

Results colour-coded for amino acid conservation

The current colourscheme of the alignment is for amino acid conservation.

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position. The colour assignments are:

Unconserved 0 1 2 3 4 5 6 7 8 9 10 Conserved

	10	20	30	40	50
HsMTA1	-----	-----	-----	M AANMYRVGDY	VYFENSSSNP
MmMTA1	-----	-----	-----	M AANMYRVGDY	VYFENSSSNP
ScaMTA1	-----	-----	---	LF-LSDY	VYFENSSSNP
CmMTA1	-----	-----	-----	M AANMYRVGDY	VYFENSSSNP
HsMTA2	-----	-----	-----	M AANMYRVGDY	VYFENSSSNP
DrMTA3	-----	-----	-----	M AANMYRVGDY	VFFENSSSNP
DmMTA1	-----	-----	-----	M ATNMYRVGDY	VYVETTPNSP
HlMTA1	MPMPAEYHEN	HGNHENANFA	LGATQDASN	M TANMYRVGDY	VYFETSSTSP
Consistency	0000000000	0000000000	0000000000	7 6 6 7 9 9 7 9 8 **	* 9 8 * 7 8 8 7 8 *
	60	70	80	90	100
HsMTA1	YLIRRIEELN	KTANGNVEAK	VVCFYRRRDI	SSTLIALA	-----
MmMTA1	YLIRRIEELN	KTANGNVEAK	VVCFYRRRDI	SSSLIALA	-----
ScaMTA1	YLIRRIEELN	KTANGNVEAK	VVCFYRRRDI	SSTLIVLA	-----
CmMTA1	FLIRRIEELN	KTANGNVEAK	VVCFYRRRDI	PSTLIGLA	-----
HsMTA2	YLVIRRIEELN	KTANGNVEAK	VVCLFRRRDI	SSSLNSLA	-----
DrMTA3	YLIRRIEELN	KTASGNVEAK	VVCFYRRRDI	SQSLIQLA	-----
DmMTA1	YLIRRIEELN	KNQTGNVEAK	VMCFYRRRDL	PNPLVQLADK	HQLATAEDSP
HlMTA1	YQIRRIEELN	KTASGNVEAK	VMCFFRRRDL	PSTLIMLADK	HQLASAEQQR
Consistency	9 8 9 * * * * * * *	* 8 8 7 * * * * * * *	* 8 * 8 8 * * * * * 8	6 7 6 * 7 4 * * * 0 0	0 0 0 0 0 0 0 0 0 0
	110	120	130	140	150
HsMTA1	-----	DKHAT	LSV	-----	-----
MmMTA1	-----	DKHAT	LSV	-----	-----
ScaMTA1	-----	DKHAS	KL	-----	-----
CmMTA1	-----	DKHAS	QEL	-----	-----
HsMTA2	-----	DSNAR	-----	-----	-----
DrMTA3	-----	DKHAK	-----	-----	-----
DmMTA1	LATKLKKTWL	RTPVSEEQAA	QAVLDPSIAA	LDEERTSPTQ	TSGGGGSATG
HlMTA1	SE-----	--SPANTQSQ	KL-----	---ENPDTTK	EMTNKDGIGP
Consistency	0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 7 6 6 9 4	2 2 3 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0
