

Supplemental Figure 2

Blast query: human 11β-HSD1

>SINCAMP00000014194 len=297 SINCAMT00000014325 SINCAMG00000009220

Length = 297

Score = 335 bits (858), Expect = 3e-92

Identities = 164/288 (56%), Positives = 221/288 (76%), Gaps = 1/288 (0%)

Query: 1 MFAMKYLILPILGLFMAYYYYSAEEFRFEMLQGGKVVIVTGASKGIGREMAHYHLAKMGAH 60
M F+KK L+ +LG+ +AYV+++ + F PEML+GK+VIVTGAS GIG +MAYHLA+MG+H
Sbjct: 1 MGFVKKMLIFLLGIALAYFFNSGDSDFPEMLRGRVIVTGASSGIGEQMAYHLAEMGSH 60

Query: 61 VVVTARSKETLQKVVSHCLLEGAASAHYIAGTMEIMDTFAEQVFAQAGKLMGGLMLILNH 120
+++TAR K+ L+ VV+ CL+LGAASA Y+AG+MEDM FA+ V +A K GGLMLILNH
Sbjct: 61 ILITARRKQRLEAVVAKCLKLGAASADYVAGSMEDMEFAKHVVKEAEKQFGGLMLILNH 120

Query: 121 ITNTSLNLFHDDIHHVRSKMEVNFSLYVVLTVAALPMLKQSNSSIVVSSLAGKIVAYRV 180
I + F D+ H+R +E+NFLSYV +IV A+PMLK+SNGSIVVSS+AGK+ P+V
Sbjct: 121 IGSAYFRYFDGVDHIRTLEINFLSYVIMTVEAMPMLKQSNSSIVVSSIAGKIGNPLV 180

Query: 181 AAYSASKFALDGFSSIRKEYSVSRVNSITLQVGLDITETAMQVSGIVHMQARKEE 240
YS++KFALDGFSS+R+E+++ NVSITLQV+ I+TE A+GA+S I+ AFK+E
Sbjct: 181 VPSYSTKFAIDGFFSSLRQEFAMLNINVSITLQVSIYINTEAAVGAISHIQQPPAKDE 240

Query: 241 CALEIKGGALRQEEVYVYDSSLWI-TLLIRNPKRKLIFLYSTSYNMD 287
CALEIKGGALR EVYV LL+R+ ++L+ +YN+D
Sbjct: 241 CALEIKGGALRNREVVYKYEFTKYVLLLRDWFPELDAFIRKYNVLD 288

Blast query: zebrafish 11β-HSD3a

>SINCAMP00000008284 len=288 SINCAMT00000008368 SINCAMG000000005417

Length = 288

Score = 310 bits (793), Expect = 1e-84

Identities = 151/281 (53%), Positives = 206/281 (73%), Gaps = 3/281 (1%)

Query: 9 LCSICVAFIAVRWSA---PSFNEESLKGARVLVTGASTGIGEQQLAYHYARLGAQIVITAR 65
+C+ AF A ++ +F+ SL G RVL+TGAS GIGEQLAY Y+ GA +VITA+
Sbjct: 7 VCAAAAAGFASFFALMSRDAFDGSLGTRVLLTGASKGIGEQQLAYQSGFGADLVITAQ 66

Query: 66 RGNVLEQVSKCREMGAQKAFYIPADMANPSSDADLVVYKAIQGLGLDYLVLNHHGSPY 125
RG+ L+V+V KC E+GA+ I ADMR+P + VV++A+E+LGLDYLVLNHHG +P+
Sbjct: 67 RGDALQKVDKCLELGAQNVRSIAADMADPRNPKRVVQFALEKGLDYLVLNHHGATFP 126

Query: 126 QMWDGVDQHTRWLLEVNFLSYLQMAQKALPTLEKSKGSIVVSSLLGKICGPFALPYAST 185
QMWD D +HTRNL++VNFLS++++A ALP L KS GSIIVVSSL GKI PF Y++I
Sbjct: 127 QMWRDRSEHTRWLMQVNFVLSFVELAGAAALPFLTKSNGSIVVSSLLCGKIATPPTASYSAT 186

Query: 186 KFALNFFGGQLQNELAMQKSNVSIITICILGLDITDSAMEKIKYINMTAYPSHEAALQII 245
KFAL GFF L++ELMQ+ +VS+T+C LGLDIT S +EKI+G ++M YP+ ++AL II
Sbjct: 187 KFALGGFFTSRLRHELMQRKHVSVTLCLFGLDITQSTLEKIQGISMQPYPASDSALAI 246

