

Results colour-coded for secondary structure

The current colourscheme of the alignment is for **secondary structure type**.

The 3-state (H, E C) secondary structure for each sequence is represented by a colour. If a sequence in the alignment has no colours assigned, this means that either there is no DSSP information available (if this was requested), or that no prediction was possible for that sequence (if this was requested).

The colour assignments are:

HELIX (H) **STRAND (E)** You have selected to perform secondary structure prediction using **DSSP** (Kabsch and Sander, 1983) and **Porter** (Pollastri and McLysaght, 2005).

	 10 20 30 40 50	
(PRED)	HsMTA1	-----	-----	-----M	AANMYRVGDY	VYFENSSSNP	
(PRED)	MmMTA1	-----	-----	-----M	AANMYRVGDY	VYFENSSSNP	
(PRED)	ScaMTA1	-----	-----	-----	---LF-LSDY	VYFENSSSNP	
(PRED)	CmMTA1	-----	-----	-----M	AANMYRVGDY	VYFENSSSNP	
(PRED)	HsMTA2	-----	-----	-----M	AANMYRVGDY	VYFENSSSNP	
(PRED)	DrMTA3	-----	-----	-----M	AANMYRVGDY	VFFENSSSNP	
(PRED)	DmMTA1	-----	-----	-----M	ATNMYRVGDY	VYVETTPNSP	
(PRED)	HlMTA1	MPMPA EY HEN	HGNHENANFA	LGATQD ASN M	TAN MYRVGDY	VYFETSSTSP	
	 60 70 80 90 100	
(PRED)	HsMTA1	YLIRRIEELN	KTANGNVEAK	VVCFYRRRDI	SSTLIALA	-----	
(PRED)	MmMTA1	YLIRRIEELN	KTANGNVEAK	VVCFYRRRDI	SSSLIALA	-----	
(PRED)	ScaMTA1	YLIRRIEELN	KTANGNVEAK	VVCFYRRRDI	SSTLIVLA	-----	
(PRED)	CmMTA1	FLIRRIEELN	KTANGNVEAK	VVCFYRRRDI	PSTLIGLA	-----	
(PRED)	HsMTA2	YLVRRIEELN	KTANGNVEAK	VVCLFRRRDI	SSSLNSLA	-----	
(PRED)	DrMTA3	YLIRRIEELN	KTASGNVEAK	VVCFYRRRDI	SQSLIQLA	-----	
(PRED)	DmMTA1	YLIRRIEELN	KNQTNVEAK	VMCFYRRRDL	PNPLVQLADK	HQLATAEDSP	
(PRED)	HlMTA1	YQIRRIEELN	KTASGNVEAK	VMCFYRRRDL	PSTLIMLADK	HQLASAEQQR	
	 110 120 130 140 150	
(PRED)	HsMTA1	-----	DKHAT	LSV	-----	-----	
(PRED)	MmMTA1	-----	DKHAT	LSV	-----	-----	
(PRED)	ScaMTA1	-----	DKHAS	KLV	-----	-----	
(PRED)	CmMTA1	-----	DKHAS	QEL	-----	-----	
(PRED)	HsMTA2	-----	DSNAR	-----	-----	-----	
(PRED)	DrMTA3	-----	DKHAK	-----	-----	-----	
(PRED)	DmMTA1	LATK LKKTWL	RTPV SEEQAA	QAVLDP	SIAA	LDEERT SPTQ	TSGG GGSATG
