNITWKLEVAQQLAWAMHFLLEDNKLHGVVCAKVLILREEDRKTG	654
HomJAK2	MSLSYKHLLLLNYGVVCGDENILVQEFVFKFGSLDTYLRANKSCVNITWKLEVAQQLAWAMHFLLEDNKLHGVVCAKVLILREEDRKTG	690
trJAK3	MSLSYKHLLLLNYGVVCGDENIMVVEYKYGALDLYLR-RGRSVSVSWKLDVAKQLASALNPLEENNIHGNITAKNILLAREGDPSQG	669
LatJAK3	MSLSYKHLLLLNYGVVCGDENIMVVEYKYGALDLYLR-RGRSVSVSWKLDVAKQLASALNPLEENNIHGNITAKNILLAREGDPSQG	669
DanJAK3	MSLSYKHLLLLNYGVVCGDENIMVVEYKYGALDLYLR-RSMCVSVSWKLDVAKQLACALNPLEENNIHGNITAKNILLAREGD---G	660
HomJAK3	MSQVSHRHLLVLLHGVVCAK-DSTMVQEFVHLCAIDMYLRKRGHLPASWKLQVVKQLAYALNYLEDKGLPHGNVSARKVILLAREGAD--G	662
trJAK1	MRVSHKHLLVLLHGVVCAKIMVVEYFQLGELDLFMRQQTTPKWKFWAKQLASALSYLEDNKLHGVVCAKVLILAREGLDGLDTE	746
LatJAK1	MRVSHKHLLVLLHGVVCAKIMVVEYFQLGELDLFMRQQTTPKWKFWAKQLASALSYLEDNKLHGVVCAKVLILAREGLDGLDTE	748
DanJAK1	MRVSHKHLLVLLHGVVCAKIMVVEYFQYGLDLFMRQQTTPKWKFWAKQLASALSYLEDNKLHGVVCAKVLILAREGLDGLD-E	729
HomJAK1	IRQVSHKHLLVLLHGVVCAKIMVVEYFQYGLDLFMRQQTTPKWKFWAKQLASALSYLEDNKLHGVVCAKVLILAREGLDGLD-E	718
trTYK2	MSQVSHRHLLVLLHGVVCAKIMVVEYFQYGLDLFMRQQTTPKWKFWAKQLASALSYLEDNKLHGVVCAKVLILAREGLEH-G	733
LatTYK2	MSQVSHRHLLVLLHGVVCAKIMVVEYFQYGLDLFMRQQTTPKWKFWAKQLASALSYLEDNKLHGVVCAKVLILAREGLEH-G	740
DanTYK2	MSQVSHRHLLVLLHGVVCAKIMVVEYFQYGLDLFMRQQTTPKWKFWAKQLASALSYLEDNKLHGVVCAKVLILAREGLEH-G	725
HomTYK2	MSQVSHRHLLVLLHGVVCAKIMVVEYFQYGLDLFMRQQTTPKWKFWAKQLASALSYLEDNKLHGVVCAKVLILAREGLAE-G	750

trJAK2a	SLPFIKLLDPGISITVLPREVLVERIPWVPEPIENPQ-NLSLAIDNWSFGTTLWEICSGGDKPLSTLDCSKKNLFYDRHQIPAKWTE	781
LatJAK2a	SLPFIKLLDPGISITVLPREVLVERIPWVPEPIENPQ-NLSLAIDNWSFGTTLWEICSGGDKPLSTLDCSKKNLFYDRHQIPAKWTE	782
DanJAK2a	TPPFIKLLDPGISITVLPREVLVERIPWVPEPIENPQ-NLSLAIDNWSFGTTLWEICSGGDKPLSTLDCSKKNLFYDRHQIPAKWTE	743
HomJAK2	NPPFIKLLDPGISITVLPKDLQERIPWVPEPIENPQ-NLSLAIDNWSFGTTLWEICSGGDKPLSTLDCSKKNLFYDRHQIPAKWTE	779
trJAK3	SSPFIKLLDPGISITVLPREVLVERIPWVPEPIENPQ-NLSLAIDNWSFGTTLWEICSGGDKPLSTLDCSKKNLFYDRHQIPAKWTE	758

LatJAK3	SSPFVKLDPGSI SL AMIGQDVLDRIPWVAPEVLEFPD-NITLEDQWWSFGATVMEIFN NN NA L RGWVLERRRFY YS FOQ Q PPSQWTE	758
DanJAK3	-SPPIKLD DP GVMS SL LGQDVLDRI PW VAPEVLD T -L-EIELEDQWWSFGTTLWEIFNGEAF L QGLDMCKLCFY IN FSN L PTLEWTE	747
HomJAK3	SPPFIKLSDPGVSPAVLSLEMLTDRI PW VAPECLREAQ-TLSLEAD K MGFGATVWEVFSGVTMP S ALDPAKKLQFYEDRQQLPAFKWTE	751
