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                          **    ▽*  *                *              ▽                                    *
NYC1         172 NVVITGSTRGLGKALAREFLLSGDRVVIA-SRSPESVLQTINELEENIQEGLSVAKKKQREILLHAKVVGTSCDVCKPEDVKKLVNFAKDELGSIDI---   267
At NYC1      163 NVVITGSTRGLGKALAREFLLSGDRVIVT-SRSSESVDMTVKELEQNLKEIMSNASESARKKLSDAKVVGIACDVCKPEDVEKLSNFAVKELGSINI---   258
NOL           75 NVLITGSTKGIGYALAKEFLKAGDNVVIC-SRSAERVESAVTDLKKEFGE----------------QHVWGIVCDVREGKDVKALVDFARDKMKYIDI---   155
At NOL        78 NILITGSTKGIGYALAREFLKAGDNVVIC-SRSAERVETAVQSLKEEFGE----------------HVWGTKCDVTEGKDVRELVAYSQKNLKYIDI---   158
Ot NOL        59 RVLITGSTRGLGLELARSFLTRGDKVFVT-SRDAEKVRETVKALREEFGD----------------DFVAGLEADVSRAESVEAVAEAVVDAFGGVDL---   138
Ot SDR        41 VCVITGGARGLGYHLARALVARSCAVVLA-SRDGARAETASRTLGAACAF-------------------ARCDVGETADVEALGRRARETAERLDVDVV   119
Ct SDR         6 GVVITGGSAGLGLAMAREFLRAGDRVVIC-SRRESNLKSALQMLGSDVPD--------------RNVYGMVCDVSLPAQAADFAAFAAAKLGIIDR---    86
Hh SDR        11 GVVITGGSRGLGLAMAQRFLAAGDAVVLC-ARDAERLEVARAELVTATGA--------------GERLHTVACDVADPEAAERLADFAVERLGSIHR---    91
Pa SDR         7 GIVITGGSRGLGYALAKGFLNVGDRVVIC-ARNPEGVDSAVSSLLQSVPD--------------GKIFGISCDVTNPEDACRLASFAVSVLGSVDR---    85
Pp SDR        33 GVVITGGSRGLGVALALEFLAAGDRVVIC-GRNPGRLDEAIQTLQQAVPS--------------GEVYGIVCDAGNPSGGRELAAFAAERLGRVDR---   113
Ha SDR        23 VIVITGGSRGLGLAMAEAMLSQGAKVVIA-GRDQASLEQALAQLKRQSSH--------------VLATTCDVGDLAAIEALRDQTIAQFGKLDV---   103
Fj SDR        20 KIVITGGTTGIGKAIADVLVSLGGRVLIF-GRDEKDFKNAVADIQKQFPG--------------SEVYGTPADVTKKEDIQKILEIADNELGGIDI---   101
Ll 3-ketoacyl  7 NVFVITGSTRGIGKAIALQFAKAGSNLIIN-GRSA-ISEELLAEFTAYGVK----------------AVGISGDISKSEDAKQMVAEAIETLGSVDI---    84
At 3-oxoacyl  77 VVVITGASRGIGKAIALALGKAGCKVLVNYARSAKEAEEVAKQIEEYGGQ----------------AITFGGDVSKATDVDAMMKTALDKWGTIDV---   156
Os 3-oxoacyl  78 VVIVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEEVSKEIEACGGQ----------------AITFGGDVSKEADVDSMMKAALDKWGTIDV---   157

                    *  *                                                       *                *      *  *
NYC1         268 -WINNAGTN-KGFRPLVNFSDEDISQIVSTNLVGSLLCTREAMNVMQHQQKG-----GHVFNMDGAGSGGSSTPLTAV-YGSTKCGLRQFQASLLKESRR   359
At NYC1      259 -WINNAGTN-KGFRPLLEFTEEDITQIVSTNLIGSILCTRGAMDVMSRQHSG-----GHIFNMDGAGSGGSSTPLTAV-YGSTKCGLRQFHGSIVKESQK   350
NOL         156 -WINNAGSNAYSYKPLVETSDEALMEVITTNTLGLMICCREAINMMRNQPRG-----GHIFNIDGAGSDGRPTPRFAA-YGATKRSVVHLTKSLQAELQM   248
At NOL      159 -WINNAGSNAYSFKPLAEASDEDLIEVVKINTLGLMLCCREAMNMMLTQSRG-----GHIFNIDGAGSDGRPTPRFAA-YGATKRSVVHLTKSLQAELQM   251
Ot NOL      139 -WINNAGSNGYAYENLEEADPLVLQEIVMINSLGSLLCTROAIRTMRKTSGR-----GHIFNMEGAGSDGSATRKFAA-YGHTKAGMAQLSKTMAVELKG   231
Ot SDR      120 YWINAAGAV-TKNAPLCDVDAREISAVVRANLLGPLLGARTCERLARETSKR-----VVVFNF-GFSDWGANLSKSAATHKSTKTGLSALTKALNAEVRA   212
Ct SDR       87 -WINNAGTAGRKRRPLWELDLSDIDETCRINLSGSMMLCAEALRVMLRQPASADEPLYHLFNM-GFSSAGLRSSPTSVPHRASKRAVAIMSKLLRQELEA   184
Hh SDR       92 -WLNNAGTAGRHKRPLVELSAADIAETCTINLTGSMQLCAAALRRMQAQPAAP-EPRYHLFNF-GFSGLGAHFSRTSIPHRVSKLGVAELSRQLRRELQA   188