	160	170	180	190	200
HsMTA1	CYKAGP	GAD	NGEEGEIEEE	MENPEMVDLP	EKLKHQLRHR
MmMTA1	CYRAGP	GAD	TGEEGEVEEE	VENPEMVDLP	EKLKHQLRHR
ScaMTA1	CVQVTS	TQN	---FQTEMEEE	MENPEMVDLP	EKQKHQLRHR
CmMTA1	DNCDPALP	SEVPEVQOET	LTKSEDLLEE	METDSLQQLT	EKQQHQLKHR
HsMTA2	-----	-----	EFEEEE	SK---QPGVS	EQQRHQLKHR
DrMTA3	-----	-----	DLEEE	KESPESDIT	EKQKHQLRHR
DmMTA1	NSGSNSSGTS	NNNSSTAIG	GGAGSGGAG	GDAEKGEALT	SKQRYQIKHR
HlMTA1	KVMNKGKGGK	GWLKAPLSEA	QEPHGMEENV	VGAGGVTELS	SKQRHQMKHR
Consistency	0 0 1 1 2 2 2 2 0 0	0 0 0 0 0 0 0 2 2 2	0 1 1 2 2 5 3 8 7 6	4 6 3 3 3 4 4 5 9 5	7 8 6 7 8 * 8 8 * *
	210	220	230	240	250
HsMTA1	ELFLSRQLES	LPATHIRGKC	SVTLLNETES	LKSYLEREDF	FFYSLVYDPQ
MmMTA1	ELFLSRQLES	LPATHIRGKC	SVTLLNETES	LKSYLEREDF	FFYSLVYDPQ
ScaMTA1	ELFLSRQLES	LPATHIRGKC	SVTLLNETES	LKSYLEREDF	FFYSLVYDPQ
CmMTA1	ELFLSRQLES	LPATHIRGKC	SVTLLNETEA	VFSYLEKEDS	FFYCLVYDPQ
HsMTA2	ELFLSRQFES	LPATHIRGKC	SVTLLNETDI	LSQYLEKEDC	FFYSLVYDFV
DrMTA3	ELFLSRQYES	LPATHIRGKC	SVALLNETEV	VLSYLEKEDT	FFYSLVYDPT
DmMTA1	ELFLSRQVES	IPATQIRGKC	SVTLLNETES	LQSYLNKDDT	FFYCLVYDFN
HlMTA1	ELFLSRQVET	MPATHIRGKC	CVTLLNETES	LLSYLNKEDS	FFYCLVYDFPA
Consistency	* * * * * * * 6 * 8	8 * * * * 8 * * * * *	8 * 8 * * * * * 9 6	8 4 8 * * * 7 8 9 * 4	* * * * 6 * * 8 * * 4
	260	270	280	290	300
HsMTA1	QKTLLADKGE	IRVGNRYQAD	ITDLLK	EGEEDGRDQS	RLETQVWEAH
MmMTA1	QKTLLADKGE	IRVGNRYQAD	ITDLLK	EGEEDGRDQS	KLETQVWEAH
ScaMTA1	QKTLLADKGE	IRVGNRYQAD	ITDLLK	EGEDDGRDQS	KLETQVWEAF
CmMTA1	QKTLLADKGE	IRVGNRYQAD	IPDLLK	EGEEDGRDQV	KLEAKIWDTD
HsMTA2	QKTLLADQGE	IRVGCYQAE	IPDRLV	EGESDNRNQQ	KMEMKVWDPD
DrMTA3	QKTLLADKGE	IRVGNRYQAD	VPEMLQ	EGEADDRDQS	KLEMKMWDPE
DmMTA1	QKTLLADKGE	IRVGSRYQCD	IPAKLK	DTATDDRKLE	ELESVWTPPE
HlMTA1	QRTLLADKGE	IRVGSRYQAD	GIAPTPLTPA	ERESDPRLQ	DLETLVWTPR
Consistency	* 9 * * * * * 8 * *	* * * * * 4 9 9 * 8 9	0 0 0 0 8 6 5 5 7 6	9 6 8 5 * 4 * 5 6 5	6 9 * 5 5 8 * 5 5 4