trJAK1	GGPFIKLDPGIDITVITREECV HR IPWIAPEV K SLT-A S IAADQWWSFGTTLWEICYD EV FLKEKKL TE KERFY TE CO LA TATDCRE	835
LatJAK1	GGPFIKLDPGIDITVITREECV HR IPWIAPEV K SLT-A S IAADQWWSFGTTLWEICYD EV FLKEKKL TE KERFY TE CO LA TATDCRE	837
DanJAK1	GGPFIKLDPGIDITVITREECV HR IPWIAPEV K SDTA-N S IAADQWWSFGTTLWEICYN GE IFL K DKKL TE KERFYA Q CC LA TATDCDE	818
HomJAK1	CGPPIKLDSPGIPITVLSRQCI ER IPWIAPEQVEDSK-NLCVAA E KKWSFGTTLWEICYNGE IF L K DKTL IE KERFY YS SR CR PVT SC KE	807
trTYK2	TTPFIKLDPGIAGVLSREERLERIPWIAPEV D SGA-P G SAADQWWSFGVTLL IC NN Q DV M SGSALSKKERFY Q KSR IP ES SM SE	822
LatTYK2	TTPFIKLDPGIAGVLSREERLERIPWIAPEV D SGT-LSDTKADQWWSFGVTLL IC NN Q DV L SSSALAKKERFY Q KGR LA ES SS QE	829
DanTYK2	TSPFVKLDPGSI SL SA S QGERVERIPWIAPEV AD GT-R G SAADQWWSFGATLL IC NN Q DLHVSNTSLSEKQRFY Q TSR LA V SS QE	814
HomTYK2	TSPFIKLDSPGVLGAL S REERVERIPWIAPECLPGGANS L STAM K WGFGATLL IC CFDGEAP L QSRSPSEKEH FY QR HR LPE SC PC	840

trJAK2a	LANL IN SCMDY EL SHR IS FR AI IR DL NSITFTPDYELLVESDMVP-NRTRGFGFPWASE-SQEPAC FE ERH LI FL K QL KG NFGSV EM CRY	869
LatJAK2a	LANL IN SCMDY EL SHR IS FR AI IR DL NSITFTPDYELLVESDMVP-NRTRGFGFPWASE-SQEPAC FE ERH LI FL K QL KG NFGSV EM CRY	870
DanJAK2a	LASV IN SCMDY EL SHR IS FR AI IR DL NSITFTPDYELLVESDTVP-SRHRGPGLAGAFE-SQEP TC Q FA ERH LI FL QL L KG NFGSV EM CRY	831
HomJAK2	LANL IN SCMDY ED DF IS FR AI IR DL NSITFTPDYELLTENDMPLPNMRIGALGFGS GA FE-DRDPT Q FEERH LI FL QL L KG NFGSV EM CRY	868
trJAK3	LADL IS QCMDYQA AF FR SC SIIR QL NSITSDYVILHATBP-VTQSP-VWRALS PQ HDQT--LFEERH LI YIT PL L KG NFGSV EM CRY	843
LatJAK3	LADL IS QCMDYQA AF FR SC SIIR QL NSITSDYVILHATBP-VTQSP-VWRALS PQ HDQT--LFEERH LI YIT PL L KG NFGSV EM CRY	843
DanJAK3	LAE L ISHCMQY Q EL R SC SI IR QL NSITSDY E ILHATDT--LPESNGFWKKLNIFKKQ Q EDVFEER Y LAF IS V L L KG NFGSV EM CRY	835
HomJAK3	LALL IQ CCMAYE EV Q R ES FR AI IR DLNSISSDYELLSDPTPGALAPRDGLWNGAQLYACQDPTIFEERH LI YIT SL L KG NFGSV EM CRY	841
trJAK1	LAE L MTDCMSY Q KKR FF RAI VR DI VM EE-----TNPSIQPQ--PTPEVDPTVFEKRL AK IREL EG HFGK VL CRY	908
LatJAK1	LAE L MTCHMSY Q KKR FF RAI VR DI VM EE-----KNPSIKPQ--PTPEVDPTVFEKRL AK IREL EG HFGK VL CRY	910
