

### **SUPPLEMENTARY MATERIAL 3**

**Amino acid sequence alignment of the OT/VP receptor family used for the phylogenetic maximum likelihood analysis.** The alignment spans between from the highly conserved arginine residue before the first transmembrane helix and the paired conserved cysteine residues in the carboxy terminal, producing an alignment of 314 amino acid positions in total. Poorly aligned sequence stretches of the amino terminus of the V2-like sequences, and of the most variable loop, ICL3, in all sequences, were removed within this span. The removal of the poorly aligned ICL3 sequences is marked in the alignment with a black line between positions 215 and 216. This segment included the expansion of ICL3 in teleost V2A sequences. Most receptor sequences span the entire length of the alignment and feature all seven transmembrane helices (see Table 1 and Supplementary Material 2), with the following exceptions: The platypus V1B sequence lacks the amino terminal, TM1-TM3 and a short portion of ICL2. The anole lizard V2B sequence lacks a segment of the amino terminal before TM1. In both these cases, this is likely due to faulty genomic sequence read in the genome database. None of the identified elephant shark scaffolds included the complete receptor sequences and the elephant shark predictions range between 120 and 255 residues in the alignment (see Table 1 and section 3.4). The positions of the three unique introns in the teleost V2A sequences have been marked with black triangles at positions 62-63, 144-145 and 196-197. The position of the conserved intron of OT/VP receptor genes has been marked with a red triangle at position 269.

## ABBREVIATIONS

Aca: *Anolis carolinensis* (anole lizard)

Cin: *Ciona intestinalis* (tunicate)

Cmi: *Callorhinchus milii* (elephant shark)

Dre: *Danio rerio* (zebrafish)

Gac: *Gasterosteus aculeatus* (stickleback)

Gga: *Gallus gallus* (chicken)

Hsa: *Homo sapiens* (human)

Mdo: *Monodelphis domestica* (opossum)

Mmu: *Mus musculus* (mouse)

Oan: *Ornitorhynchus anatinus* (platypus)

Ola: *Oryzias latipes* (medaka)

Ovu: *Octopus vulgaris* (octopus)

Tru: *Takifugu rubripes* (fugu)

Xtr: *Silurana (Xenopus) tropicalis* (frog)

