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Expanding the biocatalytic toolbox of flavoprotein monooxygenases from *Rhodococcus jostii* RHA1

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Supplementary information

Table S1: GC conditions for the determination of the conversions and enantioselectivities

The following columns were used for the determination of conversions and enantiomeric excesses of the sulfoxides by GC: A: Alltech GT-A (30 m x 0.25 mm x 0.25 μ m), B: Hewlett Packard HP-1 (30m x 0.32 mm x 0.25 μ m, 12.2 psi N₂), C: Chirasil Dex CB (30 m x 0.25 mm x 0.25 μ m, 12 psi N₂)

Substrate	Program	Column	t _R (min) substrate	t _R (min) products
thioanisole	70/5/10/200/2	B	11.4	14.9 (sulfoxide) 15.6 (sulfone)
thioanisole	40/0/10/160/8	A	7.5	14.3 (R); 16.7 (S)
p-tolyl methyl sulfide	70/5/10/200/2	B	11.5	15.1 (sulfoxide) 15.9 (sulfone)
p-tolyl methyl sulfide	40/0/10/160/8	A	8.3	15.6 (R); 16.5 (S)
benzyl ethyl sulfide	70/5/10/200/2	B	12.5	14.7 (sulfoxide) 16.9 (sulfone)
benzyl ethyl sulfide	40/0/10/160/8	A	8.8	14.4 (R); 15.5 (S) 19.0 (sulfone)
benzyl phenyl sulfide	100/5/5/200/5	B	21.7	27.3 (sulfoxide)
2-indanone	70/10/3/180/5	B	22.3	32.7
cyclopentadecanone	70/10/3/180/5	B	46.5	50.4
phenylacetone	70/7/5/120/2	B	13.5	14.9 (ester) 10.3 (alcohol)
bicyclohept-2-en-6-one	70/5/5/150/0	B	6.6	13.3 (abnormal; AB) 13.4 (normal; N)
bicyclohept-2-en-6-one	130°C isotherm	C	9.7 and 9.9	(AB: 1R,5S): 17.6 (N: 1R,5S): 18.0 (AB: 1S,5R): 18.3 (N: 1S,5R): 18.5

^a Program: initial T (°C)/ time (min)/ slope (°C/min)/T (°C)/ time (min).

Figure S1: CLUSTAL 2.1 multiple sequence alignment

```
15 -----
STMO -----
9 -----
14 -----
PAMO -----
24 -----
CHMO -----
1 -----
CPMO -----
11 -----
20 -----
3 -----
4 -----
21 -----
23 -----
ACMO -----
MEKMO -----
CPDMO -----
CDMO -----
7 -----
2 -----
12 -----
6 -----
19 -----
17 -----
5 -----
10 -----MTETIAAGLAVPSD-----RDAQLYNATAES 26
8 -----
18 -----MKAAQQVQEAGAATDDRINPDRLTESEIRTAVARA 35
HAPMO -----MSAFNTTLPSTLDYDDDTLREHLQGA 25
16 -----
EtaA -----
13 -----
F MTQTVQPAAVQTS LTPQERVDLWLASFESALAARDVDRAAGMFAVDSFWRDLVAF TWNLK 60
G MTATLDAPVDNIPQPGDIARRWLAGFGATLERGDARGAAQHFLVDGWWRD LLSFTWDLH 60
E MTTTFSDIDLRTD-----AQAWLDGFSRFLAAELAP--TAVFAPQAYWRDVLAF TGDLR 52
D -----
grogan -----
FM01Ara -----
FM02Ara -----
FM01dog -----
FM01hum -----
FM02hum -----
FM03hum -----
FM05hum -----
FM04hum -----
FM0Fish -----
FM01Dro -----
FM02Dro -----
FM0Tyr -----
H -----
IucD_Lys -----
PVDA_Orn -----
SidA_Orn -----
NRho_Orn -----
FMOMeth -----
A -----
C -----
B -----

15 -----
STMO -----
9 -----
14 -----
PAMO -----
24 -----
CHMO -----
1 -----
CPMO -----
11 -----
20 -----
3 -----
4 -----
21 -----
23 -----
ACMO -----
MEKMO -----
```

```

CPDMO -----MSQLIQE 7
CDMO -----
7 -----
2 -----
12 -----
6 -----
19 -----
17 -----
5 -----
10 DPAPLLMALVHATGDTGLLDEFGARLTIEEPGNHYRTGIRPTAPPGIYPEDVAEDIRIRA 86
8 -----MITEIRKRA 9
18 NVPSLLMVVFQTTGDEKWLAAPYRPTRGKGLGDHDSGGLEEP-----IQDEIREAAVKA 89
HAPMO DIPTLLLTVAHLTGDLQILKPNWKPSIAMGVARS-----MDLETEAQVREFCLQR 76
16 -----
EtaA -----
13 -----
F TVEGRDAVAAMLHARLDDTDPVNFRTI----ETPDEADG--VTSAWIEFETATGRGKGH 113
G TTHGRADIESRLADSVPVHEPRHLVLSPAHPAEAVADPEGD-WIQAFFTFETTLARSRGF 119
E TFS--DEIPAELLRRQELTKATNIRIAEDRTPPRLVERAGIPCLEVI FEFDTLAGSAVGV 110
D -----
grogan -----
FM01Ara -----
FM02Ara -----
FM01dog -----
FM01hum -----
FM02hum -----
FM03hum -----
FM05hum -----
FM04hum -----
FM0Fish -----
FM01Dro -----
FM02Dro -----
FM0Tyr -----
H -----
IucD_Lys -----
PVDA_Orn -----
SidA_Orn -----
NRho_Orn -----
FM0Meth -----
A -----
C -----
B -----

15 -----MSARTEVDARANR 13
STMO -----MNGQHPRSVVTAPDAT 16
9 -----MTVQDN- 6
14 -----MSKTI SAD-- 8
PAMO -----MAGQTVDSRR 11
24 -----MTTSMKAANPMNFPSTS 17
CHMO -----MSQKMD---- 6
1 -----MSTAAP---- 6
CPMO -----MTTMTTMTTEQLGMNN 16
11 -----MTTASIDTREL D-- 12
20 -----MTASQADTATRTGKH 15
3 -----MNTTLL-- 6
4 -----MTAIHAPKNDLAQS- 14
21 -----MSTTASAPTETSAT 14
23 -----MSTTASAPTETSAT 14
ACMO -----MSTTT- 5
MEKMO -----MSAQSKLAAGSCAY 14
CPDMO PAEAGVTSQKVSFDHVALREKYRQERDKRLRQDQEQYLEVAVTCDEYLKDPYADPIVRD 67
CDMO -----MTTIDREALRRKYAEERDKRIRPDGNDQYIRLDH-VDGWSDHPYMPIITPRE 51
7 -----MVSYSMLPVTDT SAPP 16
2 -----MNL P- 4
12 -----MVRSAIPVELPVDSDVHPP 19
6 -----
19 -----MTATTTQHAAAPDGG 15
17 -----MT 2
5 -----MG 2
10 REILTPDVVAELGVPDDEL FVRMATVCTSQRVDAEFAPILLEQAGFTKNRRHVPTVAP- 145
8 REVL TNDLTA VLGVPDPELFRRMASLR TAGTVAE EFV PILLEQAGFQIGRRVPTKKP- 68
18 ILDLQNGALPAVETPSPELTVRMISVCTGEEVGEYGPMLSELARRAAPDAPSLALEPV 149
HAPMO LIDFRD SGQPAPGRPTS DQLHILGTWLMGPVIEPYLPLIAEEAVTA EEDLRAPRWHKDHV 136
16 -----MSHETEAAETT G-----AK 14
EtaA -----
13 -----MKHITSHDSDQETPVTITTIPE 23
F LRLKGE----AWTFLTTMQELKGHEERRGRNRVKGAVHSGGDTLSWAEKREIEEREL 168
G VRLRRDDDG EWRAWTLISAMEEIKGHEEKKGHRRVQGTNHGAHRGKINWLD RR- TAKGEF 178
E ARLVDVPERGLLVRSLFTTLDQLADHPERTGEHRPVGQADSSKFGGPNWLD RR- IAAQAY 169
D -----

```

```

grogan -----
FM01Ara -----MASNY 5
FM02Ara -----MAYNY 5
FM01dog -----
FM01hum -----
FM02hum -----
FM03hum -----
FM05hum -----
FM04hum -----
FM0Fish -----
FM01Dro -----MMS 3
FM02Dro -----MIK 3
FM0Tyr -----MGYRTYAILLCFNWLHGGDTFPQETTPVMLDCERVIRLEAPAPLKAVLLP 53
H -----
IucD_Lys -----
PVDA_Orn -----MTQAT 5
SidA_Orn -----MESVERKSESSYLGMNRMQPEQLSLDPPRLRST 34
NRho_Orn -----MSESPETVGT 10
FMOMeth -----
A -----
C -----
B -----