DanJAK1	LAK L NIH CM TYD R QRL FF RAI VR DI VM EK-----QNPSIQPV--PMLEVDPTVFEKRL AK IREL EG HFGK VL CRY	891
HomJAK1	LADL MT RCMNY DF NQ RF FR AI MR DI NKEE-----QNPDIVSEKKPATEVDPTHEKRL AK IREL EG HFGK VL CRY	882
trTYK2	LAR F ISMCLTYE IV ER IS FR AI VR DI VMK-----KDPDIS-PSETLPD TD SSV EH KRYL AK IREL EG HFGK VL Y YL H	896
LatTYK2	LAS F ISMCLTYE IV ER IS FR AI VR DI VMK-----IDPAIS-PGETLPDSDPSV EH KRYL AK IREL EG HFGK VL Y YL H	902
DanTYK2	LAS F ISMCLTYDAA AR ISFR AI VR DI VMTEQI-----KNPDISSECESLPDKDPSEV Y KRYL AK IREL EG HFGK VL Y YL H	889
HomTYK2	LAT IT SCQITYE IV ER IS FR AI MR DI TRIQPH-----NLADVLTVNPDSPASDPTV EH KRYL AK IREL EG HFGK VL Y YL H	916

trJAK2a	DPLQDSTG IV AVKKLQ H STA--EHLRDFE IE IEL SL H HE NI IV YK GC YSAGRRN RL IMEY YP GL AD Y IL EH D H DF SK IL LHY	957
LatJAK2a	DPLQDSTG IV AVKKLQ H STA--EHLRDFE IE IEL SL H HE NI IV YK GC YSAGRRN RL IMEY YP GL AD Y IL EH D H DF SK IL LHY	958
DanJAK2a	DPLQDNTG IV AVKKLQ H STA--EHLRDFE IE IEL SL H HE NI IV YK GC YSAGRRN RL IMEY YP GL AD Y IL EH D H DF SK IL LHY	919
HomJAK2	DPLQDNTG IV AVKKLQ H STE--EHLRDFE IE IEL SL H HE NI IV YK GC YSAGRRN RL IMEY YP GL AD Y IL EH D H DF SK IL LHY	956
trJAK3	DPLGNTG HL AVKKLQPNKQ--STQEDFQ KE VNTLSVLHCDYIVKYRGV GC YSMGR LS MSLVMEY YP GL IG LYLESN HN VNTRRMLLF	931
LatJAK3	DPLGNTG HL AVKKLQPNKQ--STQEDFQ KE VNTLSVLHCDYIVKYRGV GC YSMGR LS MSLVMEY YP GL IG LYLESN HN VNTRRMLLF	931
DanJAK3	DPWGDNTG HL AVKKLQSNKQ--ATMADFQ KE IEITLSLHCDYIVKYK GC YSTGR LS TKLVMEY YP GL IG LYME TH HN VN GRKL LL F	923
HomJAK3	DPLGNTG HL AVKKLQ H SGP--DQQRDFQ KE IEITLSLHSDYIVKYRGV GC YSMGR LS MSLVMEY YP GL IG LYLESN HN VNTRRMLLF	929
trJAK1	DPRGDRTG HL AVKKLQPNKQ--EEOQNNLSSEID IL ALY HE NI IV YK GC Q BE GGQ AI KLIMEY YP GL IG LYLESN HN VNTRRMLLF	997
LatJAK1	DPRGDRTG HL AVKKLQPNKQ--EEOQNNLSSEID IL ALY HE NI IV YK GC Q BE GGQ AI KLIMEY YP GL IG LYLESN HN VNTRRMLLF	999
DanJAK1	DPRGDRTG HL AVKKLQPNKQ--EEOQNNLSSEID IL ALY HE NI IV YK GC Q BE GGQ AI KLIMEY YP GL IG LYLESN HN VNTRRMLLF	980
HomJAK1	DPE L INTG Q AVVKKLQPNKQ--GNHIADL KE IEITLSLHSDYIVKYK GC CTE EG NG CI KLIMEY YP GL IG LYLESN HN VNTRRMLLF	970