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..... 310..... 320..... 330..... 340..... 350
HsMTA1 NPLTDKQIDQ FLVVARSVGT FARALDCSSS VRQPSLHMSA AAASRDITLF
MmMTA1 NPLVDKQIDQ FLVVARSVGT FARALDCSSS VRQPSLHMSA AAASRDITLF
ScaMTA1 NPLVDKQIDQ FLVVARSVGT FARALDCSSS VRQPSLHMSA AAASRDITLF
CmMTA1 NPLTDRQIDQ FLVLARSVGT FARALDCSSS IRQPSLHMSA AAASRDITLF
HsMTA2 NPLTDRQIDQ FLVVARAVGT FARALDCSSS IRQPSLHMSA AAASRDITLF
DrMTA3 CPLTNKQIDQ FLVVARAVGT FARALDCSSS VRQPSLHMSA AAASRDITLF
DmMTA1 HSLTDRKIDQ FLVVSRSIGT FARALDCSSS VKQPSLHMSA AAASRDITLF
HlMTA1 HSLTDRQIDQ FLVVSRSVGT FARALDCSSS VKQPSLHMSA AAASRDITLF
Consistency 57*7888*** **98*89** ***** 98***** *****9***

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..... 360..... 370..... 380..... 390..... 400
HsMTA1 HAMDTLHKNI YDISKAISAL VPQGGPVLCR DEMEEWSASE ANLFEEALEK
MmMTA1 HAMDTLHKNI YDISKAISAL VPQGGPVLCR DEMEEWSASE ANLFEEALEK
ScaMTA1 HAMDTLHKNI YDISKAISAL VPQGGPVLCR DEMEEWSASE ANLFEEALEK
CmMTA1 HSMDTLHKNI YDISKAISAL VPQGGPVLCR DEMEEWSASE ANMFEEALEK
HsMTA2 HAMDTLQRNG YDLAKAMSTL VPQGGPVLCR DEMEEWSASE AMLFEEALEK
DrMTA3 HAMDTLHRHG YDLSSALSVL VPQGGPVLCR DEMEEWSASE ANLFEEALEK
DmMTA1 HAMNIIHKHE YSIEESMSSL VPSTGPVLCR DEIEDWSASE ANLFEEALEK
HlMTA1 HAMDTLHRHN YDVAKAMSSL VPSTGPVLCR DEMEEWSASE ANLFEEALDK
Consistency *9*88*8873 *887797*6* **76***** **8*9**9** *89*****9*

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..... 410..... 420..... 430..... 440..... 450
HsMTA1 YGKDFTDIQQ DFLPWKSLTS IIEYYYMWKT TDRYVQQRK KAAEAESKLLK
MmMTA1 YGKDFTDIQQ DFLPWKSLTS IIEYYYMWKT TDRYVQQRK KAAEAESKLLK
ScaMTA1 YGKDFTDIQQ DFLPWKSLTS IIEYYYMWKT TDRYVQQRK KAAEAESKLLK
CmMTA1 YGKDFSDIRQ DFLPWKALTS IVEYYYMWKT TDRYVQQRK KAAEAESRLK
HsMTA2 YGKDFNDIRQ DFLPWKSLAS IVQFYMWKT TDRYIQQRK KAAEADSKLLK
DrMTA3 YGKDFNDIRQ DFLPWKSLTS IIEYYYMWKT TDRYVQQRK KAAEAESKLLK
DmMTA1 YGKDFNDIRQ DFLPWKTLKQ IIEYYYMWKT TDRYVQQRK KAVEAELKLLK
HlMTA1 YGKDFSDIRQ DFLPWKTLKN VIEYYYMWKT TDRYVQQRK KAVEAESKLLK
Consistency ****6**7* *****7*67 9999***** ****9****8 **7**989**

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..... 460..... 470..... 480..... 490..... 500
HsMTA1 QVYIPNYNKP NPNQI----- SV NN--VKAGVV NGTGAP----
MmMTA1 QVYIPNYNKP NPNQI----- SA SS--VKATVV NGTGTP----
ScaMTA1 QVYIPNYNKP NPNQI----- NV NN--VKPGVV NGTGVQ----
CmMTA1 QVYIPNYNKP NPNQI----- NV NSTVAKSAMV NGAAVP----
HsMTA2 QVYIPTYTKP NPNQI----- IS VG--SKPG-M NGAG-----
DrMTA3 QVYIPTYTKP NPNQI----- SV SN--GKMATV NGAAAG----
DmMTA1 QVYIPQYNNN GKGNG----- TSTKAGGGIY NGTT-----
HlMTA1 QVYIPNYNKT APPTTAPSAA TIVPLGNNNS NSNGKPTNVL NGNSNGNMTT
Consistency ****6*886 68676 00000 000000044 5600463556 **65220000