```

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15 IG--DVDVVVVGAGFAGLYAVHKLR-SL-G-----LTVQGVEAAGVGGTWF 57
STMO TGTTSDVDDVVVVGAGIAGLYAIHRFR-SQ-G-----LTVRAFEAASGVGGVWY 62
9 ----DFDAVVVVGAGISGLYAVYKLR-QR-G-----MRVHGFESAEGVGGTWF 48
14 ----VDVVVVGAGFAGLYALRKLDRM-K-----LSTRVFEAGSEVGGTWF 50
PAMO QPPEEVDVLLVVGAGFAGLYALYRRL-EL-G-----RSVHVIEATAGDVG 57
24 DTG-IVDVLGVGAGFAGLYLHRLT-TA-G-----WTFAGFEAGPSVGGTWF 62
CHMO ----FDAIVIGGGFAGLYAVKLRDEL-E-----LKVQAFDKATDVAGTWF 48
1 AVTEVLDVLLVVGAGFAGLYQLENLR-SR-G-----YSVKVVEAGEGLGGI 52
CPMO SVNDKLDVLLIGAGFTGLYQLYHLR-KL-G-----YKVHLVDAGADIGGI 62
11 EANGVLDVLLVVGAGFAGLYQLDQLR-SR-G-----FSVKVVEAGDSLGGI 58
20 SNNDVLDVLLIGGGFAGLYALDRIR-DL-G-----FTAKVWDAAGGLGGI 61
3 ---EELDLVIGGGFAGLYQLDRLR-TL-G-----YVVKIYEAGTGLGGV 49
4 AETPTYDVIIVGGFAGLYQLRHLR-DR-G-----FSVILLEASGGFGGAW 60
21 -ESLELDALIIIGAGVAGLYQLHQLR-EQ-G-----LRVRAYDTAGDVGG 59
23 -ESLELDALIIIGAGVAGLYQLHQLR-EQ-G-----LRVRAYDTAGDVGG 59
ACMO ----LDAAVIGTGAGLYELHMLR-EQ-G-----LEVRAYDKASGVGGT 46
MEKMO GNVTSLDAMVIGAGVAGLYQLYRRL-EM-G-----LTVRAYDTASGVGG 60
CPDMO PVVRETDVFIIGGGFAGLYAAVRLQQAG-V-----SDYVMVERAGDVG 114
CDMO PKLDHVTFAFVIGGGFAGLYAARLRRESG-V-----ESVRIIDKAGDF 98
7 AGVRHIDTLIIIGSGFAGLGAAILKLTQAG-K-----TDFLVLERGSD 63
2 ---QHVHTLIVGAGFAGMGLAARILQTPQ-----ADVLIIEERGDDV 49
12 ---EVVDVLLVVGAGFAGLGTAIRLKQAG-I-----DDFVLDRAEDIG 63
6 ---MTHYDILIVGAGISGIGAAIRLKQSG-I-----DNFAILEKGDAL 45
19 GDERHLRVVVVVGAGLSGIAAAVKLERAG-I-----TDFVLEKSDRV 62
17 TGTTEPDLVVVGTGAGLCMAIKLKEAG-E-----ENVVVEKADRVGG 49
5 GEVHRCRVLVIGTGAGLYAIAAQLLEDMG-----IDYVILEKQPEAG 195
10 --PADFDVIVIGAGIVGNAGIKLGEAG-----FRYTIIEEREDVGG 189
8 --PADLGVIVIGAGMIGLNAAILKGEAG-----FGYRVFESRDDIG 112
18 DAPEGYSVVVIGTVAGIAAAQQLLEDMG-----IDYVILEKQPEAG 195
HAPMO ASGRDFKVVIIIGAGESGMIAALRFKQAG-----VPFVIEYKGNDDV 182
16 TPVEHVDVLLIIIGAGLSGIAAYHLQDNFPR-----RTYAILESRES 62
EtaA -MTEHLDVIVIGAGISGVSAAHWLQDRCP-----KSYAILEKRESMG 47
13 VETMDFDVLIIIGAGISGIAAYHLKTRRP-----TTFALLEGKDAIG 71
F GTRQPYVLLVIGGGGIALGARLRQLGVP-----AIVVDKNERPGDQ 214
G -ETEQPAVVIVGAGQGGALAAARLQGLGVD-----TLLVERNDRIG 223
E -ENRDPDLVIGGGQSGTLAARLQGLDVD-----ALVVDTHARPGDN 214
D -MNSEVDVAVIGAGQAGLSAAYLRRFVVEP-----ESGFVLDHAPG 49
grogan -MDS-VDVVVIGGGQSGLSAGYFLRRSGLS-----YVILDAEASPG 44
FM01Ara DKLTSSRVAVIIIGAGVSLAAAKNLVHH-----NPTVFEASDSVGG 49
FM02Ara NMHTSSRVAVIIIGAGVSLAAAKHLARH-----HPQVFEASDSIG 49
FM01dog ---MAKRVAIVGAGVSLASIKCCLEEG-----LEPTCFERSDDLGL 43
FM01hum ---MAKRVAIVGAGVSLASIKCCLEEG-----LEPTCFERSDDLGL 43
FM02hum ---MAKKVAVIGAGVSLISLCCVDEG-----LEPTCFERTEDIG 43
FM03hum ---MGKKVAIVGAGVSLASIRSCLEEG-----LEPTCFEKSNDIG 43
FM05hum ---MTKKRIAVIGGGVSLSSIKCCVEEG-----LEPVCFERTDDIG 44
FM04hum ---MAKKVAVIGAGVSLSSIKCCVDED-----LEPTCFERSDDIG 43
FM0Fish ---MVRTVAVIGAGPSGLTSIKSCLDEG-----LEPTCFESSDDIG 43
FM01Dro -----VCIIGAGTAGLCCARHSIANG-----FETTVFELSDRIG 42
FM02Dro TSVDKRRVCVIGAGTAGLCAKNSLEAG-----LDVAVYERGTIE 49
FM0Tyr QASLTPRVCIIGAGYSLATARHMIDYG-----LNLTVFEASSYIG 99
H -MLEHLDLVIGAGPSNLSVAALSAPVG-----RLRCKFLDRQPTQR 46
IucD_Lys -MKKSVDVIGVGTGPFNLSIAALSHQIG-----ELDCLFFDEHPH 46
PVDA_Orn ATAVVHDLIGVGFGPSNIALAIALQER-----AQAQGALEVLFLDK 56
SidA_Orn PQDELHDLCLVGFGPSALAIATIALHDALDPRLNKSASNIHAQPKIC 94
NRho_Orn DLP-VRDVVGVGFANLALAIATIEEHN-----AECPPRERISAQFF 63
FMOMeth ---MATRIAILGAGPSGMAQLRAFQSAQEK-----AEIPELVCFEK 49
A --MSEHQVAIVGAGTSGVAAVALADRG-----INPLLIDRADQVGS 44