trTYK2	DPSNDGTG HL AVVKKLQ EN --GYVPDGM KE IEITLSLHSDYIVKYK GC CTE EG NG CI KLIMEY YP GL IG LYLESN HN VNTRRMLLF	982
LatTYK2	DPANDGTG HL AVVKKLQ EN --GHVPDGM KE IEITLSLHSDYIVKYK GC CTE EG NG CI KLIMEY YP GL IG LYLESN HN VNTRRMLLF	988
DanTYK2	DPHNDGTG HL AVVKKLQ EN --GHVPDGM KE IEITLSLHSDYIVKYK GC CTE EG NG CI KLIMEY YP GL IG LYLESN HN VNTRRMLLF	977
HomTYK2	DPTNDGTG HL AVVKKLQ AD CG--PQHRSGW KE IEITLSLHSDYIVKYK GC CTE EG NG CI KLIMEY YP GL IG LYLESN HN VNTRRMLLF	1003

trJAK2a	ASQICKGMDYLG IK RI HR D LA TRN IL VESEM RV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1047
LatJAK2a	ASQICKGMDYLG IK RI HR D LA TRN IL VESEM RV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1048
DanJAK2a	ASQICKGMDYLG IK RI HR D LA TRN IL VESEM RV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1009
HomJAK2	TSQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1046
trJAK3	ASQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1021
LatJAK3	ASQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1021
DanJAK3	ASQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1013
HomJAK3	SSQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1019
trJAK1	SLQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1087
LatJAK1	SIQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1089
DanJAK1	SVQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1070
HomJAK1	AVQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1060
trTYK2	AQQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1072
LatTYK2	AQQICKGMEYLG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1078
DanTYK2	AQQICLGM Y LG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1067
HomTYK2	AQQICGM Y LG IK RI HR D LA TRN IL VEN EV KI ED FGL AK VL Q DK KE YY IV REP GE SP FW YAE SE TES IF SVASDVWSF FW VLYE	1093

trJAK2a	LYTYSKNCSP PP V FD K M NEKQ Q MI V YHL DL LKQGYRL AD PN CG KEI HK IMTEC W SSD PK LR PT E KT L I HS ET VRDSKDG----	1133
LatJAK2a	LFTYSKNCSP PP V FD K M NEKQ Q MI V YHL DL LKQGYRL AD PN CG KEI HK IMTEC W SSD PK LR PT E KT L I HS ET VRDIKDG----	1134
DanJAK2a	LFTYSEKSP PP V FD K M NEKQ Q MI V YHL DL LKRN Y RL AD PG CG AEI HA LMKQ CA EP AD RL FR D LA RT ED I Q DSQSG----	1095
