

Alignment of Cdal sequence (H99) with *C. gatti* (CNBG 1745) Cdal sequence

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H99      MFTFAAFSALLISLAGVVAQTTGTSVDSSILTKTADSTGPSGFSIPALSELTSGAPTDST  60
M  FAA SALL+SLAG++AQT  TSV SS+LT+TA  TGPSGFSIPALSELTSGAPTD+T
R265    MSFAAAVSALLVSLAGIMAQTASTSVASSVLTQTA-PTGPSGFSIPALSELTSGAPDST  59

H99      VALYSTFAAGATPTVSGAPVLPTSALTIADYPALDVTPTNSSLVKDWMKIDLSKVPSY  120
VALYSTF A ATPTVSGAPVLPTSALTIA+YPALDV PPTNSSLV+++W+AKID++KVP+Y
R265    VALYSTFPASATPTVSGAPVLPTSALTIANYPALDVIPPTNSSLVQEWLAKIDMTKVPNY  119

H99      NVTGDCSTDAAAISDGRCWWTGGCTRET DIVECPDKNVWGLSYDDGSPFPTLLIDYL  180
N  TTGDCSTD  A SDGRCWWTGGCTR  TDIV CPDKNVWGLSYDDGSPFPTLLIDYL
R265    NATGDCSTDPGATSDGRCWWTGGCTRATDIVACPDKNVWGLSYDDGSPFPTLLIDYL  179

H99      QEKNIKTTFVVGSRVLSRPEMLQTEYMSGHQISIHTWHPALTTLTNEEIVAELGWTMK  240
QEKNIKTTFVVGSRVLSRPEMLQTEYMSGH+ISIHTWHPALTTLTNE+IVAEL  WTMK
R265    QEKNIKTTFVVGSRVLSRPEMLQTEYMSGHEISIHTWHPALTTLTNEQIVAELAWTMK  239

H99      VIKDTLGVTNPNTFRPPYGDIDDRVRAIAAQMGLTPVIWTSYTDGSTTVNFDTNDWHISGG  300
VIKDT+GVTNPNTFRPPYGDIDDRVRAIAAQMGLTPVIWTSY+DGSTTVNFDTNDWHISGG
R265    VIKDTIGVTNPNTFRPPYGDIDDRVRAIAAQMGLTPVIWTSYSDGSTTVNFDTNDWHISGG  299

H99      TATGASSYETF EKILTEYAPKLDTG FITLEHDIYQQSVDLAVGYILPQVLANGTYQLKSI  360
TATGASSYETF EKIL  EYAPKL+TG FITLEHD+YQQSVDLAVGYILPQVLANGTYQLKSI
R265    TATGASSYETF EKILNEYAPKLNTG FITLEHDLYQQSVDLAVGYILPQVLANGTYQLKSI  359

H99      INCLGKDTSEAYIETSSNQTTTQITAATGSQSTFFQPIVGTATGAEV SAPSEATGSTAAG  420
INCLGKD SEAYIETSSNQTTTQIT+A+G  ST+FPQPIVGTATG+EV SAPSEAT  + A
R265    INCLGKDISEAYIETSSNQTTTQITSASG--STYFPQPIVGTATGSEV SAPSEAT-GSTAA  416

H99      SAASTTSGSGASASTGAASNTSSSGSGRSATMGGALIALAAVAVGMVYVA  470
+A+ ++ + + ++  AS+++SSSGSGRSATMGGALIA AAVAVG+VYVA
R265    GSAAGSAATTS GSAASGASDSSSSSGSGRSATMGGALIAFAAVAVGIVYVA  466
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400/470 identical (85%); 435/470 positive (92%)