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C      MSTERFETIVIGAGQAGLATGYHLTRCG-----QRFVILDAHDRVGDVWRE 46
B      -MTEQHTVVVIGGGQAGLSISWHLVQRG-----IDHVVLER-ESIAHEWRD 44
      : * * . :
      :
15     NRYPGAR-----CDVESVDYSYSFSRELEQEWWDWSEKYAT-----QPEILAYINH 102
STMO   NRYPGAR-----CDVESIDYSYSFSPELEQEWNNWSEKYAT-----QPEILAYLEH 107
9      NRYPGAR-----CDVESIDYSYSFDEELQEQEWWTWTERFAT-----QDEILRYLEH 93
14     NRYPGAR-----CDIESVHYSYSFDEDLQEQEWQWSERFAG-----QPEILRYLEH 95
PAMO   NRYPGAR-----CDIESIEYCYFSSEVLQEWNNWTERYAS-----QPEILRYINF 102
24     NRYPGAR-----CDVESIYYSYSFDEALQEQEWTSQRFPAP-----QAEILSYINH 107
CHMO   NRYPGAL-----TDTETHLYCYSWDKELLQSLEIKKKYVQ-----GPDVRKYLQO 93
1      NRYPGAR-----VDSEGPYQFTR-PDLWDEFASFSELYPG-----GDELRRYFKY 96
CPMO   NCYPGAR-----VDTHCQIYQYSI-PELWQEFNWKELFPN-----WAQMREYFHF 106
11     NCYPGAR-----TDSTGQIYQYSR-EDLWKDWSYDELYPS-----WSGVRDYFAY 102
20     NCYPGAR-----TDSTGQIYQFSH-KDLWKKYDFAEALYPG-----HDGVRNYFEY 105
3      NSYPGAR-----VDTWAPVYQFSR-EELWRDWNWSEMYPG-----RDELVRYFEY 93
4      NRYPGAR-----VDSHAPVYQFTD-EYLWKDWDWFSQMYPD-----HEEMRSYFNY 104
21     NRYPGAR-----FDSEAYIYQYLFSEELYKNWSWSQRFPG-----QPEIERWMHY 104
23     NRYPGAR-----FDSEAYIYQYLFSEELYKNWSWSQRFPG-----QPEIERWMHY 104
ACMO   NRYPGAR-----FDSEAYIYQYLFDEDLYKGSWSQRFPG-----QPEIERWLN 91
MEKMO  NRYPGAR-----FDSQAEIYQYWFSEELYKSWQFTERFPA-----QPETEELWLN 105
CPDMO  NRYPGAQ-----CDIESYVYMPLEEMGYIP---TEKYAF-----GTEILEYSRS 156
CDMO   NRYPGAM-----CDTAAVMYMPLEETGYMP---TEKYAH-----GPEILEHCQR 140
7      NTYPGAA-----CDVPS---HLYSFSFALNPEWTRSFST-----QPEIQKYIQS 104
2      NTYPGCA-----CDVPT---SLYSYFAPSADWSHTFAR-----QPEIHRYLK 90
12     NTYPGAQ-----CDIPS---ILYSFSFAPNPNWTRLYPL-----QPEIHDYLR 104
6      NTYPGCA-----CDVPS---ALYSYFAPNREWSRFLFAG-----QDEIRRYIER 86
19     NTYPGCG-----VDIPA---PVYSFSFHPNPRWRSNFAL-----QPELLSYIED 103
17     NTYPGCG-----CDVMS---LMYSFSFAPNRKWRMYAR-----QPEILDYIER 90
5      NTYPGCA-----CDVPS---HLYSFSFEPNPDWTRMWSG-----QEEIFDYLRG 90
10     NTYPGAA-----VDTPS---HYYSYSFELNPNWSKYPT-----GPEYQNYLLD 230
8      NVYPGAA-----VDTPS---HYYSYSFELNPDWSRYPT-----GPEYLDYMH 153
18     NTYPGAG-----VDTPS---HLYSFSFAKN-DWTTDFEL-----RNELOQAYFG 235
HAPMO  NTYPGCR-----VDINS---FWYSFSFARG-IWDDCFAP-----APQVFAFYM 222
16     FRYPGIR-----SDSDMYTLGFRF---KPWSGKSIAD-----GPSILEYVKD 102
EtaA   FRYPGIR-----SDSDMYTLGFRF---RPWTGRQAIAD-----GKPILEYVKS 87
13     FRYPGIR-----SDSDMPTFGGFG---KPWTHKKAID-----AHILDYLQE 111
F      RYKSLCL-----HDPVWYDHLPLYPMPDNWVVFAP-----KDKIGDWLEM 254
G      RYHSLVL-----HDPVWYDHLPLYNPDPHWPVFTP-----KDKLANWFEF 263
D      RYHALTL-----HNAVWLNLDLPLYPMPFATWPFQFVP-----KDKLAGWFEA 254
E      RWPSLTL-----STVNGVHDLPLGLGFADTIGVDPNDPEAALVHA---ASAVPQYFAT 98
grogan AWHSLHL-----FSPAGWSSIPGWMPASQGPYP-----A---RAEVLAYLAQ 84
FM01Ara -----CTYETTKLQARSVDYEFSDFPWPNNRDTTFPP---YLEILDYLE 92
FM02Ara -----CTYETTKLQSVRVSYELSDFLWPN-RGESSFPT--YVDVLDYLEA 91
FM01dog TEHVEEG-----RASLYKSVVNSCKEMSCYSDFPFPED-YPNYVP---NSQFLEYLKM 93
FM01hum TEHVEEG-----RASLYKSVVNSCKEMSCYSDFPFPED-YPNYVP---NSQFLEYLKM 93
FM02hum KENVEDG-----RASLYQSVVINTSKEMSCFSDFPMPED-FPNFLH---NSKLEYFRI 93
FM03hum SDHAEEG-----RASLYKSVVNSCKEMSCFSDFPFPED-FPNFMH---NSKIQEYIIA 93
FM05hum QENPEEG-----RASLYKSVIINTSKEMSCFSDYIPDH-YPNFMH---NAQVLEYFRM 94
FM04hum TESSKDG-----MTRVYKSLVTNVCKEMSCYSDFPFHED-YPNFMN---HEKFWDYLQE 93
FM0Fish KEVSEPN-----RASLYRSLTINISCKEMSCFSDFPFIPAD-YPNYMH---HSRILQYFRL 93
FM01Dro NEATGAV---NGIDVHSSMYKLNRLNLPKEVMGPFDFEIGAN-EASYVR---SDEICDFLNQ 97
FM02Dro SEEMPDK---EYDEVHSSMYEGLRNLNLPKEVMGPDYSPDDITESFIT---SNQVLEFLRS 105
FM0Tyr  TPRVGTDENGAFLFTSAYKNLRTNSFYQIMEFPDYPFPQG-SSSYLS---GPCIKYKQ 155
H      MLSAAVLQVSHLKDVLVLDPTSRYTFLNLFARTGRLHRFASLHTPLIA-RREYESYLRW 105
LucD_Lys LVPDCHMTVFLKDLVSAVAPTNPYSFVNYLVKHKKFFYRFLTSRLRTVS-REEFSDYLRW 105
PVDA_Orn LVSQSELQISFLKDLVSLRNPTSPYSFVNYLVKHKHDLVDFINLGTFFPC-RMEFNDYLRW 115
SidA_Orn LVPGSKMQISFIKDLATLRDPRSSTFLNLYLHQKGRLIHFTNLSTFLPA-RLEFEDYMRW 153
NRho_Orn LLDGATMQIAFPKDLVTFRNPRSAFTFFNYLFDQGRLVDFVNHQTFPPT-RHEFHDLQW 122
FM0Meth TWRTGLDENGEVPHSSMYRYLWSNGPKCELEFADYTFDEHFGKPIASYPPEVLWDYIKG 109
A      RYDRLRLN-----TGRQFSLPNRYPKGTPTFP---TREQVIEHLER 84
C      RFDSLRL-----YSPARYDGLPGWGIAPAWSWPG-----KDEVADYFEA 86
B      SRWDSFT-----LVTPNWQCTLPGYTYSGGDDPGFMNR-----EQTYQFVRG 86

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15     VADRFDLDRFLFGRTRVTSAELEDES-----LRWEVRTDRGDV--- 140
STMO   VADRFDLRRDIRFDTRVTSAVLDEEG-----LRWVRTDRGDGE--- 145
9      VADRHDLRSAYDFLTRVTSATYDEET-----TRWSITTDGQGN--- 131
14     VADRFDLRKDI TFDRVVGHWDDEN-----SVWVRTDDGAV--- 133
PAMO   VADKFDLRSGITFHHTVTAFAFDEAT-----NTWTVDTNHGDR--- 140
24     VADRFDLRKHFNTFRVVGATWNAAE-----RLWEVQLDNGET--- 145
CHMO   VAEKHDLKSYQFNNTAVQSAHYNEAD-----ALWEVTTEYGDK--- 131
1      VDAKLDLSKDIYNNTRIISAFFDDTA-----NTWTVTAENGSS--- 134
CPMO   ADKLDLSKDISFNTRVQSAVFDEGT-----REWTVRSIGHQP--- 144
11     VDRKLDLSRDIIFSTRVTSADFDGER-----NQWTVRTDTGRM--- 140
20     VDSQLDLTRDVVDFTFAESCTWDEET-----RQWTARSADGKV--- 143
3      VDEKLDLSKDVRYEYTRVLGRFDEET-----HRWTLVSRNERTGEEF 135
4      VDSKLDLSKDSRFNTKVVGATFDEEQ-----RMWSLETQDGAT--- 142
21     VADTLDLRRDIQLSTMITSAHYDERA-----DKWIVRTDRGET--- 142
23     VADTLDLRRDIQLSTMITSAHYDERA-----DKWIVRTDRGET--- 142
ACMO   VADSLDLRRDISLETEITSAVFDEDR-----NRWTLTTADGDT--- 129

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MEKMO VANRLNLKDKIQFNTRIASAHFCEDS-----GRWVVTTAAGET---- 143
 CPDMO IGRKFGLYERTYFQTEVKDLSWDDEA-----ARWRITDRGDK---- 194
 CDMO IGKHYDLYDDALFHTEVTDLVWQEH-----QRWRISTNRGDH---- 178
 7 VADKYKVRNKHFLGCDVQSAHWNEST-----TRWEVT----TTKG-- 140
 2 VAADTGVRSRVVTDCELQEAHWDADE-----AVWTVR----TSRG-- 126
 12 CAENFGIVPHLRMGHDVQDAAWDDDS-----QVWHVT----TSRG-- 140
 6 TAAEHGVPFAHVKFGTEMQRAQWSEQS-----RRWTVD----TSAG-- 122
 19 TVDTFGLQSRISMQTDVREAAWSDER-----RRWILD----TSRG-- 139
 17 VVRDYDLAPHIRFGAEVISYEFDETT-----DRWRVE----TRSGS- 127
 5 LADKYDLRRNIHFGRMTGGHWAER-----RRWHVH----TESGD- 127
 10 VVEKYRLREHIRFRTRVLSARWLDDE-----HRWEVVTEDEGEGSVV- 271
 8 VAEKYDLYKNIELSTAVVTAEWDEAA-----QKWTVVTRRTDGSTP- 194
 18 VLKDLGAGERVRYGTEVRSTRYDEAA-----AQWSVDMINPDGSSS- 276
 HAPMO VAREHGLYEHIRFNTEVSDAHWDEST-----QRWQLLYRDEGQ-T- 262
 16 TAAEHGIDRNIIRFRHKVVRAEWSTAD-----SHWTVDAERTDTGETV 144
 EtaA TAAMYGIDRHIRFHKKVISADWSTAE-----NRWTVHIQSHGT--LS 127
 13 TVTENHIDEHIRFGYRVSSAEFSSSA-----GRWTVTAQRSGSDETV 153
 F YTKVMEIP--YWSSTTCTSATFDDT-----KEWTVVLDLRD-GEDV- 292
 G YADAMELN--VWTGTEFTGGSYDDAT-----GEWTVTVARDDGSTR- 302
 E YVEAMEIN--FWGTTAFIGGDYDEQS-----QSWVARVRRRGGTVR- 293
 D YEQFELP--VHRPVHTRVVCARDE-----RLRIETDRG-- 130
 grogan YEQYALP--VLRPIRVQRVSHFGE-----RLRVVARDGR- 117
 FM01Ara YAKHFDDLKFMKFGSKVIEVRFIGDGETPQMVDLGAIGNLLPGKPVWEVAVQIGDSGDIQ 152
 FM02Ara YAKHFNLVKFIKFNKVVLELFIGDGKTLQMGDLGAYGNLLPGKPVWEVAVNTGD-GDIQ 150
 FM0ldog YANRFSLLKCIKIRFKTKVCKVTKCPD-----FTVTGQWEVVTO-HE-GKQE 136
 FM01hum YANHFDDLKHIQFKTKVCSVTKCS-----SAVSGQWEVVTM-HE-EKQE 136
 FM02hum FAKKFDLLKYIQFQTTVLSVRKCPD-----FSSSGQWKVVTO-SN-GKEQ 136
 FM03hum FAKEKNLLKYIQFKTFVSSVKNKHPD-----FATSGQWVDVTE-RD-GKKE 136
 FM05hum YAKEFDLLKYIRFKTTVCSVKKQPD-----FATSGQWEVVTE-SE-GKKE 137
 FM04hum FAEHFDLLKYIQFKTTVCSITKRPD-----FSETGQWVDVTE-TE-GKQN 136
 FM0Fish YAEHFLLQHIHFQTSVRSVRQRPD-----FHSQGQWEVVTEENRE-GQEE 137
 FM01dro YANHFDDLKHKIKFDSYVIRVLQRKT-----KWQVLFKDLVTN----KIE 137
 FM02dro YAEHFLLKKAHIKQLEHIVRVRPLD-----DWEVYVWDHSTD----TCD 145
 FM0Tyr YTKQFNLEKHKIKFQSLVTSVERVGD-----MWNVTYMKTDTK----ENV 195
 H YSDQLD-EVQFGCAVEEVTFDG-----QAFRVESTRTG----- 137
 TucD_Lys AAEDMN-NLYFSHTVENIDFDKRR-----RLFLVQTSQGE----- 139
 PVDA_Orn VASHFQEQSRYGEEVLRIEPMLS-----AGQVEALRVISRNAD-GEEL 157
 SidA_Orn CAQFSDVVAYGEEVVEVIPGKSDPS-----SSVDFFTVRSRNVETGEIS 199
 NRho_Orn AARRVDADVRYGTAETVIRGIRGD-----DGVIDRFEVRTADGS----- 161
 FM0Meth RVEKAGVRKYIRFNATVRRHVEFNEDS-----QTFVTVTQDHTTDTIY 151
 A HARADGIELRLGCPVERLDLTDG-----HWRLTTAAGS----- 117
 C YAQRFALPIRTGTTVDGLSRDGD-----YVVTAGTDR----- 119
 B YADTFDPPVREGVAVVAVRQSGSG-----GFDVDTTEGP----- 120