	10	20	30	40	50	60	70	80	90	100	110	120			
Hsa_V1A	RNEELAKLEI	AVLAVTFAVAVL	GNSVLLALHRT	PR---	KT	SRMHFLIR	HLSLADLAVAFFQVL	PQMCWDI	TYRFRGPDWLCR	VVKHLQVFGMFAS	AYMLVVM	ADRYIAVCHPLKTLQQP-ARRS			
Mmu_V1A	RNEELAKLEV	TVLAVTFVAVL	GNSVLLALHRT	PR---	KT	SRMHFLIR	HLSLADLAVAFFQVL	PQLCWDI	TYRFRGPDWLCR	VVKHLQVFGMFAS	SYMLVVM	ADRYIAVCHPLKTLQQP-ARRS			
Mdo_V1A	RNEELAKLEI	TVLAVTFVAVL	GNSVLLALHRT	QR---	KT	SRMHFLIR	HLSLADLAVAFFQVL	PQLCWDI	TYRFRGPDGLCR	VVKHLQVFGMFAS	AYMLVVM	ADRYIAVCHPLKTLQQP-ARRS			
Oan_V1A	RNEELAKLEV	AVLAVTFAAALL	GNSVLLALHRT	PR---	KT	SRMHFLIR	HLSLADLAVAFFQVL	PQLCWDV	TYRFRGPDGLCR	VVKHLQVFSMFAS	AYVLLAM	ADRYIAVCHPLKTLQRP-ARRS			
Gga_V1A	RDEELAKLEI	AVLAVTFAVAVL	GNSVLLALHRT	PR---	KA	SRMHFLIR	HLSLADLVVAVFQVL	PQLCWEV	THRFHGP	DGLCRVVKHLQVFGMFAS	AYMLVAM	ADRYIAVCHPLKTLQQP-TKRS			
Aca_V1A	RNEELARLEV	AVLAVTFLVAVL	GNALVLLALGRT	PRR---	KASRMHFR	IRHLSLADLAVAFFQVL	PQLCWEV	THRFHGP	DGLCRVVKHLQVFGMFAS	AYLLVVM	ADRYIAVCHPLKTLQRP-SKRS				
Xtr_V1A	RNEALAKIEI	AIALIFVAAVL	GNSVLLGLYKSK	KK---	KT	SRMHFLIK	HLSLADLAVAFFQVL	PQLCWEV	TYRFRGPDILCR	IVKHLQVFGMFAS	AYMLVVM	ADRYIAI	CHPLKTLQQP-TKRS		
Gac_V1A1	RNEEVAQIEI	IMVLCITFVAVI	GNVSVLLAMFNT	KK---	KMSRMHFLIK	HLSLADLVVAVFQVL	PQLCWKI	ITFRFYGP	DFLCRI	VKHLQVMGMFASTYMMVMT	LDRIYIAI	CHPLKTLQQP-TQRS			
Ola_V1A1	RNEEVAQIEI	IMVLSITFVAVI	GNVSVLLAMNTK	KK---	KMSRMHFLIK	HLSLADLVVAVFQVL	PQLCWEI	ITFRFYGS	DFLCRI	VKHLQVMGMFASTYMMVMT	LDRIYIAI	CHPLKTLQQP-TKRS			
Tru_V1A1	RNEEVAQIEI	IMVLSITFVAVI	GNVSVLLAMHNT	KK---	KISRMHFLIK	HLSLADLVVAVFQVL	PQLCWEI	ITFRFYGS	DFLCRI	VKHLQVMGMFASTYMMVMT	LDRIYIAI	CHPLKTLQQS-SQRS			
Dre_V1A2	RDEEVAKIEI	IAVLSVTFAVAVI	GNYSVLVAIHNT	KK---	KT	SRMHFLIK	HLSLADLVVAVFQVL	PQLCWEI	ITFRFYGP	DFLCRI	VKHLQVMGMFASTYMMVMT	LDRIYIAI	CHPLKTLQQS-TRR		
Dre_V1A1	RNEDVAKMEI	ITVLSVTFVAVV	GNLCVLLAMHNT	KK---	KSSRMHFLIK	HLSLADLVVAVFQVL	PQLCWEI	ITFRFYGP	DFLCRI	VKHLQVLGMFASTYMMVMT	LDRIYIAI	CHPLKTLQQP-TRRA			
Gac_V1A2	RNEEVAKLEI	ITVLSVAFVAAGNV	SVLLAMRRT	RR---	KXSRVHLFMR	HXS	LADLVVAVFQVL	PQLCWEV	TRFSGP	DLCRVVKKLQVMGMFASTYMMVMT	VDRIYIAI	CHPLQTLQQP-TRRA			
Ola_V1A2	RNEEVAKIEI	ITVLSLAFVAADV	GNVSVLLAMHRT	RR---	KL	SRMHLMFK	HLSLADLVVAVFQVL	PQLCWEI	ITFRFYGP	DFLCRI	VKHLQVLGMFASTYMMVMT	LDRIYIAI	CHPLKTLQQP-TQRA		
Tru_V1A2	RNEEVAKIEI	ITVLSITFVAADV	GNVSVLLATHR	---	KPSRVHLFMK	HLSLADLVVAVFQVL	PQLCWEV	TRFRFYGP	DFLCRI	VKHLQVLGMFASTYMMVMT	LDRIYIAI	CHPLQTLQRP-AQRA			
Cmi_1	RNENLAKTEI	SVLGIIFLVAVIGN	LSVLMALYKT	KK---	KMSRMHFLIK	HLSVADLVVAVFQVL	PQFIWDI	TYRFNGP	DFLCRI	VKHLQVLGMFASTYMMVMS	VDRIYIAI	CHPLKTLQQA-TK--			
Hsa_V1B	RDEELAKVEI	GLVATVLVLA	TGGNLAVLLTGLQL	GR---	KRSRMHLFVL	HLALTDLGVALFQVL	PQLLWDI	ITYRFQGP	DLLCR	AVKYLVLSMFAS	STYMLLAM	LDRIYLAVCHPLRSLQQP-GQST			
Mmu_V1B	RDEELAKVEI	GLVATVLVLA	TGGNLAVLLTGLQGH	---	KRSRMHLFVL	HLALTDLGVALFQVL	PQLLWDI	ITYRFQGS	DLLCR	AVKYLVLSMFAS	STYMLLAM	LDRIYLAVCHPLRSLQQP-SQST			
Mdo_V1B	RDEELAKVEI	IAVLAITLVLAT	TGGNSIVLLALGWP	GR---	KRSRMHLFVL	HLALTDLGVALFQVL	PQLLWDI	ITYRFQGS	DFLCR	VVKYLAQALSMFASTYMLLVM	LDRIYLAVCHPLRSLHQP-SRSA				
Oan_V1B_fragment												NHTDR--PGP-SRS-			
Gga_V1B	RDEQLARAEV	GVLAAILLVATT	GNLAVLLAVCRR	GR---	KL	SRMHFLVL	HLALS	DLGVALFQVL	PQMLWEV	TYRFAGPDLLCR	AVKYLVLSMFAS	TYMLMAM	LDRIYVAVCHPLRTLRRP-GRQP		