(PRED)	HlMTA1	SE-----	--SPANT QSQ	KL-----	---ENPD TTK	EMTN KDGIGP	
	 160 170 180 190 200	
(PRED)	HsMTA1	-- CYKAGP --	-----GAD	NGEEGEIEEE	MENPE MVDLP	EKLKHQLRHR	
(PRED)	MmMTA1	-- CYRAGP --	-----GAD	TGEEGEVEEEE	VENPE MVDLP	EKLKHQLRHR	
(PRED)	ScaMTA1	-- CVQVTS --	-----TQN	-- FQTEMEEEE	MENPE MVDLP	EKQKHQLRHR	
(PRED)	CmMTA1	-- DNCDPALP	SEVPE VQOET	LTKSEDL EEE	METD SLQQLT	EKQQHQLKHR	
(PRED)	HsMTA2	-----	-----	EFEEE	SK-- QPGVS	EQQRHQLKHR	
(PRED)	DrMTA3	-----	-----	DLEEE	KESP ESDLT	EKQKHQLRHR	
(PRED)	DmMTA1	NSGS NSSGTS	NNSSSTAIG	GGAGGSGGAG	GDAEK GEALT	SKQRYQIKHR	
(PRED)	HlMTA1	KVMNK GGGKG	GWLK APLSEA	QEPHGMEENV	VGAG GVTELS	SKQR HQMKHR	
	 210 220 230 240 250	
(PRED)	HsMTA1	ELFLSRQLES	LPATHIRGKC	SVTLLNETES	LKSYLEREDF	FFYSLVYDPQ	
(PRED)	MmMTA1	ELFLSRQLES	LPATHIRGKC	SVTLLNETES	LKSYLEREDF	FFYSLVYDPQ	
(PRED)	ScaMTA1	ELFLSRQLES	LPATHIRGKC	SVTLLNETES	LKSYLEREDF	FFYSLVYDPQ	
(PRED)	CmMTA1	ELFLSRQLES	LPATHIRGKC	SVTLLNETEA	VFSYLEKEDS	FFYCLVYDPQ	
(PRED)	HsMTA2	ELFLSRQFES	LPATHIRGKC	SVTLLNETDI	LSQYLEKEDC	FFYSLVYDPV	
(PRED)	DrMTA3	ELFLSRQYES	LPATHIRGKC	SVALLN ETEV	VLSYLEKEDT	FFYSLVYDPT	
(PRED)	DmMTA1	ELFLSRQVES	IPATQIRGKC	SVTLLNETES	LQSYLN KDDT	FFYCLVYDPN	
(PRED)	HlMTA1	ELFLSRQVET	MPATHIRGKC	CVTLLNETES	LLSYLN KEDS	FFYCLVYDPA	
	 260 270 280 290 300	
(PRED)	HsMTA1	QKTL LADKGE	IRVGNRYQAD	---- ITDLLK	EGEEDGRD	QS RLETQVWEAH	
(PRED)	MmMTA1	QKTL LADKGE	IRVGNRYQAD	---- ITDLLK	EGEEDGRD	QS KLETKVWEAH	
(PRED)	ScaMTA1	QKTL LADKGE	IRVGNRYQAD	---- ITDLLK	EGEDDGRD	QS KLETKVWEAF	
(PRED)	CmMTA1	QKTL LADKGE	IRVGPRYQAD	---- IPDLLK	EGEEDGRD	QV KLEAKIWDTD	
(PRED)	HsMTA2	QKTL LADQGE	IRVGCKYQAE	---- IPDRLV	EGESDNRN	QQ KMEMKVWDPD	
(PRED)	DrMTA3	QKTL LADKGE	IRVGPRFQAD	---- VPEMLQ	EGEADDRD	QS KLEMKMWDPE	
(PRED)	DmMTA1	QKTL LADKGE	IRVGSRYQCD	---- IPAKLK	DTATDDRKLE	ELES LVWTPE	
(PRED)	HlMTA1	QRT LADKGE	IRVGSRYQAD	GIAPT PLTPA	ERESDPRRLQ	DLET LVWTPR	
	 310 320 330 340 350	
(PRED)	HsMTA1	NPL TDKQIDQ	FLVVARSVGT	FARALDCSSS	VRQPSLHMSA	AAASRDITLF	
(PRED)	MmMTA1	NPL VDKQIDQ	FLVVARSVGT	FARALDCSSS	VRQPSLHMSA	AAASRDITLF	