15 -LSARYCIFATGAL--STAN--MPNIAGRESFTGDTHTHTGQWPH-----EGVDFT 185
 STMO -VSARFLVVAAGPL--SNAN--TPAFDGLDRFTGDI VHTARWPH-----DGVDFT 190
 9 -VTARFVLATGVL--SATN--KPDIPGRDTFGGATYHTGEWPH-----EPVDFA 176
 14 -VRSRYFISGAGNL--SVPK--PEFEGIDNFRGEVLLTGNWPR-----EGADFT 178
 PAMO -IRARYLIMASGQL--SVPO--LPNFPGLKDFAGNLYHTGNWPH-----EPVDFS 185
 24 -RRGRYLLISGAGGL--STPK--DFDVPGLGNFTGLQVSTSRWNI-----SLDDLA 190
 CHMO -YTARFLITAGLL--SAPN--LPNIKGINQFKGELHHTSRWP-----DDVSFE 175
 1 -FVKYFVLCGFA--AKPI--FPKLPGMDSFTGINHHTGLWPE-----GGIEFA 179
 CPMO -IQARFVIANLFGG--ASPS--TPNVDGIETFKGQWYHTALWFO-----EGVNMA 189
 11 -LRARSVVICTFGG--AKPH--IPSNGLNSFAGESHHTALWFO-----EGLDMA 185
 20 -QNRARQVIVATGFG--AKPL--YFNLEGLDLFAGDCYHTARWFO-----EGVDMT 188
 3 TTQAQFVIMCLGAG--SKPL--FPNIPGLEKFGGDCFHHTARWPL-----EGYDLA 181
 4 -FRARFVVFATGST--TEPY--TPSIPDMDAYQGELVHTARWR-----SDLDMT 186
 21 -ITTRFLVTCGML--SAPM--SYVFEQEEFSGPIFHTSRWPK-----EGADLD 187
 23 -ITTRFLVTCGML--SAPM--SYVFEQEEFSGPIFHTSRWPK-----EGADLD 187
 ACMO -IDAQFLITCCGML--SAPM--KDLFPQGSDFGGQLVHTARWPK-----EGIDFA 174
 MEKMO -INTQYLLISCCGML--SAPL--SDRFPQGADFGQGIYHTGLWPK-----DPVDFN 188
 CPDMO -FSARFVCMSTGPL--QRPK--LPGIPGITSFKGHSFHTSRWDYSYTGDDQDTGN-LEGLK 248
 CDMO -FTAQFVGMGTGPL--HVAQ--LPGIPGIESFRGKSFHTSRWDYDYGDDALGAPMDKLA 233
 7 NFVAKVLVSAVGAL--CEPS--LPDIKIEGFEIGEIFHSARWNH-----DADLT 185
 2 TVTADVVAATGAL--STPS--VPDMPGLETFGGTTFHSATWNH-----DHDLT 171
 12 TWEARILVGAMGPF--SEPA--VPNLPALESFRGAVFHSAAWDH-----EHDLA 185
 6 TFTANAVIAAAGPW--NEPL--VPTVPLDFTTGEVHSSRNH-----TYDLT 167
 19 TIVAQHVIFAAGPI--TEPS--TPAVPGIDRFDDGVFHSARWNH-----DVDLT 184
 17 VYHPRIVVAGPGL--HKPS--VPDLPGRKSFSGVAFHSAEWDH-----SVDLT 172
 5 EYVAQFVVSGIGAL--HIPN--VPDLPGADTFDGTTFHSSARWNH-----DYDLR 172
 10 RHRARAVITAMGML--NAAN--IPEVDGLDSFAGRVVHTAEWDS-----DLDS 316
 8 RHRASAAITGFGFL--NSPN--KTIDPGLDTFEGTVVHTAEWDP-----SLDLT 239
 18 TLRADVVISAVGVL--NRPK--TPNVPMDSFTGTSFHSAAWPD-----DLDL 321
 HAPMO QVDSNVVFAVGQL--NRPM--IPAIPGIETFKGPMFHSAAQWDH-----DVDWS 307
 16 RLTAADFLMCSGYY--RYDEGYTPEFPGDRFGGRVHPQWPE-----DLDY 191
 EtaA ALTCEFLFLCSGYY--NYDEGYSPRFAGSEDFVGP IHPQHWE-----DLDY 174
 13 QITARFLFSGTGY--NHEAGFTPEFDGIEDFTGQVHPQHWE-----ELDYS 200
 F VLHPKQLVLTGMS--GKPN--VPSFPGQDVFRGEQHSSSRHPG-----PDAYV 337
 G TLHPRHVVLATGMS--GVPN--IPRIAGADTFEGTIEHSSWFVG-----GREMQ 347
 E TLRPKHVVIATGVS--GIPY--VPELPLSQFAGRTLHSSSEYDD-----ANDFA 338

D VVSARGLINATGTW--ERPF--IPRYPGAESFTGRQVHTKDYSS-----AQDFA 175
grogan QWLARAVISATGTW--GEAY--TPEYQGLLESFAGIQLHSAHYST-----PAPFA 162
FM01Ara WHAFEFVVVCTGKYGDVPRIPAFPAKKGPEMFQGMVHSMYCKLEKEE----ASTLLS 207
FM02Ara WHAFEVVVVCGAGKYGDVPRTPFPVKKGPEIFKGGKVLHSMYCKLQKEK----ASQLLH 205
FM01dog SAIFDAVMVCTGFLL--TNPHLPLDCFPGINTFKGQYFHSRQYKHPDI-----FK 183
FM01hum SAIFDAVMVCTGFLL--TNPYLPLDSFPGINAFKQYFHSRQYKHPDI-----FK 183
FM02hum SAVFDAVMVCSGHH--ILPHIPLKSPFPMERFKGQYFHSRQYKHPDG-----FE 183
FM03hum SAVFDAVMVCSGHH--VYPNLPKESFPGLNHFKGKCFHSRQYKHPGV-----FN 183
FM05hum MNVFDGVMVCTGHH--TNAHLPLESFPFIEKFKGQYFHSRQYKHPDG-----FT 184
FM04hum RAVFDAVMVCTGHH--LNPPLLEAFPGIHKFKGQILHSEQYKIPDG-----FQ 183
FM0Fish RHMFDVIVCSGHH--SYPHLPLKDFSGIESFEGKYFHSWDYKHPDG-----LR 184
FM01Dro FQYFDKVLVANGHY--HTPNYS--QIPNMERFKGQYFHSRQYKHPDG-----FE 182
FM02Dro PVYDFVYVNCNGHY--TEPDLP--EVEGLDLFEGNKMHSRQYKHPDG-----FK 190
FM0Tyr SEECGFVVVANGEY--IAPHIP--YFAKQEDFQGMKPHSHDYRSED-----YR 240
H -YAAQHLISIGVGP--PYVP--ELATGTLGDEVFHSDFGYHTDLSA----- 179
LucD_Lys -YFARNICLGTGKQ--PYLP--PCVK--HMTQSCFHASEMNLRRPDL----- 180
PVDA_Orn VRTTRALVSPGGT--PRIPQVFRALKGDGRVFFHSSQYLEHMAKQPCS-----SGK 206
SidA_Orn ARTRKVVIAIGGT--AKMP---SGLPQDPRIHSSKYCTTLPALLK-----KSK 245
NRho_Orn TVIARNVVMGAGLR--ERIP---EWANPSARCFHNNHQLFLRLEGMP-----APV 205
FM0Meth SEEFDYVVCCTGHH--STPY--VPEFEGFEKFGGRI LHAHDFR-----ALEFK 196
A -VDAAEVVVATGFD--HEPF--VPDWPGRGDWRGALVHSSQYRN-----PSQYN 161
C -FEADNVVVASGTW---QSPVVPDLAERLDPRIQLHSSDYRN-----PSQLQ 163
B -MHADHVVAVGGY---HTPVVPRFAERLPADITQLHSSQYRS-----AGALP 164