Aca_V1B	RDEELAKAEI	GVLAAILAVTL	GNLGVLLTMYHL	RK---	KMSRMHFLI	HLALTDLVVALFQVL	PQMIWEV	TYRFQGP	DPLCK	LVKYLVLSMFAS	TYMLIAM	LDRIYMAVCHPLRTLQQT-SCQA			
Cmi_2	RDEELARAEI	SVLA AVLIVAVAG	NLAVLTALCRM	KR---	KL	SRTHLFVL	HLALTDLCAVLFQVL	PQLCWEI	TYRFQGP	DALCR	SVKYLVVGMFASTNMLVM	ADRIYLAVCHPLRTLQQP-VRQV			
Xtr_V1B	RNEDLAKAEV	ALLGAILVIT	TGSNLIVLFAIYQR	RK---	KMT	SRMHFLIV	HLTFTDLAVALFQIL	PQMIWDI	ITFRFIS	DI	LCRAV	YKTVMSMFAS	TYMLMMT	IDRIYIAVCHPLKTLQQP-SKQA	
Hsa_OTR	RNEALARVE	AVLCLILLAL	SGNACVLLALRTT	RQ---	KHSRLFFFMK	HLSIADLVVAVFQVL	PQLLWDI	ITFRFYGP	DLLCR	LVKYLVVGMFASTYLLLM	LDRLCIAI	CQPLRSLRRR-TDRL			
Mmu_OTR	RNEALARVE	AVLCLILLFAL	SGNACVLLALRTT	RH---	KHSRLFFFMK	HLSIADLVVAVFQVL	PQLLWDI	ITFRFYGP	DLLCR	LVKYLVVGMFASTYLLLM	LDRLCIAI	CQPLRSLRRR-TDRL			
Mdo_OTR	RNEAMAKVE	VTLSVILFLALT	GNLCVLLALRTT	RH---	KHSRMFFFMK	HLSIADLVVAVFQVL	PQLLWDI	ITFRFYGP	DFLCRI	LVKYLVVGMFASTYLLLM	LDRLCIAI	CQPLRSLRRQ-SDHL			
Oan_OTR	RNEAMAKVE	VTLSVILFLALT	GNLCVLLALHTT	RH---	KHSRMFFFMK	HLSIADLVVAVFQVL	PQLLWDI	ITFRFYGP	DFLCRI	LVKYLVVGMFASTYLLLM	LDRLCIAI	CQPLRSLRRR-ADRA			
Gga_OTR	RNEDMAKVE	VTLSVILFLALT	GNLCVLLAIHTT	RQ---	KHSRMFFFMK	HLSIADLVVAVFQVL	PQLIWDI	ITFRFYGP	DFLCRI	LVKYLVVGMFASTYMLLM	LDRLCIAI	CQPLRSLHRR-ADRV			
Aca_OTR	RNEDVAKVE	AVLCLIFFLALT	GNLCVLMAIYTT	RH---	KHSRMFFFMK	HLSIADLVVAIFQVL	PQLIWDI	ITFRFYGP	DYLCRI	LVKYLVVGMFASTYMLLM	LDRLCIAI	CQPLRSLHRR-SDRL			
Xtr_OTR	RNEDVAKVE	AVLALILFLALAGN	ICVLAIAHNR	H---	KHSRMFFFMK	HLSIADLVVAVFQVL	PQLIWDI	ITFRFYAP	DFVCR	IVKYLVVGMFASTYMLLM	LDRLCIAI	CQPLRSLHRR-SDCV			
Cmi_3															
Gac_OTR	RNEEVAKVE	AVLALVLFAL	TGNLCVLLAIHTT	KH---	SQSRMYFFMK	HLSIADLVVAIFQVL	PQLIWDI	ITFRFYGP	DMLCR	LVKYLVVGMFASTYMLVLM	VDRLCIAI	CQPLRSLHRR-KDRV			
Ola_OTR1	RNEEVAKVE	VTLSVILVFLALAGN	LCVLLAIHTT	KH---	SQSRMYFFMK	HLSIADLVVAIFQVL	PQLIWDI	ITFRFYGP	DILCR	LVKYLVVGMFASTYMLVLM	VDRLCIAI	CQPLRSLHRR-KDRI			
Tru_OTR1	RNEEVAKVE	VTLSVILVFLALAGN	LCVLLAIHTT	KH---	SQSRMYFFMK	HLSIADLVVAIFQVL	PQLIWDI	ITFRFYGP	DILCR	LVKYLVVGMFASTYMLVLM	VDRLCIAI	CQPLRSLHRR-KDRF			
Dre_OTR1	RNEEVAKVE	VTLSVILVFLALAGN	LCVLLAIHTT	KH---	SQSRMYFFMK	HLSIADLVVAVFQVL	PQLIWDI	ITFRFYGP	DILCR	LVKYLVVGMFASTYMLVLM	VDRLCIAI	CQPLRSLHRR-KDRC			
Dre_OTR2	RNEEVAKVE	VTLSVILLLALAGN	LCVLLAIQTS	KH---	QSRMYFFMK	HLSIADLVVAVFQVL	PQLIWDI	ITFRFYGP	DFLCRI	LVKYLVVGMFASTYMLVLM	VDRLCIAI	WQPLRSLRRR-KDRF			
Tru_OTR2	RNEDVAKVE	AVLVLLVLLAL	TGNLCVWATHAT	KH---	SQSRMYFFMK	HLSIADLVVAVFQVL	PQLIWDI	ITFRFYGS	DVLCRI	LVKYLVVSMFASTYMLVLM	VDRLCIAI	CQPLRLVDRK-KDRL			
Ola_OTR2	RNEEAAKVE	VTLSVILVLFALM	GNLCVLLAIHTT	KH---	SQSRMYFFMK	HLSIADLVVAVFQVL	PQLIWDI	ITFRFYGP	DILCR	LVKYLVVGMFASTYMLVLM	VDRLCIAI	CLPFRFVNKR-KDRI			
Dre_V2B	RNEQLAQIEI	ALLSVIFLCAST	LFSLLLVLWKR	RQ---	QMSRMRVFV	HLCLADLVVAVFQVC	PQLMWDI	ITDRFVGP	DVLCRI	LVKYLVVGMFASTYMI	VMTVDRIYQAI	CNPMTVFQRR-RARW			
Gac_V2B	RDES LAKLEI	ALLSVVFIGAAILNTS	LLLVLWQR	RQ---	HMSRMRVFV	HLCLADLVVAVFQVC	PQLIWDI	ITDRFVGP	DPVCR	LVKYLVVGMFASTYMI	VMTVDRIYQAV	CNPMTVFQRR-HTRL			
Ola_V2B	RDES LARAEI	ALLSVIFVSA	LNTSLLNALLVLWQR	RK---	QMSRMRI	IFVHLCLADLVVAVFQVC	PQLIWDI	ITDRFVGP	DVLCRI	LVKYLVVGMFASTYMI	VMTVDRIYQAV	CNPMTVFQRR-RTRI			
Tru_V2B	RDERLAQVEI	ALLSVIFITAGIL	NLGVLLVLWKR	RK---	QLSRMRVFV	HLCLADLVVAVFQVC	PQLMWDI	ITDRFVGP	DVLCRI	LVKYLVVGMFASTYMI	VMTVDRIYQAI	CNPMTVFQRR-RARC			
Cmi_4															