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(PRED) ScaMTA1 NPLV DKQIDQ FLVVARSVGT FARALDCSSS VRQPSLHMSA AAASRDITLF
(PRED) CmMTA1 NPLT DRQIDQ FLVLARSVGT FARALDCSSS IRQPSLHMSA AAASRDVTLF
(PRED) HsMTA2 NPLT DRQIDQ FLVVARAVGT FARALDCSSS IRQPSLHMSA AAASRDITLF
(PRED) DrMTA3 CPLT NKQIDQ FLVVARAVGT FARALDCSSS VRQPSLHMSA AAASRDITLF
(PRED) DmMTA1 HSLT DRKIDQ FLVVSRSIGT FARALDCSSS VKQPSLHMSA AAASRDITLF
(PRED) HlMTA1 HSLT DRQIDQ FLVVSRSVGT FARALDCSSS VKQPSLHMSA AAASRDITLF

..... 360..... 370..... 380..... 390..... 400
(PRED) HsMTA1 HAMDTLHKNI YDISKAISAL VPQGGPVLCR DEMEEWSASE ANLFEEALEK
(PRED) MmMTA1 HAMDTLHKNI YDISKAISAL VPQGGPVLCR DEMEEWSASE ANLFEEALEK
(PRED) ScaMTA1 HAMDTLHKNV YDISKAISAL VPQGGPVLCR DEMEEWSASE ANLFEEALEK
(PRED) CmMTA1 HSMDTLHKNN YDVSKAISAL VPQGGPVLCR DEMEEWSASE ANMFEEALEK
(PRED) HsMTA2 HAMDTLQRNG YDLAKAMSTL VPQGGPVLCR DEMEEWSASE AMLFEEALEK
(PRED) DrMTA3 HAMDTLHRHG YDLSSALSVL VPQGGPVLCR DEMEEWSASE ANLFEEALEK
(PRED) DmMTA1 HAMNILLKHE YSIEESMSSL VPSTGPNVLCR DEIEDWSASE ANLFEEALEK
(PRED) HlMTA1 HAMDTLHRHN YDVAKAMSSL VPSTGPNVLCR DEMEEWSASE ANLFEEALDK

..... 410..... 420..... 430..... 440..... 450
(PRED) HsMTA1 YGKDFTDIQQ DFLPWKSLTS IIEYYMVKKT TDRYVQQRK KAAEAESKLLK
(PRED) MmMTA1 YGKDFTDIQQ DFLPWKSLTS IIEYYMVKKT TDRYVQQRK KAAEAESKLLK
(PRED) ScaMTA1 YGKDFTDIQQ DFLPWKSLTS IIEYYMVKKT TDRYVQQRK KAAEAESKLLK
(PRED) CmMTA1 YGKDFSDIRQ DFLPWKALTS IVEYYMVKKT TDRYVQQRK KAAEAESRLK
(PRED) HsMTA2 YGKDFNDIRQ DFLPWKSLAS IVQFYMVKKT TDRYIQQRK KAAEADSKLLK
(PRED) DrMTA3 YGKDFNDIRQ DFLPWKSLTS IIEYYMVKKT TDRYVQQRK KAAEAESKLLK
(PRED) DmMTA1 YGKDFNDIRQ DFLPWKTLKQ IIEYYMVKKT TDRYVQQRV KAVEAELKLLK
(PRED) HlMTA1 YGKDFSDIRQ DFLPWKTLKN VIEYYMVKKT TDRYVQQRV KAVEAESKLLK

..... 460..... 470..... 480..... 490..... 500
(PRED) HsMTA1 QVYIPNYNKP NPNQI-----SV NN--VKAGVV NGTGAP----
(PRED) MmMTA1 QVYIPNYNKP NPNQI-----SA SS--VKATVV NGTGTP----
(PRED) ScaMTA1 QVYIPNYNKP NPNQI-----NV NN--VKPGVV NGTGVQ----
(PRED) CmMTA1 QVYIPNYNKP NPNQI-----NV NSTVAKSAMV NGAAMP----
(PRED) HsMTA2 QVYIPTYTKP NPNQI-----IS VG--SKPG-M NGAG-----
(PRED) DrMTA3 QVYIPTYNKP NPNQI-----SV SN--GKMATV NGAAAG----
(PRED) DmMTA1 QVYIPQYNNN GKGNG-----TSTKAGGGIY NGTT-----
(PRED) HlMTA1 QVYIPNYNKT APPTTAPSAA TIVPLGNNNS NSNGKPTNVL NGNSNGNMTT