HomJAK2	LFTYIEKSP PP V FD K M NEKQ Q MI V YHL DL LKNN GR L AD PG CG DEI Y IMTEC W NN N V N Q RP FR D LALR DQ VRDNMAG----	1132
trJAK3	LFSY CM MNCN PK RL Y Q EI HN VO PSISM HL AN IL KT N W RL SAP PH CP PK V Y SL M QC WA YN FD ER PC SS LN Q EI IMQDDR----	1106
LatJAK3	LFSY CM MNCN PK RL Y Q EI HN VO PSISM HL AN IL KT N W RL SAP PH CP PK V Y SL M QC WA YN FD ER PC SS LN Q EI IMQDDR----	1106
DanJAK3	LFSY CD ISQNP KL C Q KI RY VH SP SM AI HL TL KN N W RL SAP AC CL LK V Y SL M QC WE FN SE NR PS SS LD L EN SLDER----	1098
HomJAK3	LFTY CD KSC PS AE FR MM CC ERD V PAL CR -L LE L EG QRL AP PAC AE V HL ML K W AP SP QD RE PS AL GP Q DM WSGSRGCETH	1108
trJAK1	LITY CD SSK SP MTL FL SM IG -RTH Q MT IR L K VL Q EG RL R EP SP CE PV Y EL MR K RC WE QL PERRI EF KRL IEE T N V Q QLQ P QNSF	1176
LatJAK1	LITY CD SSK SP MTL FL SM IG -RTH Q MT IR L K VL Q EG RL R EP SP CE PV Y EL MR K RC WE QL PERRI EF KRL IEE T N V Q QLQ P QNSF	1177
DanJAK1	LLTY CD ASC SP MSV FL K LI E-PTH Q MT VR L K VL Q EG RL R EP SP CE PV Y EL MR K RC WE QL PERRI EF KRL IEE T N V Q QLQ P QNSF	1153
HomJAK1	LLTY CD SS SP ML FL K LI E-PTH Q MT VR L K VL Q EG RL R EP SP CE PV Y EL MR K RC WE QL PERRI EF KRL IEE T N V Q QLQ P QNSF	1141
trTYK2	ILTR CD QRQ SP PL FL SEM MD -EPR Q MT VM V L K LE K QL RL CP DK CH EV K ML ME QC WA SE PG QR PE FT SL IER EA IRRSYD W QSGI	1161
LatTYK2	ILTR CD HRQ SP PP VK SEM MD -ATO Q MT VM V L K LE K QL RL CP DK CH EV K ML ME QC WA AD PA QR PS HG PL IEK EA IRRTYD W QSGI	1167
DanTYK2	ILTN CS SHRL SP SK SD MM CG -TVH Q MT VM V L K LE K QL RL CP DK CH EV K ML ME QC WA FN ED QR PS FL SA ES EA IRG PY K Q PSL	1156
HomTYK2	ILTH CS SSQ SP PK FL EL IE -IAQ Q MT VR L K VL Q EG RL R EP SP CE PV Y EL MR K RC WE QL PERRI EF KRL IEE T N V Q QLQ P QNSF	1182

trJAK2a	-----	-
LatJAK2a	-----	-
DanJAK2a	-----	-

HomJAK2	-----	-
trJAK3	---ENPKG-----	1111
LatJAK3	---ENLKG-----	1111
DanJAK3	---EGCKG-----	1103
HomJAK3	AFTAHPEGKHSLSFS	1124
trJAK1	-----	-
LatJAK1	-----	-
DanJAK1	-----	-
HomJAK1	-----	-
trTYK2	NFSLAQIC-----	1169
LatTYK2	NFSLAQIC-----	1175
DanTYK2	QLAQLNHR-----	1164
HomTYK2	VFSVC-----	1187