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Appendix A

Supplementary data for chapter 2

CLUSTALX protein colouring:

Green	Thr, Ser, Gln, Asn
Cyan	Ala, Val, Ile, Leu, Met, Phe, Trp
Blue	Tyr, His
Magenta	Asp, Glu
Yellow	Pro
Orange	Gly
Pink	Cys, Lys, Arg

Swissprot accession numbers for multiple sequence alignment

<i>Bos taurus</i>	P50243
<i>Homo sapiens</i>	P17707, Q9BWK4
<i>Mesocricetus auratus</i>	P28918
<i>Mus musculus</i>	P31154
<i>Rattus norvegicus</i>	P17708
<i>Xenopus laevis</i>	P79888
<i>Drosophila melanogaster</i>	P91931, P91925, Q9VKY9
<i>Caenorhabditis elegans</i>	O02655
<i>Onchocerca volvulus</i>	Q27883
<i>Leishmania donovani</i>	Q25264
<i>Trypanosoma brucei brucei</i>	P50244
<i>Trypanosoma cruzi</i>	O76240, Q9UAD2
<i>Arabidopsis thaliana</i>	Q96286, Q96531, Q9M893
<i>Brassica juncea</i>	Q42613
<i>Catharanthus roseus</i>	Q42679

<i>Datura stramonium</i>	Q96555
<i>Dianthus caryophyllus</i>	Q39676
<i>Helianthus annuus</i>	O65354
<i>Hordeum chilense</i>	Q42829
<i>Zea mays</i>	O24575
<i>Nicotiana sylvestris</i>	O80402
<i>Oryza sativa</i>	O24215, O81269
<i>Pisum sativum</i>	Q43820
<i>Pharbitis nil</i>	Q96471
<i>Solanum tuberosum</i>	Q04694
<i>Spinacia oleracea</i>	P46255
<i>Nicotiana tabacum</i>	O04009, O49005
<i>Saccharomyces cerevisiae</i>	P21182