Gga_V2B	RDEQLAQVEI	IAVLGVIFLTASV	GNFILI	VLWRR	RK---	KL	SRMYVFML	HLSIADLVVAVFQVL	PQLIWDI	ITDVFI	IGP	DFLCRI	IVKYLVVGMFASTYMI	VMTVDRIYQAV	CNPMTVFQRR-RALW
Xtr_V2B	RSEQLAYVEI	SVLGVIFMVASAGN	LILVLWNKR	RK---	KL	SRMYVFML	HLSLADLVVAVFQVL	PQMIWDI	ITDVFFGP	DMCR	LIRYLVVGMFASTYMI	VMTVDRIYQAI	CNPMTVFQRR-RALW		
Aca_V2B_fragment															
Hsa_V2A	RDPLLARAEI	ALLSVIFVAVALS	GNLVLAAL-ARR	GRGR	HWAP	IHVFI	GHCLADLAVAFFQVL	PQLAWKAT	DRFRGP	DALCR	AVKYLVQVMGYASSYMI	LAMTLDRHRAI	CRPMLAYRHSGAHW		
Mmu_V2A	RDPLLVRAE	ALLSVIFVAVALS	GNLVLAGAL-IRR	GRGR	HWAP	MHVFI	SHCLADLAVAFFQVL	PQLAWDAT	DRFHGP	DALCR	AVKYLVQVMGYASSYMI	LAMTLDRHRAI	CRPMLAYRHGGGARW		
Mdo_V2A_fragment	GDPWLAQAE	ALLVAMFVCV	TLSNIVL	GAL-ARR	GRGR	HWAP	MHVFI	GHCLADLAVAFFQVL	PQLAWDI	DRFQGP	DFLCRI	AVKYLVQVMGYASSYMI	LAMTLDRHRAI	CRPMLAFRHG-GAHW	
Oan_V2A	RDEALARAEI	ITLAVMFVGVAGS	NTLVLGAL-ARR	GRGR	HWAP	MHVFI	HLCLADLAVAFFQVL	PQLLWDI	ITDRFQGP	DLLCR	AVKYLVQVMGYASSYMI	LAMTLDRHHAICRPMTFRRG-GARW			
Aca_V2A_fragment	RDVALAQAEI	AILASIFLLATLS	GNLVLGALFLR	-GHRAAP	TPMHRFI	HLCLADLTVALFQVL	PQLIWDI	ITDRFQGP	DILCRAI	ITYLVQVMGYASSYMI	VAMTVDRIYQAI	CNPMTVFRRG-PGTW			
Xtr_V2A	RDPIVAQNI	IAVLAVIFSFAT	GNCLVLF	TL-LRR	RKHN--	ALMHTFM	HLCLADLVVS	FFQVL	PQLVWDI	ITDRFRGP	DVLCRI	GVKYLVQVMGYASSYMI	VAMTVDRIYQAI	CRPMTVFRRG-SARW	
Gac_V2A1_unsolved	RDPGLARAEI	IAVLGVVLA	TTLGN	SVFLWVL-LRR	RKYN--	APMHVFMN	LCVADLVVAVFQVL	PQLIWDI	ITGRFQGP	DFLCRI	SVKYLVQVMGYASSYMI	VAMTVDRIYQAI	CRPMTVFRRG-SARW		
Ola_V2A1	RDLTLARAEI	IAVLGVVLA	TTLGN	SVFLWVL-LRR	RKHN--	APMHVFMN	LCVADLVVAVFQVL	PQLIWDI	ITGRFQGP	DFLCRI	SVKYLVQVMGYASSYMI	VAMTVDRIYQAI	CRPMTVFRRG-SARW		
Tru_V2A1	RDLNLARAEI	IAVLGVVLA	TTLGN	SVFLWVL-LRR	RKYN--	APMHVFMN	LCVADLVVAVFQVL	PQLIWDI	ITGRFQGP	DLLCR	SVKYLVQVMGYASSYMI	VAMTVDRIYQAI	CRPMTVFRRG-SARW		
Dre_V2A2	RDVALAQAEI	GLILGLVLA	TTLGN	SVFLWVL-LRR	RKYN--	APMHVFMN	LCVADLVVAVFQVL	PQLMWDI	ITGRFQGP	DVLCRI	SVKYLVQVMGYASSYMI	VAMTVDRIYQAI	CRPMTVFRRG-SARW		
Gac_V2A2	RDALLAVA	EVVLTIVLVMALL	GNLVLVVL-LRR	RQHH--	NPLHQF	MLNLCVADLVVAVFQVL	PQLVWDI	AKGLFPGP	DFLCRI	LVKYLVQVMGYASSYMI	VAMTMDRIYQAI	CRPMTVFRRG-SARW			
Tru_V2A2_unsolved	RDAA LAVA	EVVLTIVLVMALL	GNLVLVVL-LRR	KRRH--	NPLHQF	MLNLCVADLVVAVFQVL	PQLVWDI	AKGLFPGP	DFLCRI	LVKYLVQVMGYASSYMI	VAMTMDRIYQAI	CRPMTVFRRG-SARW			
Ola_V2A2_unsolved	RDAL LAVA	EVVLTIVLVMALL	GNLVLVVL-LRR	KRRH--	NPLHQF	MLNLCVADLVVAVFQVL	PQLVWDI	AKGLFPGP	DFLCRI	LVKYLVQVMGYASSYMI	VAMTMDRIYQAI	CRPMTVFRRG-SARW			
Dre_V2A1	RDQALAQAEI	GVGLVLVLA	TALGN	SVFLWVL-LRR	RKHN--	APMHVFMN	LCVADLVVAVFQVL	PQLVWDI	ITGRFHGP	DALCR	SVKYLVQVMGYASSYMI	VAMTMDRIYQAI	CRPMTVFRRG-SARW		
Cmi_5															
Dre_V2-like															
Gac_V2-like															
Cin_VPR	LQRQIRI	TELYIATVFIL	GLGNSCVL	VLA	WQYS--	KHTRMHILI	FHLAVADLIVL	FEMLE	EWIIR	FGFFAS	DAMCFV	KYMQIL	LGMYGSTY	VL	LCAAFDRIYRAIRYPMQSFQLT-AKRV
Ovu_CTR2	RDEKLVKIEI	IAVLGCTCT	FLAIINNL	GVLLVLR	RK---	KVRMQMFI	HLSIADLVVAVFQVL	PQLIWDI	ITDRFMAG	DAMCF	FLKYAQMFS	LYASTY	ILIMTAV	DRIYRAI	CHPLSNQWTW-PCMV
Ovu_CTR1	RNQDLANAEI	ITLAVVIT	ITVIGNSIVL	TLFQR	RK---	KLTRMHFLI	HLSVITDLFVAFNNL	PQMIWDI	ITFLGL	TDL	LCRLVLY	QSSVAM	LYASSV	VLVATAIDRIYFAI	CHPLSNHKTW-TARV
Ovu_OPR	YDDELGKFEI	IMVLCILCFM	ALFGNAV	LIVLR	IKT---	TLTRMQLLI	VYLSVTDIS	VAFHIL	PTIIL	IK	INVY	FLGDI	SACRY	VYQFIT	VAELYASSFVLIVTALDRIYISICHPLLAHMTW-NRRV