*

15 GRRVGIIGTSSGSIQSIPLIAEQ--AEHLYVQRSANYSVPAGNQAWDDMERRAIKAGYEE 244
STMO GKRVGVIIGTSSGSIQSIPIIAEQ--AEQLFVQRSANYSIPAGNVPLDDATRAEQKANYAE 249
9 GKRVGVIIGTSSGSIQSIPIIAEE--AAELVVFQRTPNFATPLGNGMDDPNELADIKSNYAD 237
14 GKRVAIVIGTGASGIIQAIPIFAED--AAELVVFQRTPNFATPLGNGMDDPNELADIKSNYAD 237
PAMO GQRVGIIGTSSGSIQSVQIAKQ--AAELFVQRTPHFVAVPARNAPLDPEFLADLKKRYAE 244
24 GKRVAIVIGTSSGSIQAIPIIAEV--AEHVTVFQRTPNYVMPARNAELPLERVDISKDDYPA 249
CHMO GKRVGVIIGTSGTGVQVITAVAPL--AKHLTVFQRTSAQYVPIGNDPLSEEDVKKIKDNYDK 234
1 GKRVAIVIGTGASGVQVAQEASKK--AAQLTVFQRTPVQALPMRQRLTDEDNAKIKFDLAD 238
CPMO GKRVAIVIGTSSGSIQVAQEAALD--AKQVTVFQRTPNLALPMHQQLSAEDNLRMKPELPA 248
11 GKRVAIVIGTSSGSIQVQTEAALD--AEQITVFQRTPNLALPMRQQLTGLQKLEKLENPE 244
20 GRKVVVMTGSSGSIQVQVQEAAGHV--AEHVTVFQRTPNLALPMRQQLTGLQKLEKLENPE 247
3 GKRVAIVIGTGASGVQVQEAASKV--ADHLTVFQRTPNLALPMRQQLTGLQKLEKLENPE 247
4 GKRVAIVIGTGASAVQVQEAAGPV--VENLTVFQRTPNLALPMRQQLTGLQKLEKLENPE 245
21 GKRVAIVIGTGATGIQVITVADK--VEHLKVFIRTPQYALPMKNTPFDESVAAYKSRFAE 246
23 GKRVAIVIGTGATGIQVITVADK--VEHLKVFIRTPQYALPMKNTPFDESVAAYKSRFAE 246
ACMO GKRVAIVIGTGATGIQVITVADK--VEHLKVFIRTPQYALPMKNTPFDESVAAYKSRFAE 246
MEKMO GKRVAIVIGTGATGIQVITVADK--VEHLKVFIRTPQYALPMKNTPFDESVAAYKSRFAE 246
CPDMO DKRVAIVIGTGATSIQAVPHLAAY--AQELVYVQRTPI SVGFRGNKPTDPEWAKSLQ---PG 304
CDMO DKRVAIVIGTGATAVQCPPELAKY--CRELYVQRTPSAVDERGNHP IDEKWFQAIAT---PG 290
7 GKRVAIVIGTGASAIQIVPAIGKK--VSHLDVYQRTAPWILPRADR---EYTKLEHTAFKYL 242
2 GERVAIVIGTGASAVQVPEIAPV--AEHLTVFQRTPAWVIRPLDR---ELSGSEKRLYRRL 228
12 GERVAIVIGTGASAVQVPIRQPI--VGSMTVFQRTPTWILPHPDQ---PMTGWPRKLFARVP 242
6 GKRVAIVIGTGASAVQVPAIQPT--VESLHLVQRTAQVWLPKPDH---TLPGERAILRRVP 224
19 GKRVAIVIGTGASAVQVPEIQPD--VEELYVQRTPAWVIRPLDR---PPRIAQWAFARVP 241
17 GKRVAIVIGTGASAVQVPEVAKT--AAHVDVQRTPHWILPKLDR---PITAGEKAVFKAVP 229
5 GKRVAIVIGTGASAVQVPEIVGD--VAELHLVQRTPPWVIGPLNF---GIPPEARRLFRV 229
10 GKRVAIVIGTGCTSVQVIVANVDQ--VEALDVVVRSPHWVPEKAVSGDVTEGEKAWALANLP 375
8 GKRVAIVIGTGCTAVQIVASIVDD--VATVDAIVRSPHWVPEKLVSTRYRPRGRSGQCGTCR 298
18 GKRVAIVIGTGASSMQIAPAIADR--VAHLSIYQRTSPQVWAPPEKFRAPIMPELRRMLQTC 380
HAPMO GKRVAIVIGTGASATQFIPQLAQ--AAELKVFARTTNWLLPTPDLHEKISDSCKWLLAHVP 366
16 GKRVAIVIGTGATAVTLAPASMAAD--AAHVTMLQRSPTYIISMPAKDKLANLRRHLPKLA 250
EtaA AKNIVVIGSGATAVTLVPLADSGAKHVTMLQRSPTYIVSQPDRDGAIEKLNRLWLPETMA 234
13 GKRVAIVIGTGATAATLIPAMAGT--AAHITMLQRSPTYVLSLPAEDAIAANTLNKLIQPKRA 259
F GKRVAIVIGTGANNASAHDIKALFEN--GADVITMLQRSSTHIVKSDSLMDLGLDLYSERAVAA 396
G GKRVAIVIGTGANNASAHDIKALFEN--GADVITMLQRSSTHIVKSDSLMDLGLDLYSERAVAA 396
E GQRVVIIGTGNSAHDVAQDLHAH--GIDVTMQRSSSTIVSVDPSAAAAADASYLTA--- 392
D GQHVLVVGGGSIQVQLLDEISRV--TTTWTWTRRP----- 208
grogan GMRVAIVIGGNSGAQIILAEVSTV--AETTWTIQTQE----- 195
FM01Ara GKKVAIVIGFKKSAIDLALLESALA----NQGGEGKACTMVVTRTHWGIPIHYWVWGLPFFL 262
FM02Ara GKKVAIVIGFKKSAIDLALLESALA----NQGGEGKACTMVVTRTHWGIPIHYWVWGLPFFL 262
FM01dog DKRVLVIGMGNSTGDI AVE-----TSRLAKKVFLSTTGGAWMSRVFDSGYPWDM 233
FM01hum DKRVLVIGMGNSTGDI AVE-----ASHLAEKVFLSTTGGGWIISRI FDSGYPWDM 233
FM02hum GKRVLVIGMGNSTGDI AVE-----LSKNAQVFLSTRHGTWVMSRI SEDGYPWDM 233
FM03hum GKRVLVIGMGNSTGDI AVE-----LSRTAEQVMISSRSWSVMSRVWVNDGYPWDM 233
FM05hum GKRVIIVIGMGNSTGDI AVE-----ISQTAQVFLSTRGAWILNRVGDYGYPADV 234
FM04hum GKRVLVIGMGNSTGDI AVE-----LSRTAAQVLLSTRGTWVLRSSDWDGYPYDM 233
FM0Fish GKRVAIVIGMGNSTGDI AVE-----SSRVAEQVFLSTRGAWIRVMSDNDGYPWDM 234
FM01Dro GKSVLVIGAGPSGMDLSNI-----ISRTADRVTISHH----- 214
FM02Dro DARVLIIGAGPSGMDITNH-----VRLAAKQVFLSHH----- 222
FM0Tyr GLRVLVIGAGPSAFDLATH-----LINVTSMFISHH----- 272
H GRDVVVGGGQSGAEVVEHLLQRSGRDVAVGLTWSARRIGFQPLDESPTNEWFHDPVVR 239
LucD_Lys GKRIVVIGGQSGADLFLNALRGEWGEAA--EINWVSRNNFNALDEAAFADEYFTPEYIS 239
PVDA_Orn PMKIAIIGGQSAEAFIDLNDS---YPSVQADMILRASALKPADDSPFVNEVFAPKFTD 263
SidA_Orn PYNFVAVLGGQSAEAFIDLQKR---YPSNRTLLIMRDSAMRPSDDSPFVNEIFNPERVD 302
NRho_Orn HHRFVVLGAGQSAEAFIVQYLHGN---YPEAEVHSVFSRYGYSFADDSFYANRIFDPEAVD 262
FM0Meth DKTVLLVGGSSYSAEDIGSQYKYGAKLLISCYRTAPMGYKWPENWDERPNLVRVDTENAY 256

A GKRVLVVGAGCSGMEIAYDLATGGAAKVLWSARTPPNIMLRQGGGIPG----- 210
 C DGPVLVVGCSHSGADIALEASRS-----HRTTICGPVRGEVFPDIEG----- 205
 B AGEVLVVGNGQSGAQIAEDLHLAAGRTVHLVTGGAPRVARFYGRDCVAVLHDMGTVDVSI 224
 : : * : .