Pa SDR       86 -WLNNAGTSGYRKRPLWELDERDLLETCTINLYGSMLMSKTAVGIMRSQPVKA-TEVYHIFNF-GFTSFGARFSRSPVPHKASKTGVAAITRHLSREIRQ   175
Pp SDR      114 -WINNAGTAGLFKRPLWELHAEDILETCTINLSGSVMLCAEAVRVMDRQPLSP-EPVYHIFNM-GFSSIGAKFSRSALSHKASKRGVAELTHFLYRELKA   201
Ha SDR      104 -WVNNAGVA-GPYGATVAIHPRDYRRVIDINIFGTYHGSITALKYFQQQGH------GHIINI-GSMSAESKEAKSTI-YVATKSAIRGFSTSLRKELNP   200
Fj SDR      102 -LINNAALG---APGITNESYDDYKYIIDINITGYLAFAQEAASRVKQQKS------GHIINI-GSMSAESKEAKSTI-YVATKSAIRGFSTSLRKELNP   188
Ll 3-ketoacyl 85 -LVNNAGIT--RDGLSLKMSEEDFESVLKINLTGAFNMTQAVLKPMTRARS------GAIINI--SSVVGLMGNAGQANYAASKAGLIGLTKSIAREVAA   173
At 3-oxoacyl 157 -VVNNAGIT--RDTLLIRMKQSQWDEVIALNLTGVFLCTQAAVKIMMKKR------GRIINI--SSVVGLIGNIGQANYAAAKGGVISFSKTAAREGAS   245
Os 3-oxoacyl 158 -LVNNAGIT--RDTLLMRMKKSQWQDVIDLNLTGVFLCTQAATKIMMKKKK------GKIINI--ASVVGLVGNIGQANYSAAKAGVIGLTKTVAREYAS   246

                                        **
NYC1         360 SKVG----VHTASPGMVLTDLLLSG                                                                                380
At NYC1      351 TNVG----LHTASPGMVLTELLLSG                                                                                371
NOL         249 NEVN-NVMVHNLSPGMVITDLLMSG                                                                                269
At NOL      252 QDVK-NVVVHNLSPGMVTTDLLMSG                                                                                275
Ot NOL      232 SSIG----VHTISPGMVFTELISSG                                                                                255
Ot SDR      213 MSPPIRCEFHQLSPGLALTRVLLGN                                                                                237
Ct SDR      185 AGIR-SVGIHELSPGLVLTDLLLRD                                                                                208
Hh SDR      189 SGEQ-GIGVHELRPGLVRTELLLAD                                                                                212
Pa SDR      176 AGIS-GIGVHEVSPGLVLTDLLLRD                                                                                196
Pp SDR      202 AGKT-SIGVHEVSPGLVLTDLLFQD                                                                                222
Ha SDR      201 QGIE----ILGFNPGLMTIDMLTDV                                                                                224
Fj SDR      189 LGIK----VSLIEPGAVTSDMQPGT                                                                                222
Ll 3-ketoacyl 174 RNVR----VNAVAPGFIESDMTEVL                                                                               194
At 3-oxoacyl 246 RNIN----VNVVCPGFIASDMTAEL                                                                                266
Os 3-oxoacyl 247 RNIN----VNAIAPGFIASDMTAEL                                                                                267
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**Supplemental Figure 4.** Multiple alignment of SDR sequences.
SDR domains of NYC1, NOL and related sequences are aligned. Identical amino acid residues are reversed out. Important residues conserved in the 'classical SDR' are marked with asterisks. The numbers start from the first methionine of each sequence. Triangles indicate the residues important for the selection of the cofactor.