	130	140	150	160	170	180	190	200	210	ICL3 edit	220	230	240	250																																																																																																												
Hsa_V1A	R	L	M	I	A	A	A	W	V	L	S	F	V	L	S	T	P	Q	Y	F	V	F	S	M	I	E	V	N	-	N	V	T	K	A	R	D	C	W	A	T	F	I	Q	P	W	G	S	R	A	Y	V	T	W	M	T	G	G	I	F	V	A	P	V	V	I	L	G	T	C	Y	G	F	C	Y	N	I	W	C	N	V	R	G	K	T	---	---	V	S	S	V	K	S	I	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	T	A	Y	I	V	C	W	A	P	F	F	I		
Mmu_V1A	R	L	M	I	A	A	S	W	G	L	S	F	V	L	S	I	P	Q	Y	F	I	F	S	V	I	E	V	N	-	N	G	T	K	A	Q	D	C	W	A	T	F	I	P	P	W	G	T	R	A	Y	V	T	W	M	T	S	G	V	F	V	V	P	V	I	L	G	T	C	Y	G	F	C	Y	H	I	W	R	N	V	R	G	K	T	---	---	V	S	S	V	K	S	I	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	S	A	Y	I	L	C	W	T	P	F	F	I			
Mdo_V1A	R	V	M	I	A	A	A	W	L	S	F	V	L	S	T	P	Q	Y	F	I	F	S	M	V	E	N	-	N	V	T	K	A	R	D	C	W	A	N	F	I	Q	P	W	G	L	R	A	Y	V	T	W	M	T	G	G	I	F	V	A	P	V	I	L	G	T	C	Y	G	F	C	Y	H	I	W	R	N	V	R	G	K	T	---	---	V	S	S	I	K	S	I	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	T	A	Y	I	V	C	W	T	P	F	F	I					
Oan_V1A	R	A	M	I	A	A	A	W	L	S	F	V	L	S	V	P	Q	Y	F	I	F	S	F	G	E	V	N	-	N	G	T	K	A	R	D	C	W	A	N	F	I	Q	P	W	G	K	A	Y	V	T	W	M	T	A	S	I	F	L	A	P	V	L	V	L	A	T	C	Y	G	F	C	Y	H	I	W	R	N	V	R	G	K	T	---	---	V	S	S	I	K	S	I	S	R	A	K	I	R	T	V	K	M	T	L	V	I	V	T	V	V	V	C	S	A	P	F	F	V					
Gga_V1A	Y	A	M	I	A	A	A	W	A	L	S	L	L	S	T	P	Q	Y	F	I	F	S	L	S	E	V	E	-	R	G	S	R	V	D	C	W	A	H	F	I	M	P	W	G	P	R	A	Y	I	T	W	I	T	G	G	I	F	V	A	P	V	L	I	A	T	C	Y	G	F	C	F	R	I	W	R	S	A	R	G	R	A	---	---	V	S	G	V	K	T	I	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	S	A	Y	V	V	C	W	A	P	F	F	T					
Aca_V1A	R	W	M	I	A	G	A	W	L	S	F	V	L	S	T	P	Q	Y	F	I	F	S	L	S	E	V	E	-	R	G	S	E	V	D	C	W	A	H	F	V	M	P	W	G	P	R	A	Y	I	T	W	I	T	G	S	I	F	V	A	P	V	L	A	T	C	Y	G	F	C	F	R	I	W	S	N	A	R	R	K	A	---	---	V	G	S	V	K	N	F	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	S	A	Y	I	V	C	W	A	P	F	F	T						
Xtr_V1A	Y	V	M	I	S	A	W	I	L	S	F	L	L	S	I	P	Q	Y	F	I	F	S	F	S	P	V	-	-	N	G	S	E	V	D	C	W	A	H	F	I	Q	P	W	G	A	K	A	Y	I	T	W	I	T	G	S	I	F	L	V	P	V	L	I	T	C	Y	G	F	C	Y	H	I	W	R	N	I	C	K	T	---	---	V	S	S	V	K	T	I	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	S	A	Y	I	V	C	W	A	P	F	F	I							
Gac_V1A1	Y	I	M	I	T	S	T	W	M	V	L	L	S	S	P	Q	Y	F	I	F	S	L	S	E	I	K	-	N	G	S	N	V	D	C	W	A	H	F	V	I	Q	P	W	G	A	K	A	Y	I	T	W	I	T	V	G	I	F	L	V	P	V	I	L	M	L	C	Y	G	F	C	H	S	I	W	K	N	I	K	Y	K	---	---	V	S	S	I	T	I	S	R	A	K	L	R	T	V	K	M	T	L	V	I	V	L	A	Y	I	V	C	W	A	P	F	F	T							
Ola_V1A1	Y	I	M	I	T	S	T	W	M	C	S	L	V	L	S	T	P	Q	Y	F	I	F	S	L	S	E	I	K	-	N	G	S	D	V	D	C	W	A	H	F	I	Q	P	W	G	A	K	A	Y	I	T	W	I	T	V	G	I	F	L	V	P	V	I	L	M	L	C	Y	G	F	C	H	S	I	W	K	N	I	K	Y	K	---	---	V	S	S	V	T	I	S	R	A	K	L	R	T	V	K	M	T	F	V	I	V	L	A	Y	I	V	C	W	A	P	F	F	T						
Tru_V1A1	Y	I	M	I	S	T	W	M	C	S	L	A	S	T	P	Q	Y	F	I	F	S	L	S	E	I	E	-	K	G	S	E	V	D	C	W	A	H	F	I	Q	P	W	G	A	K	A	Y	I	T	W	I	T	V	G	I	F	L	V	P	V	I	L	M	M	C	Y	G	F	C	H	S	I	W	K	N	I	K	Y	K	---	---	V	S	S	I	T	I	S	R	A	K	L	R	T	V	K	M	T	F	V	I	V	L	A	Y	I	V	C	W	A	P	F	F	T								