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..... 510..... 520..... 530..... 540..... 550
HsMTA1 --G--QSPG AGRACESCYT TQSYQWYS--
MmMTA1 --G--QSPG AGRACESCYT TQSYQWYS--
ScaMTA1 --A--QNTG AGRACESCYT TQSYQWYS--
CmMTA1 --G--QNGG AGRACESCYT TQSYQWYS--
HsMTA2 -----FQ KGLTCECHT TQSAQWYA--
DrMTA3 --TGSFHTAG GGRACESCFV VQSAQWYS--
DmMTA1 --NGSTDLS NGKPCESC GT TKS SQWNS VS SGHSTRRLCL SCWEYWRRYG
HlMTA1 DNSGILMVG VSGKPCESC QV MQSPQWY--
Consistency 0031004335 5*66***47 78*4**7600 0000000000 0000000000

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..... 560..... 570..... 580..... 590..... 600
HsMTA1 -----W GPPNMQCRLC ASCWTYWKKY GGLKMPTRLD GE-----
MmMTA1 -----W GPPNMQCRLC ASCWTYWKKY GGLKMPTRLD GE-----
ScaMTA1 -----W GPPNMQCRLC ASCWTYWKKY GGLKMPTRLD GE-----
CmMTA1 -----W GPPNMQCRLC ATCWNYWKKY GGLKMPTRLE GE-----
HsMTA2 -----W GPPNMQCRLC ASCWIYWKKY GGLKTPQLE GA-----
DrMTA3 -----W GPPNMQCRLC VSCWYWKKY GGLKMPSPRAE GAE-----
DmMTA1 SMKSATKGD A GEGDAKKKSS SAASTPTATL AGLATTPTAV VDL-----
HlMTA1 -----AW GPSHMQCRLC QSCWTYWKKY GGLKVP SRMD DVDLERKRGG
Consistency 0000000007 *867887988 6887577888 8**8686766 6500000000

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..... 610..... 620..... 630..... 640..... 650
HsMTA1 -----RPGPNR-- --SNMSPH GLPA--RSS-
MmMTA1 -----RPGPNR-- --NNMSPH GIPA--RSS-
ScaMTA1 -----RPGPNR-- --NNLSPH GVPV--RNS-
CmMTA1 -----RPGPNR-- --SSANPH GYVW--KN--
HsMTA2 -----TRGTTEPHS RGHLSPPEAQ SLSPYTTSA-
DrMTA3 -----EKTP PSPAPNESRS RGHCARQSSH MVPI--RNS-
DmMTA1 --NDDEKISD LTNRQLHRCS IVNCGKEFKL KTHLARHYAQ AHGIAISS--