..... 510..... 520..... 530..... 540..... 550
(PRED) HsMTA1 --G---QSPG AGRACESCYT TQSYQWYS--
(PRED) MmMTA1 --G---QSPG AGRACESCYT TQSYQWYS--
(PRED) ScaMTA1 --A---QNTG AGRACESCYT TQSYQWYS--
(PRED) CmMTA1 --G---QNGG AGRACESCYT TQSYQWYS--
(PRED) HsMTA2 -----FQ KGLTCESCHT TQSAQWYA--
(PRED) DrMTA3 --TGSFHTAG GGRACESCFV VQSAQWYS--
(PRED) DmMTA1 --NGSTDLS NGKPCESCGT TKSSQWNSVS SGHSTSRLCL SCWEYWRRYG
(PRED) HlMTA1 DN SGILMVG V SGKPCESCQV MQSPQWY---

..... 560..... 570..... 580..... 590..... 600
(PRED) HsMTA1 -----W GPPNMQCRLC ASCWTYWKKY GGLKMPTRLD GE-----
(PRED) MmMTA1 -----W GPPNMQCRLC ASCWTYWKKY GGLKMPTRLD GE-----
(PRED) ScaMTA1 -----W GPPNMQCRLC ASCWTYWKKY GGLKMPTRLD GE-----
(PRED) CmMTA1 -----W GPPNMQCRLC ATCWNYWKKY GGLKMPTRLE GE-----
(PRED) HsMTA2 -----W GPPNMQCRLC ASCWIYWKKY GGLKTPPTLE GA-----
(PRED) DrMTA3 -----W GPPNMQCRLC VSCWYWKKY GGLKMPSRAE GAE-----
(PRED) DmMTA1 SMKSATKGD GEGDAKKKSS SAASTPTATL AGLATTPTAV VDL-----
(PRED) HlMTA1 -----AW GPSHMQCRLC QSCWTYWKKY GGLKVP SRMD DVDLERKRGG

..... 610..... 620..... 630..... 640..... 650
(PRED) HsMTA1 ----- -RPGPNR--- ----SNMSPH GLPA--RSS-
(PRED) MmMTA1 ----- -RPGPNR--- ----NNMSPH GIPA--RSS-
(PRED) ScaMTA1 ----- -RPGPNR--- ----NNLSPH GVPV--RNS-
(PRED) CmMTA1 ----- -RPGPNR--- ----SSANPH GYVW--KN--
(PRED) HsMTA2 ----- -TRGTTEPHS RGHLSPPEAQ SLSPYT TSA-
(PRED) DrMTA3 ----- -EKTP PSPAPNESRS RGHCARQSSH MVPI--RNS-
(PRED) DmMTA1 --NDDEKISD LTNRQLHRCS IVNCGKEFKL KTHLARHYAQ AHGIAISS--
(PRED) HlMTA1 TGSDEESKGI GGAHRPHRCS IPSCGKEFKL KAHLRHYAS AHGVDLRGSG

..... 660..... 670..... 680..... 690..... 700
(PRED) HsMTA1 -----GSP KFAMKTRQAF YLHTTKLTRI ARRLCREILR PWHAAARHPYL
(PRED) MmMTA1 -----GSP KFAMKTRQAF YLHTTKLTRI ARRLCREILR PWHAAARHPYM
(PRED) ScaMTA1 -----GSP KFAMKTRQAF YLHTTKLTRI ARRLCRDILR PWHAAARHPYL
(PRED) CmMTA1 -----ANP KFTLKTRQAF CLQTTKLT KI ARYFCRSLFH TRQSARRPFT
(PRED) HsMTA2 -----NRA KLLAKNRQTF LLQTTKLT RL ARRMCRDLIQ PRRAARRPYA
(PRED) DrMTA3 -----GSP KSSMKTKQAF LLQATRLTKL ARHMCRDLIR LRRRAARRPFV
(PRED) DmMTA1 -----GSP RPIMKTRTAF YLHTNPMTRV ARAICRSIVK PKKAARQSA