Dre_V1A2	Q	V	M	I	G	G	T	W	V	C	S	L	V	L	S	S	P	Q	Y	F	I	F	S	L	S	E	I	Q	-	N	G	S	E	V	D	C	W	A	H	F	I	Q	P	W	G	V	R	A	Y	I	T	W	I	T	A	G	I	F	L	V	P	V	I	L	M	T	C	Y	G	F	C	H	S	I	R	M	S	I	R	Y	K	---	---	V	S	S	V	S	I	S	R	A	K	L	R	T	V	K	M	T	F	V	I	V	L	A	Y	I	V	C	W	A	P	F	F	T						
Dre_V1A1	Y	I	M	I	C	S	T	W	L	C	S	L	L	S	T	P	Q	Y	F	I	F	S	L	S	E	I	Q	-	N	G	S	D	V	D	C	W	A	H	F	I	Q	P	W	G	I	R	A	Y	I	T	W	I	T	V	G	I	F	L	P	V	V	I	L	C	Y	G	F	C	H	S	I	W	K	N	F	K	C	K	T	---	---	V	S	S	V	T	I	S	R	A	K	L	R	T	V	K	M	T	F	V	I	V	L	A	Y	I	V	C	W	A	P	F	F	T								
Gac_V1A2	H	V	M	I	G	S	S	W	A	C	S	L	A	L	S	L	P	Q	Y	F	I	F	S	L	S	E	V	H	-	P	G	S	G	V	D	C	W	G	H	F	E	P	W	G	L	R	A	Y	I	T	W	M	T	V	G	I	F	L	P	V	A	A	L	V	F	C	Y	G	L	I	C	R	T	I	W	R	N	L	K	Y	K	T	---	---	V	S	G	V	G	N	I	S	R	A	K	L	R	T	V	K	M	T	F	V	I	V	L	A	Y	V	V	C	W	A	P	F	F	T				
Ola_V1A2	Y	I	M	I	G	S	T	W	A	C	S	L	V	L	S	T	P	Q	Y	F	I	F	S	L	S	E	V	R	-	P	G	S	A	V	D	C	W	G	H	F	M	P	W	G	L	R	A	Y	I	T	W	I	T	A	G	I	F	L	L	P	V	A	I	L	V	F	C	Y	G	F	C	R	T	I	W	M	N	I	K	Y	K	T	---	---	V	S	S	V	S	T	I	S	R	A	K	L	R	T	V	K	M	T	F	V	I	V	L	A	F	V	V	C	W	A	P	F	F	T				
Tru_V1A2	Y	V	M	I	G	G	T	W	A	G	S	L	A	L	S	A	P	Q	Y	F	I	F	S	L	S	E	V	S	-	P	G	S	A	V	D	C	W	G	H	F	E	P	W	G	L	R	A	Y	I	T	W	M	T	A	G	I	F	V	V	P	V	A	A	L	V	F	C	Y	G	F	C	R	T	I	W	K	N	L	K	C	K	T	---	---	V	S	S	V	S	T	L	S	R	A	K	L	R	T	V	K	M	T	F	V	I	V	L	A	Y	V	L	C	W	A	P	F	F	T				
Cmi_1	Y	L	L	I	A	A	P	W	L	L	A	A	I	F	S	L	P	Q	V	F	I	F	S	L	R	E	V	I	-	Q	G	S	G	V	L	D	C	W	A	D	F	I	Q	P	W	G	P	R	A	Y	L	T	W	T	T	L	A	I	F	V	L	P	V	T	M	L	T	A	C	Y	S	L	I	C	H	E	I	C	K	N	L	K	V	K	T	---	---	R	V	S	S	I	N	T	I	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	L	A	Y	I	A	C	W	A	P	F	F	S
Mmu_V1B	Y	P	L	I	A	A	P	W	L	L	A	A	I	F	S	L	P	Q	V	F	I	F	S	L	R	E	V	I	-	Q	G	S	G	V	L	D	C	W	A	D	F	I	Q	P	W	G	T	R	A	Y	I	T	W	T	T	M	A	I	F	V	L	P	V	V	I	L	G	T	C	Y	G	L	I	C	H	E	I	Y	K	N	L	K	V	K	T	---	---	R	V	S	S	I	S	T	I	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	L	A	Y	I	A	C	W	A	P	F	F	S
Mdo_V1B	Y	P	F	I	A	A	T	L	L	A	A	G	L	S	L	P	Q	V	F	I	F	S	L	R	E	V	S	-	Q	G	T	G	V	L	D	C	W	A	D	F	I	Q	P	W	G	L	Q	A	Y	I	T	W	T	T	L	A	I	F	V	L	P	V	A	V	I	A	C	Y	S	L	I	C	H	E	I	C	K	N	L	K	V	K	T	---	---	R	V	S	S	I	S	T	I	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	L	A	Y	I	A	C	W	A	P	F	F	S		
Oan_V1B_fragment	Y	P	L	I	A	A	T	L	L	A	A	G	L	S	L	P	Q	L	F	I	F	S	L	R	E	V	S	-	R	D	S	G	V	L	D	C	W	A	H	F	R	V	P	W	G	P	R	A	Y	V	T	W	T	T	L	A	I	F	V	L	P	V	A	V	L	T	A	C	Y	G	L	I	C	H	E	I	C	K	N	L	R	G	K	S	---	---	R	V	S	S	V	R	A	I	S	R	A	K	I	R	T	V	K	M	T	F	V	I	V	L	A	Y	V	A	C	W	A	P	F	F	S	
Gga_V1B	C	A	M	V	G	A	A	W	L	L	S	C	L	L	S	T	P	Q	I	F	I	F	S	L	R	E	V	Q	-	P	G	S	G	V	L	D	C	W	A	D	F	I	Q	P	W	G	A	R	A	Y	I	T	W	T	T	L	C	I	F	L	L	P	V	I	L	T	A	C	Y	S	L	I	C	H	E	I	C	K	N	L	K	G	K	T	---	---	R	V	S	S	V	R	T	I	S	R	A	K	I	R	T																					