15 RRRLSRESGGGSPYNAHPK-----SALDVSDEERREAYETRWK-LGGV-LFAKTFPDQT 296
 STMO RRRLSRESGGGSPHRPHK-----SALEVSEERRAVYEERWK-LGGV-LFAKAFPDQL 301
 9 RRRLSRMSGGGTPNSAYPK-----GALEVDAEERRRVYDEWQ-RGGY-LFAKAFPDQT 287
 14 VRTAARNHFLGVFPFNQVQP-----SALAVDAEERRRTFDERWN-AGGFRLFIDSYQDIL 290
 PAMO FREESRNTPGGTHRYQGPK-----SALEVSEELVETLERYWQ-EGGP-DILAAYRDIL 296
 24 IREECRHSPGGIPDRPVD-----KAFDVSAEERQRRYEAAE-RSGFNGVGGFADLL 302
 CHMO IWDGVWNSALAFGLNESTV-----PAMSVSAEERKAVFEKAWQTGGGFRFMFETFGDIA 288
 1 RFSRRSASFSGDFDFIPK-----SALGVSDEERITTYERLWE-CG-FEFWLGTYQDVF 290
 CPMO AFERRGKCFAGDFDFIAK-----NATELSAERTEILEELWN-AGGFRYLANFQDYL 301
 11 RFAQRRRSFAGFDMDFIPK-----SVFEVSDEERADTYERMWA-TGGFELWLANYQDIL 297
 20 RFEARYKAFAGDFDFLQ-----NAADLSMEERDAIYEKMW-EGGFEMWLGNFQDIL 300
 3 RFANRKNWAGDFDYDFLKE-----NIQDLTEERRNEILEELWT-NGGLQPWLGGLNLV 293
 4 VAAKRETHAAIDYDFDPR-----SGFETPEDERNAVFERLWN-QGGFAFWLGNFSDYL 298
 21 LKETLPNTFSGFEYDFEH-----VWADLTPEQRNDVLEETYE-NGSLKWLWLSFGEMF 298
 23 LKETLPNTFSGFEYDFEH-----VWADLTPEQRNDVLEETYE-NGSLKWLWLSFGEMF 298
 ACO LKDTLPHTFTGFEYDFD-----AWEDLTPEQRARLEDDYE-NGSLKWLWLSFAEIF 285
 MEKMO LKKRVRETFAGFDYDFDAG-----PWAETPDERQAVLEQLWK-DGSLAMWLSFPEMF 300
 CPDMO WQQARMDNFNAITHGMPVD-----VDLVQDSWTKIFGELGVFLGSD-----G 346
 CDMO WQKRWLDSTAIWDGVLTDPSLAIEHEDLVQDGTALGQRMRAAVGSVPIEQYSPENVQ 350
 7 GFQKLCRTGIYWMR-----ESQVVGL 263
 2 LVQKAVRGTVYGF-----EALGGVL 249
 12 VAQRLARSGLDLVQ-----EAMVPGF 263
 6 GAIRALRRVEYAIM-----ESLGLGF 245
 19 AVQRALRRLLDVIL-----RTLWVM 262
 17 GVQKAYRGAIYWSH-----ESLIAGF 250
 5 LARRMVRAAVYWTY-----ESLALGF 250
 10 FYDRWFLRSLYWFASDNLY-----PLPRIDKEWAATHL 408
 8 TSRISSGSEPTGLPQNNLY-----MMPRIDPEWAATHL 331
 18 IYHSWYWRLEFWQFQDKVI-----ESLRVDEPEWHEPER 413
 HAPMO HYSLWYRVAMAMPQSVGFL-----EDVMVDVGYPPTEL 399
 16 YGLTRLKN-----ASVATAIY 266
 EtaA YTAVRWKN-----VLRQAAYV 250
 13 YPIIRRN-----IMMHRGIF 275
 F GMTTEKADLTFASLPYKIM-----HEFQIPIY 423
 G GPAVQDADLIFASLPYPLL-----AGIHAGAT 429
 E -PTLEDCDLLSMATVYDDL-----YTGSQMIT 418
 D -----
 grogan -----
 FMO1Ara FYSSRASQFLHDRPNQSF----- 281
 FMO2Ara -----
 FMO1dog VFMTFRFQNMFRN----- 245
 FMO1hum VFMTFRFQNMFLRN----- 245
 FMO2hum VFHTFRFRSMLRN----- 245
 FMO3hum LLVTRFGTFLKN----- 245
 FMO5hum LFSRLTHFIWK----- 246
 FMO4hum MVTRRCCSFTIAQ----- 245
 FMOFish KYNTRFVHILFQ----- 246
 FMO1Dro -----
 FMO2Dro -----
 FMO1Tyr -----
 H YFHGLSQS----- 247
 IucD_Lys GFSGLEED----- 247
 PVDA_Orn LIYSREHA----- 271
 SidA_Orn KFYSQSAA----- 310
 NRho_Orn DLHGAPEA----- 270
 FMO1Meth FADGSSEK----- 264
 A -----
 C -----
 B ADHPGGLGKRENTNHYVTG-----R 244

15 KTEAANA-TAREFAEEKIRLLVDD-PAVADKLIIPNDH--PIGTKRIVTDTH-YFETYNRP 351
 STMO TDPAAND-TARAFWEEKIRAVVDD-PAVAELLTPKDH--AIGAKRIVTDGSG-YYETYNRD 356
 9 ISQAAND-TAREYVEAKIREMVD-PDIADQLVPTDH--PIGTKRIVTDNG-YFKTFNRG 342
 14 FDKKAND-TIADYIRDRIHERVQD-PAKAATLAPTGY--AYGTRKRPLETN-YYEAFNRD 345
 PAMO RDRDANE-RVAEIRNKRINTVRD-PEVAERLVKPGY--PFGTKRLILEID-YYEMFNRD 351
 24 TDVEANR-TASEFIHDKIREIVED-PATAELLVPRYH--PLGAKRSVFGTD-YYETYNRP 357
 CHMO TNMEANI-EAQNFIKGKIAEIVKD-PAIAQKLMPOD---LYAKRPLCDSG-YYNFTNRD 341
 1 VDDDAND-TAYEWRDRTRARIKD-PVIAEKLAPTKKAYFVGKVRPSLEQT-YYDIFNQD 347
 CPMO FDDKAND-YVEFWRDKVRARIKD-PKVAEKLAPMKKHPYGAKRPSLEQW-YYEIFNQD 358
 11 LDERANR-IMYDFWRDKVRQRTD-PVKAELKAPMDPPHFGTKRPSLEQN-FYDVVNQE 354
 20 VDEANR-TFYDFWRNKVLERVTD-PKKAIVAPETPPHPYGVKVRPSLEQD-YFDVINQS 357
 3 FDKDND-ILYAFWRDKTRQIRTR-PELVELLAPTEPIHPWGVKVRPSLEQN-YFESLCRD 350
 4 FNDKTNA-LTYEFWKNKIKPKIKD-PVKAELLVPEIAPHFPGAKRPSLEQN-YYEVMNQ 355
 21 YDEI SE-EISEFVRRKMRARLQD-PHLCDLLIPTD--YGFGTHRVPLETN-YLETYHRP 353
 23 YDEI SE-EISEFVRRKMRARLQD-PHLCDLLIPTD--YGFGTHRVPLETN-YLETYHRP 353

ACMO SDEQVSE-EVSEFVREKMRARLVD-PELCLDLLIPSD--YFGTHRVPLETN-YLEVYHRD 340
MEKMO FDEQVNE-VVSQFVRIKMRERLRSRDLCDLLIPTD--YFGTHRVPLENN-YLEVYLSQ 356
CPDMO SRAQMVDFQLEQIRARVDQEVKD-PATAESLKPYYN---IMCKRPGFHDS-YLPSFNKP 401
CDMO RALEEADDEQMERIRARVDEIVTD-PATAAQLKAWFR---QMCKRPFHDD-YLPFNRP 405
7 AKAPVFMKPLQFAAERHLRRQIKD-KALRKKVTPNFQ---IGCKRMLISNN-YYPTLAQD 318
2 AHATGLLEPVFEMVAKAHLRRQVRD-PELRRKLTPNFT---IGCKRMLLSND-WLRTLDRP 304
12 VYKPALLKGLAALGRAHLRRQVHD-PELRTKLTPTYA---FGCKRPTFSNS-FYPALAQF 318
6 R-HPWILRVIQQVGKAQLRAQVRD-PKLRAKALTPDYT---LGCKRLLLSNT-YYPALTRP 299
19 R-CERTARLLNPIGTRWLAQVRD-PALRAALTPNF---LGCKRLLLSNT-YLPALTKS 316
17 L-HPRLMTVLESAARGLRRQVRD-PELRATLTPDYI---IGCKRILVSSN-FYPALQRG 304
5 NGH SRLMRPIESMARKNLNRTVAD-PELRRKLTPSYR---IGCKRILGSDV-YYPALISP 305
10 SASPANDMVLRTAQEYLQTSFTDR-PDLIAKLTPDFR---PYAKRIVKDPG-FFAALNRE 463
8 SVSPVNDLVMQTSLQYLEQLTPDR-PDLREKLTPSIR---PYAKRIVKDPG-FLEALERD 386
18 SVNARNDAHREYFTRYITISQVQDR-TDLLDKVMPDYP---PFGRKILLDNG-WYSTLRKD 468
HAPMO AVSARNDRLQDIIASWMEPQFADR-PDLREVLIPDSP---VGGKRIVRDNGTWISTLRKD 455
16 QLCQRYPEFMKGRIRQLQEKWLPKYDIDTHFTPRYN--PWDQRLCLVPNGDLFRAIRND 324
EtaA SACQKWPRMRKMFSLIQRQLPEGYDVRKHFGPHYN--PWDQRLCLVPNGDLFRAIRHG 308
13 KACRRSPKLMRKLIANARQLPKNFVDVTHFTPRYN--PWDQRLCMVNGDLFKAISTG 333
F QKIAERDRDFYDRLEKAGFKLDFGDDGSGLFMKYLRR---GGYYIDVGAS-----ELVA 475
G EAIAEKDAEMLDGLRKAGFKVDFGDDGSGLFMKYLRR---GGYYIDVGAS-----ELIA 481
E ATMKELDKDLVAALNRIGFRDYEEDTGGQMKFMRR---GGYYLNVGCS-----DLII 470
D PFTKDEPFTP--EIGRAAVALVEDRVR---GLPPGSV---VSVTGLPVTPA-----IRAA 256
grogan PAFIADDDVGRVLFERATERWKAQQEGREPDLPPG-----GFGDIVMVPV-----VLDA 244
FMO1Ara RTFLCFLSLLRAVVSKEIESYVLWKLPLEKYGLKPNHSEEDYASCQMAIIPENFFEEA 321
FMO2Ara -----RATVSKFIESYVLWKLPLEKYGLKPDHAFEEDYASCQMALVPEKFFEEA 301
FMO1dog -----SLPTPIVTLWLMARKMNSWFNHNANYGLVPEDETRQLREPVLNDELPGCIIITGV 297
FMO1hum -----SLPTPIVTLWLMERKINNWLHNHANYGLIPEDRTQLKEFVNLDELPGRIITGV 297
FMO2hum -----VLPRTAVKMWIEQQMNRWFNHNENYGLEPQNKYIMKEPVLNDDVPSRLCGAI 297
FMO3hum -----NLPTAISDWLYVKQMNARFKHENYGLMPLNGVLRKEPVFNDELPAIILCGI 297
FMO5hum -----ICGQSLANKYLEKKINQRFDHMFGLKPKHRALSQHPHNLNDDLPNRIISGLV 298
FMO4hum -----VLPFRFLNWIQERKLNKFNHEDYGLS-I TKGKAKFIVNDELPNCLCGAI 296
FMOFish -----LLPVNWSLWFGKELKNAMYDHTMYALKPKHRLFSTIPVINDELPNKILTGGV 298
FMO1Dro -----ERERLLREYHNNTYSVVDTLIERIYGVFYRQKVSIGIPRHAFCMTTVER--ATATA 301
FMO2Dro -----LSTPNTAFMGNV 235
FMO1Tyr -----LDAK-LPEVYGY 284
H ---RRSLLDAQQLASDGIS-KGLESYRRLYNDVSDRIRTTLLPGRELTGLCRGP 303
IucD_Lys ---IRHQLLEDEQKMTSDGIT-ADSLTIYRELYHRFEVLRKPRNIRLLPSRSVTTLE--S 326
PVDA_Orn ---ERERLLREYHNNTYSVVDTLIERIYGVFYRQKVSIGIPRHAFCMTTVER--ATATA 301
SidA_Orn ---ERQSLADKATNYSVVRLELIEEYNDMYLQVRKNPDETQWQHRLPERKITRVEH 367
NRho_Orn ---ERLRLLDVHRSTNYSVVDIELINELYATEYQERVRG--RRRLFMRRASEI IAVDETS 325
FMO1Meth -----VDAILLCTGYIHHFFFLNDDLRLVNNRNLWPLNLYKGVVWEDNPKFFYIGM 315
A -----DFIATPLYHAPVPIADAIARFRGRERSIGDLREFGLPIPEGIFARSARL 259
C -----RLAHLAVPIMWFMANHVLTERTPVGRKMCETHVR---SGGGPLLRVKR-----ADL 252
B DGGRDIDLRAFALAGMRLYGRLLDQVVDGTLRFAPATLESLLDAADAVSESIKDSIDAYIDR 304