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(PRED) HlMTA1 ASGGGGGGSP R PVMKTRSAF YLR T S A L A R A A R R L C A A Q L R T R H A A R A P H Q
..... 710..... 720..... 730..... 740..... 750
(PRED) HsMTA1 P I N S A A I K A E C T A - R L P E A S Q - S P L V L K Q A V - - - - - R K P L E A V L R Y L E T H
(PRED) MmMTA1 P I N S A A I K A E C T A - R L P E A S Q - S P L V L K Q V V - - - - - R K P L E A V L R Y L E T H
(PRED) ScaMTA1 P I N S A A I K A E C T A - R L P E A S E - N P L L L K Q V V - - - - - R K P L E A V L R Y L E S H
(PRED) CmMTA1 P I N S A A I K A E C T A - R L P E I G E - K P I K L K P S V - - - - - R K T L E S I A K Y L E L H
(PRED) HsMTA2 P I N A N A I K A E C S I - R L P K A A K - T P L K I H P L V - - - - - R L P L A T I V K D L V A Q
(PRED) DrMTA3 P I N C G A I K A E Y M I - R V S E G M T G R P L K P K S S P - - - - - R S T L T S V L Q Y L E S R
(PRED) DmMTA1 A I N A M L V K Q E F T N - R I S G K S Q - A E I K K L L L L K - P K D R G S V T K I A N R L G A P
(PRED) HlMTA1 P V N A A P L R H L C A S P Q L T S K S S - V E L R I L A R A V R P R P R P R V T D I A T R L G D H
..... 760..... 770..... 780..... 790..... 800
(PRED) HsMTA1 P - - - - - - - - - - - - - - - - - - - - - R P P K P D P V K S V - - - - - - - - - - - S S V
(PRED) MmMTA1 P - - - - - - - - - - - - - - - - - - - - - R P P K P D P V K S S - - - - - - - - - - - S S V
(PRED) ScaMTA1 P - - - - - - - - - - - - - - - - - - - - - C P P K P D P A K S L - - - - - - - - - - - S S S
(PRED) CmMTA1 P - - - - - - - - - - - - - - - - - - - - - S V K P I C S L A - - - - - - - - - - - V H
(PRED) HsMTA2 A - - - - - - - - - - - - - - - - - - - - - P L K P K T P R G T - - - - - - - - - - - K - -
(PRED) DrMTA3 P - - - - - - - - - - - - - - - - - - - - - A T H V Q R P H R T - - - - - - - - - - - P G L
(PRED) DmMTA1 G - - - - S G P H E W L V L T P K D K M P L P A V V S F P K P P K A P D G S L V Y D R V P N K S P D
(PRED) HlMTA1 P A P R Q P G D W D W L A L T A A A Q R K Q P D R V S F P R P P K A P D G S L L Y E R V P N K S E V
..... 810..... 820..... 830..... 840..... 850
(PRED) HsMTA1 L S S L T P A K V A P V I N N G S P T I L G K R - - S Y E Q H N G V D G N M K K R L L M P S R G L A
(PRED) MmMTA1 L S S L T P A K S A P V I N N G S P T I L G K R - - S Y E Q H N G V D G N M K K R L L M P S R G L A
(PRED) ScaMTA1 L N N L T P A K F T P V I N N G S P T I L G K R - - S Y E Q H N G M D G N M K K R L L M P S R G L P
(PRED) CmMTA1 S G S V T P A K I L P V L N H G S P T I L G K R - - G Y E Q H N G I D G T M K K R L L M P F R G K T
(PRED) HsMTA2 - T P I N R N Q L S Q - - N R G L G G I M V K R - - A Y E T M A G - - - - - - - - - - - - - - - -
(PRED) DrMTA3 Q V Q P P R R L L S S L P S H G P L G M L G K R - - S Y H H H S R V E S A E R R A G A T G - - - - -