Query: 246 QAGATRQSESYFYWYFYATLFRDNWFFYLDRKVIQNSYTYN 286
+ G TR E ++PW+ + DWFP D++I+N+Y Y+
Sbjct: 247 KGGMTRAREIYFPWWDLVSKLHDWFPEASDQHIRNAINYS 287

Blast query: zebrafish 11β-HSD3b

>SINCAMP00000008284 len=288 SINCAMT00000008368 SINCAMG000000005417

Length = 288

Score = 303 bits (775), Expect = 2e-82

Identities = 145/254 (57%), Positives = 199/254 (78%)

Query: 16 SLMWRDFFDFESIRGTRVLTIGASSGIGEQMAYHYAKFGAEIVITARRLEALKKVTQKCE 75
+LM RD FDP S+ GTRVL+TGAS GIGEQ+AY Y+ FGA++VITA+R +AL+KV KC
Sbjct: 20 ALMGRDAFDGSLGTRVLLTGASKGIGEQQLAYQYSGFGADLVITAQRGDALQKVDKCL 79

Query: 76 KLGAKKIMYVIGMSDPADPERVLKYITIEKGLGLDYLVLNHHGVTNVLWNRDADHVRSL 135
+LGAK + + IM+DP +P+RV+++ +EKGLGLD+LVLNH+G T +W+RD++H R L
Sbjct: 80 ELGAKQVRSIAADMADPRNPKRVVQFALEKGLDYLVLNHHGATFPQWDRDSEHTRWL 139

Query: 136 MQVNFVSYVQMAAALPVLLETSGSSIVVSSLAGKIASPFVYPSSTKFMANGFFGALQK 195
MQVNF+S+V++AGAALP L S GSI+VSSL GKIA+PF YS+TKFA+ GFF +L+
Sbjct: 140 MQVNFVSLFVELAGAAALPFLTKSNGSIVVSSLLCGKIATPPTASYSATKFAFGGFFTSRHR 199

Query: 196 ELAIQKSNVSVSIQILGLDITDSAMRKIRYTIMTAYPASEAALSIIKAGATRQKVAFY 255
ELA+Q+ +VSV++ LGLDIT+S +KI+G +M YPAS++AL+I+IK G TR + ++P
Sbjct: 200 ELAMQRKHVSVTLCLFGLDITQSTLEKIQGISMQPYPASDSALAIKGGMTRAREIYFP 259

Query: 256 WFHYLTCLINDIFF 269
W+ L ++D FP
Sbjct: 260 WWVDLVSKLHDWFP 273

Blast query: human 11β-HSD3

>SINCAMP00000008284 len=288 SINCAMT00000008368 SINCAMG000000005417

Length = 288

Score = 238 bits (608), Expect = 3e-63

Identities = 123/234 (52%), Positives = 155/234 (66%)

Query: 20 DNFDPASLQGARVLLTGANAGVGEELAYHYARLGSLSHLVLTATHEALLQKVVGNCRKLGAP 79
D FDP SL G RVLLTGA+ G+GE+LAY Y+ G+ LV+TA LQKV C +LGA
Sbjct: 25 DAFDPSGSLGTRVLLTGASKGIGEQQLAYQYSGFGADLVITAQRGDALQKVDKCLELGA 84

Query: 80 KVFYIADMASFEAPESVVQFALDKLGLDYLVLNHHGAGPAGTRARSPQATRWLMQVNF 139
V IAADMA P P+ VVQFAL+KLGGLDYLVLNHHG P R +TRWLMQVNF
Sbjct: 85 NVRSIAADMADPRNPKRVVQFALEKGLDYLVLNHHGATFPQWDRDSEHTRWLMQVNF 144

Query: 140 VSYVQLTSRALPSTLDSKGGXXXXXXGRVFTSFSTPYSAAKALDGGFGLRRELDVQ 199
+S+V+L ALP LT S G G++ T F+ YSA KFAL GFF SLR EL +Q
Sbjct: 145 LSFVELAGAAALPFLTKSNGSIVVSSLLCGKIATPPTASYSATKFAFGGFFTSRLRHELMQ 204

Query: 200 DVNVAITMCVLGLRDRASAAEAVRGVTRVGAAPGPKAALAVIRGGATRAAGVFY 253
+V+T+C LGL D S E ++G+ ++ P +ALA+I+GG TR + ++
Sbjct: 205 RKHVSVTLCLFGLDITQSTLEKIQGISMQPYPASDSALAIKGGMTRAREIYFP 258