15 NVTLVLDKAAPIESITPSGITTADA--DYALDTLVFATGFDAMTGALDR---MRIVGRGG 406
STMO NVELVDRSTPIVGMDETGI VTTGA--HYDLDMLVATGFDAMTGLSLDK---LEIVGRGG 411
9 NVTLVNLRRTPIITEAGVLTINS--FYGLDMLVATGFDAMTGLSLDR---IDIRGRAG 397
14 SVSVVDVKSTPIDEITPTGVRVGDG--VYEVDTIVLATGFDAMTGPLMA---MDIRGRGG 400
PAMO NVHLVDTLSAPIETITPRGVRTSER--EYELDSLVLATGFDALTGALFK---IDIRGVGN 406
24 NVSLVSLRDEPIETMTANAVTSKG--TYEADAVVLAIGFDAFTGPLYG---LGLTGASG 412
CHMO NVRLEDVKANPIVEITENGKLENGD-FVELDMLICATGFDVAVDGNVYR---MDIQKNG 397
1 NVRVVDLHEDPIETITPTGLKTTSE--QHEFDIIVYATGFDVAVTGGLTA---MDIRGTDG 402
CPMO NVTLVVDNETPVLRIETEKGI VTAEG--EAEFDLIVFATGFDVAVTGGLTS---IDFRNQQG 413
11 NVDIVVDNEDPIERITPAGVQTKSG--LHEFDLIVFATGFDANRGGITS---IDIRGTND 409
20 NVEVIDSNLPIRRVLPHGIE TDDG--VIECDLLVLATGFDNNSGGGIMA---IDITGVGD 412
3 NVELVDTSANPIREVASDAIITADGT-RHEVDVIVLATGFDVAVTGGLTA---IDIRGTGN 406
4 NVSLVSTKETPIVGFTEGTIRTADGVEHGFEDIIVLATGFNNNTGALTS---IDVQNANG 412
21 NVEAIGVRDNPITRIVPQGLVLADG-TLHEVDVIVMATGFDAGTGLSLTR---IDIRGRGG 409
23 NVEAIGVRDNPITRIVPQGLVLADG-TLHEVDVIVMATGFDAGTGLSLTR---IDIRGRGG 409
ACMO NVTAVLVRDNPITRIRENGIELADG-TVHELDVIMATGFDAGTGALTR---IDIRGRDG 396
MEKMO NVKAVDCKQSPIERIVPQGIQTADG-KIHEVDIIVLAVGFDAGSGALSR---IDIRGRDS 412
CPDMO NVTLVDTQGAGVERITEKGLVVNGR--EYEVDCIYATGFYEQ-TKLSRRNGYIEHGRNG 458
CDMO NTHLVDTGGKVERITENGVVVAGV--EYEVDCIYASGFELGTGYTDRAGFDPTGRDG 463
7 NVDLVTDG---IAEVTADSVVSKDG-TVREVDIVVATGFHVTDSPTEFEG---IFGKDG 370
2 DVTLVTDG---LAGVTPDGVVDALG-NEHKVDTIIFATGFTPTPEPPVAHA---LRGANG 356
12 NVDVITDG---IREVRNNGIVTEDG-VLHEVDVIVMGTGFRITDNPAPFDV---VRGRDG 370
6 NVEVHANA---VESVRGNVVGSDG-AEREVDVIFGTGFHLDMPIGSK---VFDGDG 351
19 NVELLPHA---LAEVDGRVVVGADG-TRREVDVIFGTGFDVSHPPIASR---IRGRDG 368
17 NVDLVTSG---ISEVTERGIRTTDDG-TMHEADVIVYGTGFAAGDRFENEH---IVGRRG 356
5 KTVVITEG---IAEVRPHSIVAGDG-AERVDVAIYATGFHVTDGFDNVE---LTGVGG 357
10 HVSLHRAS---FEKVTPGVYTTTEG-AFIPADVILATGFKLQ-FTTSIE---IEGRDG 514
8 HVSLHRAS---PKHVHPGGVSLSSG-EFVEADVIVLATGFKVE-YASFD---ITGRNG 437
18 NVDLVDRS---VTAVRPEGLVDDQG-AENDVDVIVWATGFEAARFVSSMD---VVGMDG 520
HAPMO NVSMIRQP---IEVITPKGICCVDDG-TEHEFDLIVYGTGFHASKFLMPIN---VTGRDG 507
16 EVSIVTDH---IDFTTETGITLKSQ-EELHADVVVATGLNLLAFGGMT-----LAVDG 374
EtaA KVEVVTDT---IERFTATGIRLNSG-RELPAIIITATGLNLQFLGGAT-----ATIDG 358
13 HASVVTDR---IERFTATGIRLESQ-QUEADIVVATGLNMLAFGAIQ-----LSVDG 383
F DGSIHVSG-QVDHLTEDAVVLTG-TELPADLVVYATGYGSMNGWAAD-----522
G SGEVSVKQGTIEDHFTPDGVVFDG-TEMPVDVVVATGYKNMRESARK-----529

E SQQVGLVQYADTAGFVAEGLSLTNG--DVVEADAVILATGYQTQQEGVRA----- 518
D RERGVLARQPMFGEITADGVRWPDG--RELKVDVILWCTGFRSLDLHLAP----- 304
grogan RARGVLAAPPPARFSPGMQWADG--TERAFDAVIWCTGFRPALSHLKG----- 292
FM01Ara DKGMIRFKKSSKWWFYEEGIVFEDGT--LEADVILATGYDGKKLKAIVPEPFRWLEF 400
FM02Ara DKGMIREFKRTTNWFFYDEGIEFEDGT--LEADVILATGYDGMKLLKAIVPEPFRSWLEF 360
FM01dog LI-----KPSIKEVKENSVFNNTSKEEPIDIVFATGYT---FAFPFLDET---VVKV 345
FM01hum FI-----RPSIKEVKENSVFNNTSKEEPIDIVFATGYT---FAFPFLDES---VVKV 345
FM02hum KV-----KSTVKELETSAIFEDGTVEENIDVIFATGYS---FSFPFLDES---LVKV 345
FM03hum SV-----KPNVKEFTTSAIFEDGTIFEGIDCVIFATGYS---FAYPFLDES---I IKS 345
FM05hum KV-----KGNVKEFTTAAIFEDGSRREDDIDAVIFATGYS---FDFPFLDES---VKV 346
FM04hum TM-----KTSVIEFTTSAVFEEDGTVEENIDVIFATGYT---FSFPFFEEP---LKSL 344
FM0Fish MV-----KPNVQQIRGSSVVFEDGVSVDKVDVIFATGYN---YDFPFLPPN---VMHK 346
FM01Dro QQ-----KPDVRELDKGAFFVDGS--YQEFDTVFFCTGYK---YAFPFLTVD--SGIYVE 276
FM02Dro TQ-----KPDVKRFTKDGAVFTDGS--TESFDHVMFCTGYK---YTFPCLSTD--VGQVI 284
FM0Tyr KR-----KPDIKHFTPTGAVFVDGS--TEEFDVAILCTGYK---YSFPFLNYKSSGVAWT 334
H GKGKWRITLTHI-----DTGEIDSVGADIVVLATGYHFPLPEFLHT----- 344
IucD_Lys SGPGWKLMEHH-----LDQGRESLESVDVIFATGYRSALPQILPS----- 342
PVDA_Orn QG----IELALR-----DAGSGELSVETYDAVILATGYERQLHRQLE----- 365
SidA_Orn HGPQSRMRIHLKSKPESEGAANDVKETLEVDALMVAATGYNRNNAHERLLS----- 417
NRho_Orn DG----IEVAVR-----SGVDGLTDTLACDALILATGFTPAPLEPLLG----- 364
FM0Meth QDQWYSFNMFDAQAWYARDVIMGRPLPSKEEMKADSMAREKELTLVT----- 364
A GVAPAIVDKELIAAIRDSIEVVRGVELESDADSVLVDGVRIDPEAMVC----- 308
C AAAAVEHFPAKVTGVHDGRPVLDG--TAFDVRNVWCTGFRKDTSWIQIP----- 301
B AGIDAPREERYVWVRPEREVTELELPTSGITSVVWSIGFRTDYRWLHAG----- 354