(PRED) DmMTA1 V V A V P A D K E L T I I P T Q A T S T I R K R A H E D Q Q L N G T E V T I V P S G P P A K R P N K
(PRED) HlMTA1 D R L T V T P P Q P Q P S M Q A Q Q T I L K R T R P P F D E I N G S D G I A L S A G L P G G P P A K
..... 860..... 870..... 880..... 890..... 900
(PRED) HsMTA1 - - - - - - - - - - - - N H G Q A R H M G P - S R N L L L N G K S Y P T K V R L I R G G S L P P V K
(PRED) MmMTA1 - - - - - - - - - - - - N H G Q T R H M G P - S R N L L L N G K S Y P T K V R L I R G G S L P P V K
(PRED) ScaMTA1 - - - - - - - - - - - - N H G Q T R Q M G P - S R N L L L N G K S Y P T K V R L I R G G S M P P V K
(PRED) CmMTA1 L A Q S C S R L H S H P N H G Q V R Q M A A V N R G Y M I N G K P Y S R S S K I L K P G S L P P M K
(PRED) HsMTA2 - - - - - - - - - - - - - - - - - - - - - A - - G V P F S A N G R P L A - - - S G I R S S S Q P A A K
(PRED) DrMTA3 - - - - - - - - - - - - - - - - - - - - - Q E N P A H I V - - G P I L Q H N G S S T G - - - G S S L R G S G L M L R
(PRED) DmMTA1 D P M P S H C P S P E Q F A A M M A A S G Q P L S R H H L N G K Q - - - - - K I A Q M A R G G N G R
(PRED) HlMTA1 R A H H S Q Q L H P K H T L E H T A P T V L P L A P P L N G R A A H P H T L P H G P P L S R S N A R
..... 910..... 920..... 930..... 940..... 950
(PRED) HsMTA1 R R R M N W I D A P D D V F Y M A T E E T R K I R K L L S S S E T K R A A R R P Y K P I A L R Q S Q
(PRED) MmMTA1 R R R M N W I D A P D D V F Y M A T E E T R K I R K L L S S S E T K R A A R R P Y K P I A L R Q S Q
(PRED) ScaMTA1 R R R M N W I D A P D D V F Y M A T E E T R K I R K L L S S S E A K R A A R R P Y K P I I L R P - -
(PRED) CmMTA1 G R R M N W I D A P D D V L F I A T E E T R K I R K L L G P V D M K R A A R Q P Y K Q I F I R Q A R
(PRED) HsMTA2 R Q K L N P A D A P N P V V F V A T K D T R A L R K A L T H L E M R R A A R R P N L P L K V K P T L
(PRED) DrMTA3 K R R P N W I D A P D D S F F L V S R E T R K A R R M L S R S Q L R R A C R Q P C E Q I S L R R V P
(PRED) DmMTA1 K Q V I S W M D A P D D V Y F R A N D T H K K T R K I L S A V D L R R A A R K P W R T L P I K P - -
(PRED) HlMTA1 K Q V I S W M D A P D D V Y F R A S D Q T K R L R K T L S S V E L R R A A R K P W R R L P A P L - -
..... 960..... 970.....
(PRED) HsMTA1 A - - - - L P P R P P P P - A P V N D E P I V I E D
(PRED) MmMTA1 A - - - - L P L R P P P P - A P V N D E P I V I E D
(PRED) ScaMTA1 - - - - - M Q A V Q L R - Q P M N D E P I I I E D
(PRED) CmMTA1 V - - - - S C A V S Q P S R Q P V N E E P I I I E D
(PRED) HsMTA2 I A V R P P V P L P A P S H P A S T N E P I V I E D
(PRED) 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
(PRED) DmMTA1 - - - - - - - A A P E P S - S R P I E S Q I V I L D
(PRED) HlMTA1 - - - - - - - H P P H P Q R A V R G D D M V V I L D

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