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HlMTA1	TGSDEESKGI	GGAHRPHRCS	IPSCGKEFKL	KAHLSRHYAS	AHGVDLRGSG					
Consistency	000000000	000000000	0455566011	1021663556	5435006640					
	660.....	670.....	680.....	690.....	700.....				
HsMTA1	-----	GSP	KFAMKTRQAF	YLHTTKLTRI	ARRLCREILR	PWHAARHPYL				
MmMTA1	-----	GSP	KFAMKTRQAF	YLHTTKLTRI	ARRLCREILR	PWHAARHPYM				
ScaMTA1	-----	GSP	KFAMKTRQAF	YLHTTKLTRI	ARRLCRDILR	PWHAARHPYL				
CmMTA1	-----	ANP	KFTLKTRQAF	CLQTTKLTKI	ARYFCRSLFH	TRQSARRPFT				
HsMTA2	-----	NRA	KLLAKNRQTF	LLQTTKLTRL	ARRMCRDLLQ	PRRAARRPYA				
DrMTA3	-----	GSP	KSSMKTQAF	LLQATRLLTKL	ARRMCRDLIR	LRRRAARRPFV				
DmMTA1	-----	GSP	RPIMKTRTAF	YLHTNPMTRV	ARAI CRSIVK	PKKAARQSAY				
HlMTA1	ASGGGGG	GSP	RPVMKTRSAF	YLRTSALARA	ARRLCAAQLR	TRHAARAPHQ				
Consistency	0000000	778	8357*8978*	5*68769887	**57*85676	5459**5854				
	710.....	720.....	730.....	740.....	750.....				
HsMTA1	PINSAAIKAE	CTA	RLPEAS	Q-SPLVLKQA	V-----	RKPL	EAVLRYLETH			
MmMTA1	PINSAAIKAE	CTA	RLPEAS	Q-SPLVLKQV	V-----	RKPL	EAVLRYLETH			
ScaMTA1	PINSAAIKAE	CTA	RLPEAS	E-NPLLLKQV	V-----	RKPL	EAVLRYLESH			
CmMTA1	PINSAAIKAE	CTA	RLPEIG	E-KPIKPKPS	V-----	RKTL	ESI AKYLELH			
HsMTA2	PINANAIAKAE	CSI	RLPKAA	K-TPLKIHP	V-----	RLPL	ATIVKDLVAQ			
DrMTA3	PINC GAIAKAE	YMI	RVSEGM	TGRPLPKPKSS	P-----	RSTL	TSVLQYLESR			
DmMTA1	AINAMLVKQE	FTN	RISGKS	Q-AEIKKLL	LK-PKDRGSV		TKIANRLGAP			
HlMTA1	PVNAAPLRHL	CASP	QLTSKS	S-VELRILAR	AVRPRPRPRV		TDIATRLGDH			
Consistency	89*	6569967	6650	886646	5047855544	600000*	448	559654*	545	
	760.....	770.....	780.....	790.....	800.....				
HsMTA1	P-----				RPP	KPDPVKS	V-----	SSV		
MmMTA1	P-----				RPP	KPDPVKS	V-----	SSV		
ScaMTA1	P-----				CPP	KPDPAKSL	V-----	SSS		
CmMTA1	P-----				SV	KPICSLA	V-----	VH		
HsMTA2	A-----				PL	KPKTPRGT	V-----	K--		
DrMTA3	P-----				AT	HVQRPHRT	V-----	PGL		
DmMTA1	G----	SGPHE	WLVLT	PKDKM	PLPAVVS	FPK	PPKAPDGS	LV	YDRV	PNKSPD
HlMTA1	PAPRQPGDWD	WLALTA	AAAQR	KQPD	RVSFPR	PPKAPDGS	LL	YERV	PNKSEV	
Consistency	6000000000	0000000000	00000001	63	58434354	00	0000000	532		
	810.....	820.....	830.....	840.....	850.....				
HsMTA1	LSSLTPAKVA	PVINNGSPTI	LGKR--	SYEQ	HNGVDGNMCK	RLLMPSRGLA				
MmMTA1	LSSLTPAKSA	PVINNGSPTI	LGKR--	SYEQ	HNGVDGNMCK	RLLMPSRGLA				