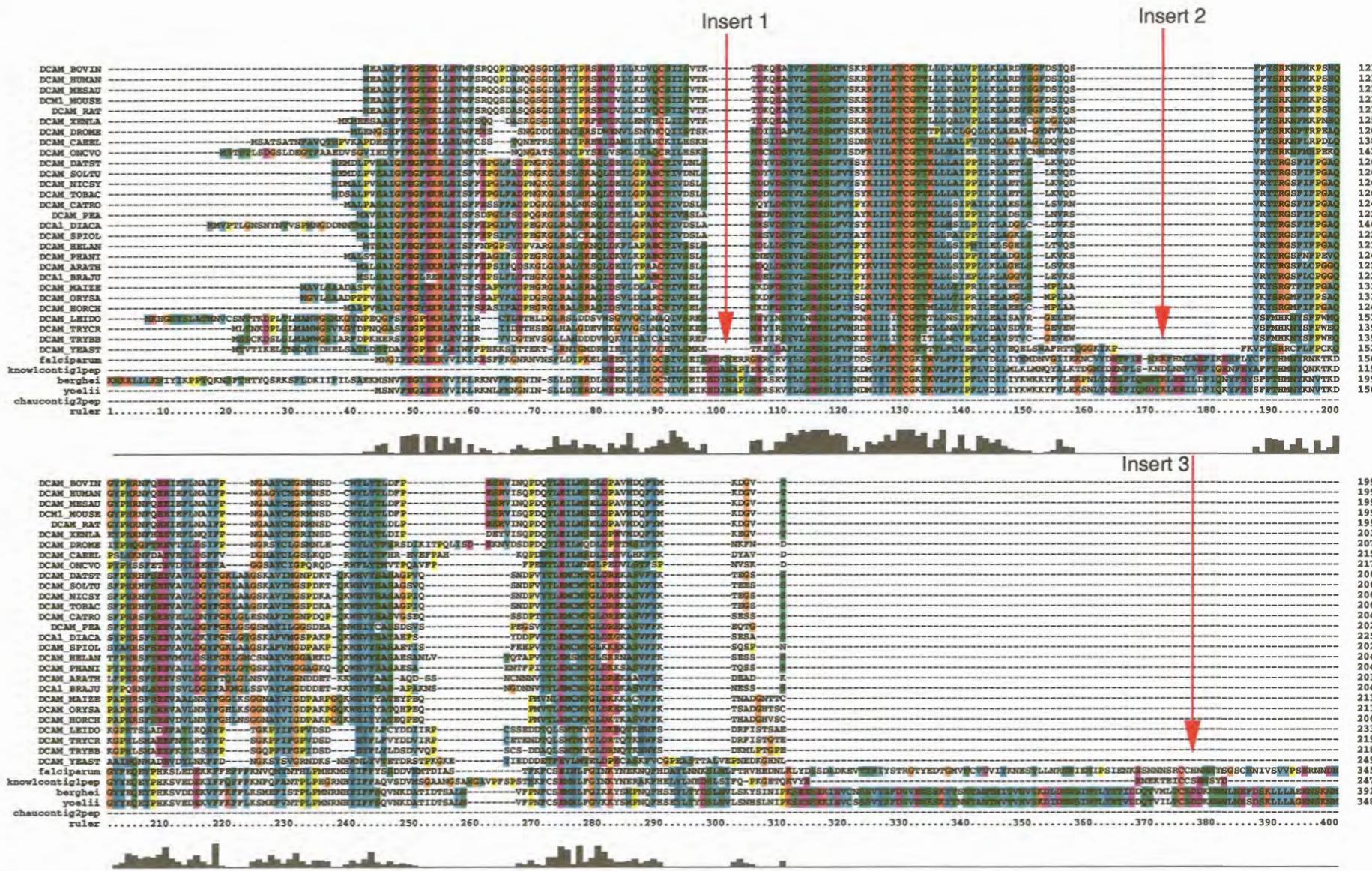


Figure A.1: Multiple alignment. All sequences used are included. Colouring of conserved and similar residues is as according to CLUSTALX defaults.

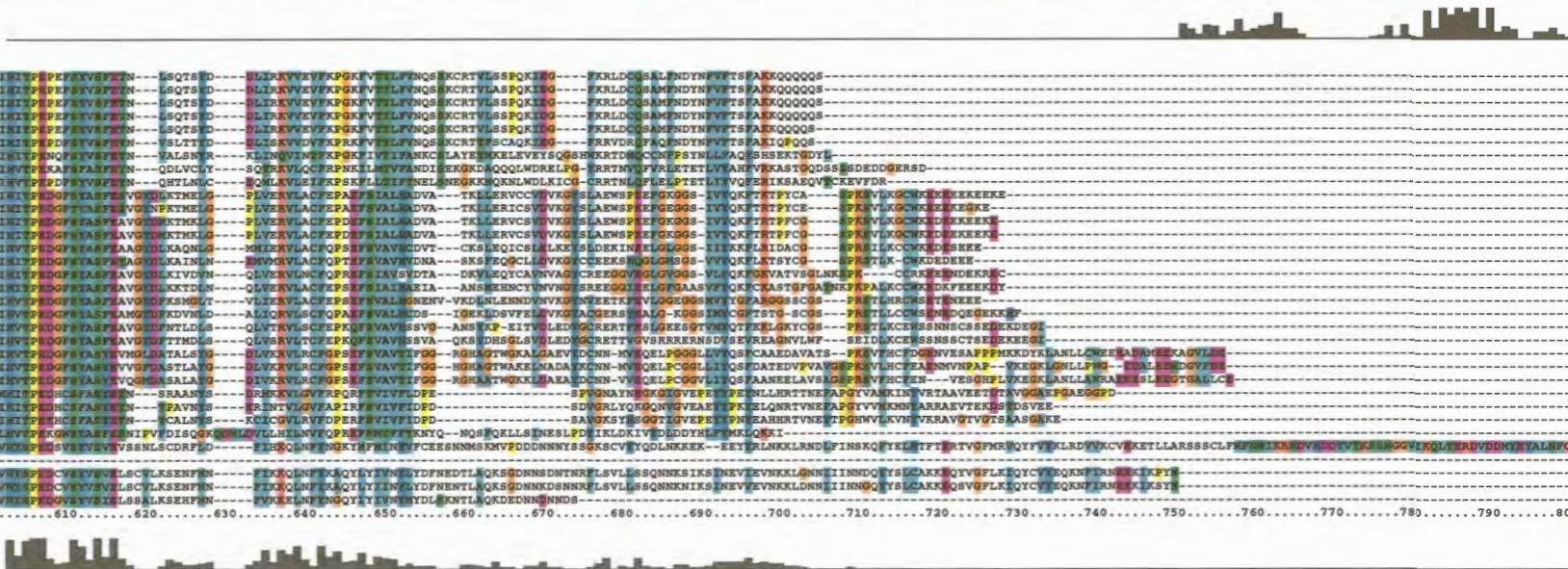


Figure A.1: Multiple alignment continued.

DCAM_YEAST 396
 falciaparum 825
 knowcontigpep 310
 berghel 885
 yoelii 842
 chaucontig2pep 214
 ruler810.....820.....830.....840.....850.....860.....870.....880.....890.....900.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000

DCAM_YEAST 396
 falciaparum 1025
 knowcontigpep 310
 berghel 1085
 yoelii 1042
 chaucontig2pep 214
 ruler1010.....1020.....1030.....1040.....1050.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200

DCAM_YEAST 396
 falciaparum 1225
 knowcontigpep 310
 berghel 1284
 yoelii 1242
 chaucontig2pep 214
 ruler1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350.....1360.....1370.....1380.....1390.....1400

DCAM_YEAST 396
 falciaparum 1419
 knowcontigpep 310
 berghel 1446
 yoelii 1399
 chaucontig2pep 214
 ruler1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600

Figure A.1: Multiple alignment concluded.