	260	270	280	290	300	310	
Hsa_V1A	I Q M W S V W D P M -	S V W T - E S E N P T I T I	T A L L G S L N S C C N P W I Y M F F	S G H L L Q D C V Q S F P -	C C		
Mmu_V1A	V Q M W S V W D T N -	F V W T - D S E N P S T T I T I	T A L L A S L N S C C N P W I Y M F F	S G H L L Q D C V Q S F P -	C C		
Mdo_V1A	V Q M W S V W D Q Q -	S S W T - D S E N P A I T I T I	T A L L G S L N S C C N P W I Y M F F	S G H L L Q D C V Q S F P -	C C		
Oan_V1A	V Q M W S T W D V R -	F V W L - A S E D A V V T I	T A L L A S L N S C C N P W I Y M F F	S G H L L Q D C I Q S F P -	C C		
Gga_V1A	I Q M W S V W D Q H -	F P W V - D S E N T A T T V T	T A L L A S L N S C C N P W I Y M F F	S G H L L Q D C V Q S F P -	C C		
Aca_V1A	V Q M R S V W E D H -	A S W V - E S E D I L I T V T	T A L L A S L N S C C N P W I Y M F F	S G H L L Q D F I Q S L L C C			
Xtr_V1A	V Q M R S V W D K N -	F E W T - D S E D I A T T V T	T A L L G S L N S C C N P W I Y M F F	S G H L L Q D F I H S F P -	C C		
Gac_V1A1	V Q M W S V W D D N -	F Q W A - D S E N T A V T L S	A L L A S L N S C C N P W I Y M I F	S G H L L Q D F V H C F S -	C C		
Ola_V1A1	V Q M W S V W D E N -	F L W D - D S D N T A V T L S	A L L A S L N S C C N P W I Y M I F	S G H L L Q D F V H C F S -	C C		
Tru_V1A1	V Q M W S V W D E N -	F Q W A - D S E N T A V T L S	A L L A S L N S C C N P W I Y M I F	S G H L L Q D F V H C L P -	C C		
Dre_V1A2	V Q M W S V W D Q S -	F N W D - D S K N T A V T L S	A L L A S L N S C C N P W I Y M V F	S G H L L Q D F A L C F P -	C C		
Dre_V1A1	V Q M W S V W D E N -	F S W D - D S E N A A V T L S	A L L A S L N S C C N P W I Y M L F	S G H L L H D F L G C F P -	C W		
Gac_V1A2	V Q M W S V W D K S -	F S F A - D S E S T T V T L X	A L L A S L N S C C N P W I Y M V F	S G H L L S D - - - -	L P - C C		
Ola_V1A2	V Q M W S V W D Q T -	F S W D - D S E N T T V T L S	A L L A S L N S C C N P W I Y M I F	S G H L L S D F F S G L P -	C C		
Tru_V1A2	V Q M W S V W D H T -	F S W D - D S E S T A V T L S	A L L A S L N S C C N P W I Y M L F	G G R L L S D C A G S L P -	C C		
Cmi_1							
Hsa_V1B	V Q M W S V W D K N -	A P D E - D S T N V A F T I	S M L L G N L N S C C N P W I Y M G F	N S H L L P R P L R H L A -	C C		
Mmu_V1B	V Q M W S V W D E N -	A P N E - D S T N V A F T I	S M L L G N L S S C C N P W I Y M G F	N S H L L P R S L S H R A -	C C		
Mdo_V1B	V Q M W S V W D E N -	A P D E - D S T N V A F T I	T M L L G N L S C C N P W I Y M C F	S S Y L L P A P L R D L S -	C C		
Oan_V1B_fragment	V Q M W S V W D E N -	I R T E - D S S D V A F T I	T M L L G S L S C C N P W I Y M S F	N S H L L P E S L R C F S -	C L		
Gga_V1B	M Q M W S V W D E D -	A P D D - E S A D A A F T I	T M L L A S L S S C C N P C I Y M F F	S G R P L Q D T A R C L A -	L W		
Aca_V1B	V Q M W S V W D K D -	A P N D - E S S N V T F T I	T M L L A S L S S C C N P W I Y M F F	S G H L F H V F H F F A -	C C		
Cmi_2	V Q M W S V W D L A -	A P D D -					
Xtr_V1B	V Q M W S V W D E N -	S P D E - D S T D F A F T I	T M L L A S L S S C S N P W I Y M C Y N S	P Q L C R G T S R P H -	G H		
Hsa_OTR	V Q M W S V W D A N -	A P K E - A S - - - A F I I	V M L L A S L N S C C N P W I Y M L F	T G H L F H E L V Q R F L -	C C		
Mmu_OTR	V Q M W S V W D V N -	A P K E - A S - - - A F I I	A M L L A S L N S C C N P W I Y M L F	T G H L F H E L V Q R F L -	C C		
Mdo_OTR	V Q M W S V W D P D -	A P K E - T S - - - L F I I	A M L L A S L N S C C N P W I Y M L F	T G H L F H D L V H R F F -	C C		
Oan_OTR	V Q M W S V W D K D -	A P K E - A S - - - P F I I	A M L L A S L N S C C N P W I Y M L F	T G H L F H D L V Q R F L -	C C		
Gga_OTR	V Q M W S V W D T N -	A P Q E - A S - - - P F I I	A M L L A S L N S C C N P W I Y M L Y T	T G H L F H D L M R R F L -	C C		
Aca_OTR	V Q M W I W D E N -	A P K E - E L - - - A F I I	T L L A S L N S C C N P W I Y M L F	T G H L F H D L L H R F L -	C C		
Xtr_OTR	V Q M W S V W D P D -	A P K E - D S - - - L F I I	A M L L G S L N S C C N P W I Y M L F	T G H L F H D L L Q R F L -	C C		
Cmi_3	V Q M W T A W D P H -	A P K E -					
Gac_OTR	V Q M W T A W D S A -	A P R E - A L - - - P F I I	S M L L A S L N S C C N P W I Y M C F A	G H L F Q D L R Q N F L -	C C		
Ola_OTR1	V Q M W S A W D Q A -	A P R E - A M - - - P F I I	S M L L A S L N S C C N P W I Y M C F A	G H L F H D L R Q N L L -	C C		