ScaMTA1	LNNLTPAKFT	PVINNGSPTI	LGKR--	SYEQ	HNGMDGNMCK	RLLMPSRGLP				
CmMTA1	SGSVTPAKIL	PVLNHGSPTI	LGKR--	GYEQ	HNGIDGTMCK	RLLMPPFRGKT				
HsMTA2	-TPINRNQLS	Q--NRGLGGI	MVKR--	AYET	MAG-----					
DrMTA3	QVQPPRRLLS	SLPSHGPLGM	LGKR--	SYHH	HSRVESAERR	AGATG-----				
DmMTA1	VVAVPADKEL	TIIPTQATST	IRKRAHEDQ	Q	LNGTEVTIVP	SGPPAKRPNK				
HlMTA1	DRLTVTPPQP	QPSMQAQQTI	LKRTRPPFDE	INGSDGIALS	AGLPGGPPAK					
Consistency	2345444534	5435465367	849800	5766	5784643444	4343323322				
	860.....	870.....	880.....	890.....	900.....				
HsMTA1	-----	NHGQARHM	GP-SRNLLL	N	GKSYP	TKVRL	IRGGS	LPPVK		
MmMTA1	-----	NHGQTRHM	GP-SRNLLL	N	GKSYP	TKVRL	IRGGS	LPPVK		
ScaMTA1	-----	NHGQTRQM	GP-SRNLLL	N	GKSYP	TKVRL	IRGGS	MPPVK		
CmMTA1	LAQSCSRLHS	HPNHGQVRQM	AAVNR	GYMIN	GKPY	SRSSKI	LKPGS	LPPMK		
HsMTA2	-----		A--GVP	FSAN	GRPLA	---SG	IRSSS	QPAAK		
DrMTA3	-----	QENPAHI	V--GPI	LQHN	GSSTG	---GS	SLRGS	GLMLR		
DmMTA1	DPMPSHCPSP	EQFAAMMAAS	GQPLSRHHLN	GKQ----	KI	AQMARGGNGR				
HlMTA1	RAHHSQQLHP	KHTLEHTAPT	VLPLAPPLNG	RAAHPHTLPH	GPPLSRSNAR					
Consistency	0000000000	0023343434	5204434448	8653312243	4535834458					
	910.....	920.....	930.....	940.....	950.....				
HsMTA1	RRRMNWIDAP	DDVIFYMATEE	TRKIRKLLSS	SETKRAARRP	YKPIALRQSQ					
MmMTA1	RRRMNWIDAP	DDVIFYMATEE	TRKIRKLLSS	SETKRAARRP	YKPIALRQSQ					
ScaMTA1	RRRMNWIDAP	DDVIFYMATEE	TRKIRKLLSS	SEAKRAARRP	YKPIILRP--					
CmMTA1	GRRMNWIDAP	DDVLFIMATEE	TRKIRKLLGP	VDMKRAARQP	YKQIFIRQAR					
HsMTA2	RQKLN PADAP	NPVV FVATKD	TRALRKAL	TH	LEMRRARRP	NLPLKVKPTL				
DrMTA3	KRRPNWIDAP	DDSFFLVSRE	TRKARRMLSR	SQLRRACRQP	CEQISLRRVP					
DmMTA1	KQVISWMDAP	DDVYFRANDT	HKKTRKILSA	VDLRRAARKP	WRTLPIKP--					
HlMTA1	KQVISWMDAP	DDVYFRASDQ	TKRLRKTLSS	VELRRAARKP	WRRLPAPL--					
Consistency	6756876***	8886858766	7876*96*75	5758**8*7*	4648376411					
	960.....	970.....							
HsMTA1	A----	LPPRP	PPP-APV	NDE	PIVIED					
MmMTA1	A----	LPLRP	PPP-APV	NDE	PIVIED					
ScaMTA1	-----	MQAV	QLR-QPM	NDE	PIIIED					
CmMTA1	V----	SCAVS	QPSRQP	VNEE	PIIIED					
HsMTA2	I	AVRPPVPLP	APSH	PASTNE	PIVLED					

DrMTA3	Q	G	P	S	Q	V	P	I	L	A	P	P	H	P	S	L	R	M	R	G	P	I	V	I	H	D			
DmMTA1	-	-	-	-	-	-	-	-	-	-	A	A	P	E	P	S	-	S	R	P	I	E	S	Q	I	V	I	L	D
HlMTA1	-	-	-	-	-	-	-	-	-	-	H	P	P	H	P	Q	R	A	V	R	G	D	D	M	V	V	I	L	D
Consistency	1	0	0	0	1	2	3	3	5	4	7	4	0	5	4	3	4	6	6	6	9	9	9	5	*				