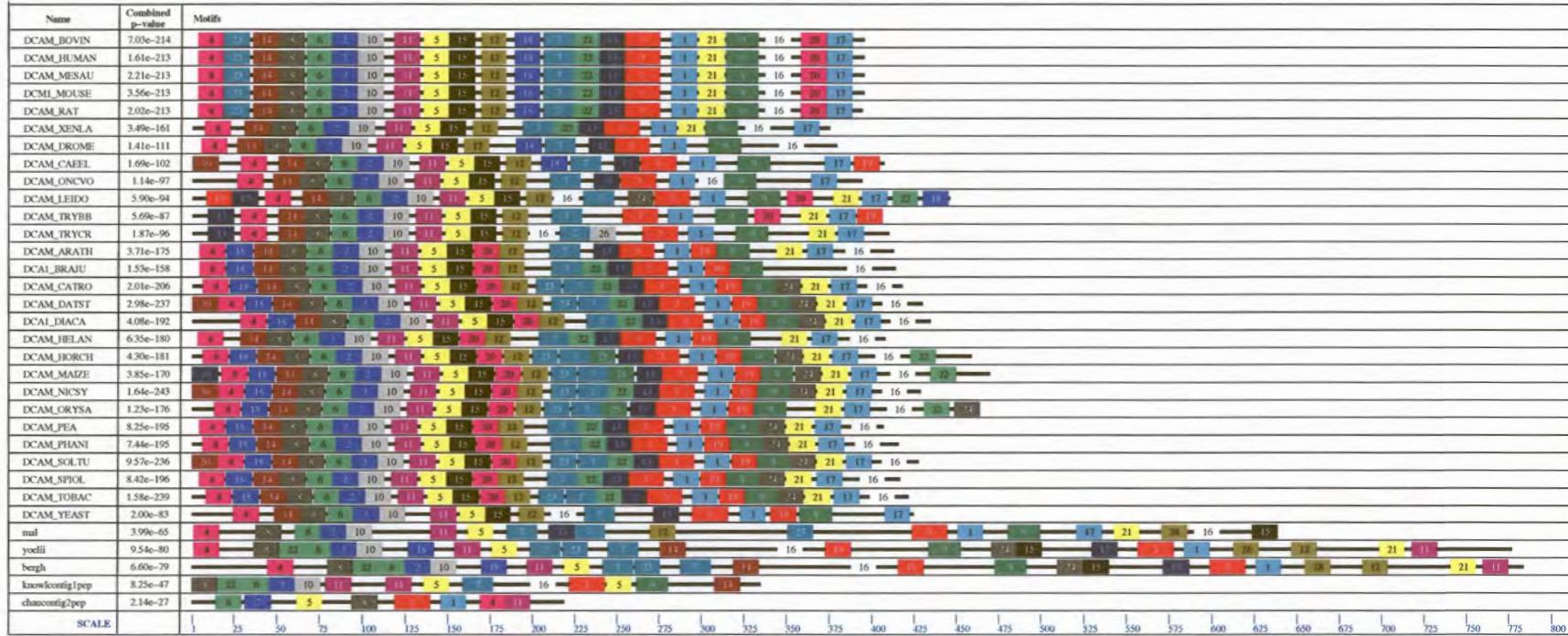


Figure A.2: Meme motifs of the set of unaligned sequences. Homologous motifs are numbered and coloured the same. Higher numbers indicate greater conservation. Motif 5 which roughly corresponds to helix 6 of the human enzyme was used to adjust the alignment.

Appendix B

Supplementary data for chapter 4

Table B.1: Hits identified from virtual screening against the internal LUDI BIOSYM database

Human	Score	Model	Score	Human	Score	Model	Score
	638		680		524		549
	614		676		521		545
	585		667		518		538
	577		658		505		530
	563		625		503		524
	547		581		500		519
	544		574		500		515
	542		563		498		512
	534		563		487		508
	530		561		486		508

Table B.2: Hits identified from virtual screening against the ACD database

Human	Score	Model	Score	Human	Score	Model	Score
	718		832		674		709
	711		817		670		702
	709		747		668		698
	701		731		658		693
	698		729		655		692
	692		725		648		689
	688		722		646		687
	685		722		645		684
	683		714		643		676
	683		710		643		676

Table B.3: Hits identified from virtual screening against the NCI database

Human - NCI	Score	Model - NCI	Score	Human - NCI	Score	Model - NCI	Score
	717		832		649		709
	701		817		645		702
	690		747		645		698
	673		731		643		693
	672		729		641		692
	665		725		636		689
	661		722		636		687
	658		722		635		684
	656		714		635		676
	655		710		628		676