Alignment of Cda2 sequence (H99) with *C. gatti* (CNBG 0964) Cda2 sequence

H99	MIPSTAAALLTLTAGAAFAHTGCGGHEIGRRNVGGPMLYRRAVTDEASAAVSTDINTECT	60
	MIPSTAAA LTLTAG AFAH GCGG EIGRRNVGGPML+ RAVTDEASAAVSTD++TECT	
R265	MIPSTAAAFLLTLTAGTAFAHIGCGGQEIGRRNVGGPMLHSRAVTDEASAAVSTDVSTECT	60
H99	AYSYAPVTELISSFPTIWQTASIPSNDTEAQQLFKGKINSTLNKIPNDVPHGTPTGDWTG	120
	AY YAPVT++ SSFP IWQTASI S D+EAQQLF IN+T+N+K+PNDVPHGTPTG+WTG	
R265	AYGYAPVTQIASSFP AIWQTASILSTDSEAQQLFASINATVNSKLPNDVPHGTPTGNWTG	120
H99	VNYSNSDPDCWVTHNKCTTPSNDTGLQADISIAPEPMTWGLGFDDGPNC SHNALYDLLLE	180
	V+YS+SDPDCWVTHNKCTTPS+DTGL+ADI+ PEPMTWGLGFDDGPNC SHNALYDLLLE	
R265	VSYSSSDPDCWVTHNKCTTPSSDTGLKADITTVPEPMTWGLGFDDGPNC SHNALYDLLLE	180
H99	NNQKATMFFIGSNVLDWPLQAMRAHDEGHEICVHTWSHQYMTALSNEVVFAELYTQKAI	240
	NNQKATMF+IGSNV+DWPLQAMRAHDEGHEICVHTWSHQYMTALSNEVVFAELYTQKAI	
R265	NNQKATMFYIGSNVMDWPLQAMRAHDEGHEICVHTWSHQYMTALSNEVVFAELYTQKAI	240
H99	KAVLGVTPQCWRPPYGDVDNRVRMIAEGLNLTTIIWSDDTDDWAAGTNGVTEQDVTNNYQ	300
	KAVLGVTP CWRPPYGDVDNRVRMIA LNL+TI+WSDDT+DW AGTNGVT+QDVTNNYQ	
R265	KAVLGVTPLCWRPPYGDVDNRVRMIAAALNLSTIVWSDDTNDWEAGTNGVTQQDVTNNYQ	300
H99	SVIDKAGNGTYTTHGPPVVLNHELTNYTMSVFMFMPKIKSAFNIVPICTAYNITQPYAE	360
	SVIDKAGNGTYTTHGPPVVLNHELTNYTMSVF++MFPKIKSAF+YIVPICTAYNITQPYAE	
R265	SVIDKAGNGTYTTHGPPVVLNHELTNYTMSVFMFMPKIKSAFSYIVPICTAYNITQPYAE	360
H99	SNITCPNFETYISGVTNISSSTTQKDGSSSTNTASGSGAAGSASATSSSDSSSSGGSSG	420
	SN+TCPNFETYISGVTNIS+STTQKDGSSSTNT+ + + S SA+S+ +SS	
R265	SNVTCPNFETYISGVTNISTSTTQKDGSSSTNTSYTASGSTSPSASSTGKIASS-----	414
H99	SSGSNNASSGALGMFDSLGSVGLILGGVVAGVMML 455	
	A SGALGM+D LSG+GLILGGVVAGVMML	
R265	-----AKSGALGMYDGLSGMGLILGGVVAGVMML 443	

79/455 identical (83%); 414/455 positive (90%)

Alignment of Cda3 sequence (H99) with C. gatti (CNBG 0806) Cda3 sequence

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H99   MYGHL SLSALS LFAVVA AAPFRESWLQPRDSPVSQLFRRTAPDPNSNDYMSYYPGPGSTP 60
      MYGHL SLSALS L AVVAAAPF ESWLQPRDSPVSQLFRR APDPN++DY+S+YP PGSTP
R265  MYGHL SLSALS L LAVVA AAPFHESWLQPRDSPVSQLFRRAAPDPNASDYLSHYPSPGSTP 60

H99   NVSTIPQAWLDK LATVNLPNVPVATPDGGRPTYPNNEDDGDSTICSFTDQCRVEDDL YSP 120
      NVSTIPQAWLDK LATV LPNV VAT G PTYPNNE+DGDSTICSFTDQC DDL+SP
R265  NVSTIPQAWLDK LATVQLPNVSVATASGEIPTYPNNENDGDSTICSFTDQCV EPDDL FSP 120

H99   PGEKIWALS FDDGPTDVSPALYDYLAQNNISSATHFMIGGNVITSPQSVLVAVKAGGHL 180
      PGEKIWALS FDDGPTDVSP LYD+LAQNNISS ATHFMIGGNV+TSPQSVL+AV+AGGHL
R265  PGEKIWALS FDDGPTDVSPGLYDFLAQNNISSKATHFMIGGNVVTSPQSVLIAVQAGGHL 180

H99   AVHTW SHPYMTTLTNEQVVGELGWTMQALS DLNGGRIPMYWRPPYGDVDNRVRAIAKEVF 240
      AVHTW SHPYMTTLTNEQVVGELGWTMQALS DLNGGR+P +WRPPYGDVDNRVRAIAK VF
R265  AVHTW SHPYMTTLTNEQVVGELGWTMQALS DLNGGRV PKFWRPPYGDVDNRVRAIAKGVF 240

H99   GLVTVLWSDTNDWAI TDEPGQYSVASVEAYFDTLVTGNRTQGLL LLEHELDNNTVEVFE 300
      L TVLWD DTNDWAI DEP QYS+ASVEAYFDTLVTGNRTQGLL LLEHELDNNTV VFE
R265  DLETVLWDEDTNDWAI ADEPSQYSIASVEAYFDTLVTGNRTQGLL LLEHELDNNTVTVFE 300

H99   TEYPKAVGNGWTVKNVADAFNMEWYLN SGKGNNDVVTMSVAGTLTTATPTNTSTYVASS 360
      TEYPKA+ NGW VKNVADAFNMEWYLN SGKGN+ VTTMSV GTL TA PTNTST VAS+
R265  TEYPKAIANGWIVKNVADAFNMEWYLN SGKGN DATVVTMSVGGTLPTAAPTNTSTSVASA 360

H99   TAASSASV TDSAGVSIASAASSEASSSWAIA NRPSHFVIAIACGLALAAIMV 412
      +A SS SVTDSAGVSIASAASSE+SSSWAIA RPS F+ IACGL AA +V
R265  SATSSGSV TDSAGVSIASAASSESSSSWAIA ERPSLFI--IACGLVFAAAVV 410
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352/412 identical (85%); 372/412 positive (90%)