Tru_OTR1	V Q M W S A W D P S -	A P R E - A T - - - P F I I	S M L L A S L N S C C N P W I Y M F F A	G H L F Q D L R Q T F L -	C C		
Dre_OTR1	V Q M W S A W D P E -	A P R E - A M - - - P F I I	S M L L A S L N S C C N P W I Y M F F A	G H L F H D L K Q N L F -	C C		
Dre_OTR2	V Q M W S A W D P M -	A P R E - A M - - - A F I I	A M L L A S L N S C C N P W I Y M F F A	G H L F R D L M Q - - - -			
Tru_OTR2	V Q L W S A W D P A -	A P R E - D M - - - A F I I	A M L L A S L N S C C N P W I Y M F F A	G H L F Q D L R R G F S -	C C C		
Ola_OTR2	V Q M W S A W D P A -	A P R E - D M - - - A F I I	A M L L A S L N S C C N P W I Y M F F A	G H L F H D L I Q C F F S -	C C		
Dre_V2B	V Q L W S V W D D D -	A P T E - T A - - - T F T I	L M L L A S L N S V A N P C I Y L L F	T V K F P E L L - G S L L -	C M		
Gac_V2B	V Q L W S A W D T N -	A P K E - T A - - - T F T V	L M L L A S L N S C A N P C I Y L L F	S G Q F P K K M - R T F L -	W Q		
Ola_V2B	V Q L W S A W D T H -	A P K E - T A - - - T F T I	L M L L A S L N S C A N P C I Y L L F	S G Q F P K K L - L T L L -	C R		
Tru_V2B	V Q L W S V W D D E -	A P T H - T A - - - T F T I	L M L L A S L N S C A N P C I Y L L F	N G S C S T G S - C P T G -	C -		
Cmi_4	V Q L W S V W D P K -	A P R E -					
Gga_V2B	A Q L W S V W F P S -	G I T E - G S - - - A F T I	I M L L G N L N S C T N P W I Y M Y F	C G H I P Y C T - N K Q L -	E N		
Xtr_V2B	V H L W V A W S E D V -	T E - G A - - - A F T I	I M L L G N L N S C A N P W I Y M Y F	S G H I P R C V - S H R E -	T L		
Aca_V2B_fragment	A Q L W T A W H P S D A R T E -	G P - - - S N S Y	L M L L A N L N S C V N P W I Y M Y F	G Q I P H C S - K N Q T -	K P		
Hsa_V2A	V Q L W A A W D P E -	A P L E - G A - - - P F V L	L M L L A S L N S C T N P W I Y A S F	S S S V S S E L - R S L L -	C C		
Mmu_V2A	V Q L W A A W D P E -	A P L E - R P - - - P F V L	L M L L A S L N S C T N P W I Y A S F	S S S V S S E L - R S L L -	C C		
Mdo_V2A_fragment	V Q L W S V W D P X G T P G -	R P - - - P F V L	L M L L A S L N S F T N P W I Y A S F	S S S V S S E L - R S L L -	C C		
Oan_V2A	V Q L W A V W D P H -	S P K N - G P - - - A F T I	L M L L A S L N S C T N P W I Y A S F	S S S V S S E L - R Q L L -	C C		
Aca_V2A_fragment	V Q L W S V W D P E -	A P I D - G P - - - A F T I	L M L V A S L N S C T N P W V Y A A F	S S S I S N E L - C R I F -	C P		
Xtr_V2A	A Q L W N V W N Q E S A A -	G S S - - A I K V	L M I L A S L N S C T N P W I Y T I	F S S S V S K D V - K E I L -	C F		
Gac_V2A1_unsolved	V Q L W A A W D P N -	P A S H T G V - - - A F T I	L M L L A S L N S C T N P W I Y T A F	S S S V S R E L - Q N L L -	Q C		
Ola_V2A1	V Q L W A A W D P N -	P P D Q - G V - - - A F T I	L M L L A S L N S C T N P W I Y T A F	S S S V S R E L - Q N L L -	H C		
Tru_V2A1	V Q L W A A W D P N -	S P D Q - G V - - - A F T I	L M L L A S L N S C T N P W I Y T A F	S S S V S R E L - Q N L L -	H C		
Dre_V2A2	V Q L W A A W D P N -	P P D Q - G V - - - A F T I	L M L L A S L N S C T N P W I Y T A F	S S S V S R E L - L A L L -	R C		
Gac_V2A2	V Q L W A A W D P N -	P P Q N - G A - - - V F T L	L M L L A S L N S C T N P W I Y S A F	S S S V S L E L - R L L L -	L C		
Tru_V2A2_unsolved	V Q L W A A W D P D -	P P Q N - G A - - - V F T L	L M L L A S L N S C T N X W I Y S A F	S S S V S P E L - R L L L -	L C		
Ola_V2A2_unsolved	V Q M W A A W Y P D -	P P Q R - D A - - - A F T I	L L L L S S L N S C T N P W I Y S A F	S S S V S P E L - R - L L -	L C		
Dre_V2A1	V Q L W A A W D P N -	P P I Q - G A - - - V F T I	L M L L A S L N S C T N P W I Y T A F	S S S V S R E L - L A L L -	R C		
Cmi_5							
Dre_V2-like	V Q L W S A W S P S S A P T Q -	G P - - - V F V T	I M L L A S L N S C T N P W I Y L Y Y S				
Gac_V2-like	V Q L W S A W S P S S T P T Q -	G P - - - V F A I	I M L L A S L N S C T N P W I Y L Y Y S				
Cin_VPR	V Q M L A A W G A I N -	E D - H I - - - A A S C	I K L L A S L N S C T N P W I Y M A F S				
Ovu_CTR2	S Q I W W L F D E T V V G -	- - - N A - - - G V V V	I L M A C L N S C T N P W I Y L I F N				
Ovu_CTR1	C Q M W A A W D E N A P Y S -	- - - G A - - - I Y T I	L L L L S S L N S C T N P W I Y M I F S				
Ovu_OPR	V L M A R T Y D A E L S S A Q -	T P - - - A L V I	L S L L P S L N S C T N P W I Y L A F S				