15 VPLSEYWE--GPKTYLGLGVGFPNLFVVTGPGSP--SVLANMVLGAEQHVWDIADCIH 463
STMO RTLKETWAA--GPRTYLGLGIDGFPNFFNLITGPGSP--SVLANMVLHSELHVDVADAIAY 468
9 RNLREDEWSA--GPRTYLGLSVAGFPNMFILAGAGSP--SVLANMVLMAEQHVWDVSNCLDY 454
14 LPLAEKWEH--GPRTYLGLMVFNFPNLFITGPGSP--SVLYNMLPLAIEDHVDVFDATDAIDY 457
PAMO VALKEKWA--GPRTYLGLSTAGFPNLFITAGPGSP--SALSNNMLVSEIQQHVEWVDHAIY 463
24 RKLQETWQD--GIRTYLGMMTDFPNFMMVAGPQSP--ALASNVMVIEQAVDVIADLIEH 469
CHMO LAMKDYWKE--GPSYMGVTVNNYPMFMVGLGNGP---FTNLPPSIESQVEWISDTIQY 452
1 TLLRDKWSN--GVRANLGVATAGFPNLLFLYGLPLSP--SGFCNGPSCAEIQGDLIVNTIDY 459
CPMO QSFKDVWSD--GIRTQLGVATAGFPNLLFGYGPQSP--AGFCNGPSSAEYQGDLLIQLMNY 470
11 LLLSHKWE--RLDTFMGLTTAGFPNLMFVYGPQSP--AGFCNGPTCAEVQGEIVVDFLTH 466
20 LSIQDKWKS--GVDTCMGLSTRGFPNMMFLYGPQSP--SGFCNGPTSAEYQGEIVVEFLQH 469
3 ETFEVEFRG--GSRTALGKATVGFNLLYVYGPQSP--NAFCNGPTCAELEGEHLIQIVEH 463
4 VTLRDKWSQ--GVDAYLGAVTAGFPNAIFVYGPQSP--AAFANGSTNAELQGEVMDVDFEF 469
21 RALKDDWNR--DIRTMGLMVHGYPNMLTTGAPLAPSAALCNMTTCLQQQTEWIAECIRY 467
23 RALKDDWNR--DIRTMGLMVHGYPNMLTTGAPLAPSAALCNMTTCLQQQTEWIAECIRY 467
ACMO RTLADDWSR--DIRTMGLMVHGYPNMLTTAVPLAPSAALCNMTTCLQQQTEWISAIH 454
MEKMO RSLKEQWQQ--EIRTAMGLQIHGYPNLFITGAPLAPSAALCNMTTCLQQQVWDTGCIH 470
CPDMO QPLSDKWKD--GLSTLWGYHIRDFPN--CFILNGQK--SAVTPNFTHMLNEAGKHVAYVVKH 514
CDMO VKLSEHWAQ--GTRTLHGMMHTYGFPN--LFVLQMLQGAALGSNIPNHFVEAARVVAIVDH 520
7 RSLADVFE--GGQGGYKGAANFNPMMFFLVGPNTGLGHTSMVFMIES--QLNYLDALQT 428
2 RTLAEHWD--GSPSAYKGTIVAGFPNLFVLMYGPNTNLGHSSIVYMLLES--QSAYIADALNV 413
12 RTLAEAWN--GNARAYLGTTSIGFPNFFMLLGPNS--VVYTSQVVTIEA--QIAYILSCLQE 426
6 RSLDDHWK--GSPQAYLGTIVAGFPNAFVLLGALGTGHTSAFMILEA--QLDYLIQAVTA 408
19 TLLSEKWS--KSPRAYLATTTPGAPNAYIMLGNILV--YNSFLGLAET--QLDYVIDGLTT 424
17 LTIQRAWRD--GMEAYLGVAVAGFPNFFLMMGPNSGGGNSQIVFVIEA--QAHYITRCLAL 413
5 RRLADEWEE--HGIRTHLGITVAGYPAFVLLGALGTGHTSMVFMIES--QIRYALELMDL 415
10 RTLSEVWNGDDPRAYLGVQVAGFPNLFITAGPNSAPNHGAGHNIILSEEHVHYIVECLQY 574
8 KKLADKWDHGDPRAYLQVSGFPNLFVITAGPNAAPNHGAGHNIITSEERVHYIVECLQY 497
18 RTLREVVND--DDPKAYLGVSVPGFPNFFMLGPNNSFPGSGS--FMFMVEQMRIRGLLTE 578
HAPMO VALHDVWKG--DDARAYLGMTVPQFPNMFVFPNMFVFPNMFVFPNMFVFPNMFVFPNMFV 566
16 HDIDLTE--AYKGMMLSGVNPFAFVIGYTN----ASWTLKADLVCEYVCRLLAH 424
EtaA QQVDITTTM--AYKGMMLSGIPNMAITVGYTN----ASWTLKADLVSEFVCRLLNY 408
13 EPVNPDDT--VYKSMMLSGLPNFVVALGYTN----ISWTLKVDLISEHFVCRLLDH 433
F -----LMGQEVADKVKGCWGLGSDTTKDPGPWEQERN 555
G -----FLGDAVADRCQDVWGLDA-----EGELRT 553
E -----LLGDEIADAVGPIWGYDD-----EGEVRN 542
D -----LRLRGPGGITMTGRLATQVVD-----PRIHLV 333
grogan -----LDLVTPQQQVEVDG--SGLRALAV---PSVWLL 320
FM01Ara PSGVMPLYR--GTIHP--LIPNMGFVGYV--QSSSNLHTSELRSMWLSRLVDEKFRLPSKEK 456
FM02Ara PWGIMPLYR--GTIHP--LIPNMGFVGYV--QSSSNLKSSELHSRWLSQLLDGKFTLPSKEK 416
FM01dog ENGQASLYK--YIFPVHLKPTLAVIGLIKPLGSMIPTGETQARWAVRVLKGVINKLPPQSA 404
FM01hum EDGQASLYK--YIFPAHLKPTLAVIGLIKPLGSMIPTGETQARWAVRVLKGVINKLPPQSA 404
FM02hum ENNMVSLYK--YIFPAHLKPTLAVIGLIKPLGSMIPTGETQARWAVRVLKGVINKLPPQSA 404
FM03hum RNNEIILFK--GVFPPLLEKSTIAVIGFVQSLGAAIPTVDLQSRWAAQVIGKGTCTLPSMED 404
FM05hum KN--KISLYK--KVFPNLERPTLAVIGLIKPLGSMIPTGETQARWAVRVLKGVINKLPPQSA 404
FM04hum CTKKIFLYK--QVFPNLERATLAVIGLIKPLGSMIPTGETQARWAVRVLKGVINKLPPQSA 403
FM0Fish SGHRLGLYK--HVFPPTLEHPTMAVVGFIHALGAIMPQAEQSRWVTRVFKGKHKLPSNRA 405
FM01Dro DNYVQELYK--QCIN--IRNPSMALIGLP--FYVCAAQMMDIQARFIMSYNNGNELPSTED 332
FM02Dro DNFVQLWK--HCIN--INHPTMAFVGLP--FNVIPTHIFDMQVRFLLKFTGQRKFPSTED 340
FM0Tyr DKYVMPLYN--QLIN--INYPMTFVGTG--KYSIG--LVRDRQGHYSQAALAGLVKLSQDE 389
H -----LGGRARTNCLGLPQLAADYSVSWAGP---AGNMK 375
IucD_Lys -----LMPLITMHDKNTFKVRDDFTLEWSP---KENNI 373
PVDA_Orn -----PLAET--LGDHEIG--RDYRLQTDER---CKVAI 392
SidA_Orn -----KVQHLRPTGQDQWKPHRDYRVEDMPSKVSSEAGI 451
NRho_Orn -----DLAPK--IHPREVG--RDYRLAVSPD---VTAGI 392

FMOMeth	-----AEMMYTYQGDYIQNLIDMTDYPSPFDIPATNKTFLEWKHHKKENIMTFRD	413
A	-----ATGFRQLEKLVGHLGVLDERGWPHATGEKP	339
C	-----VTGSDGWPEQSRGVSPDHPGLYFVGLPFLQAFAS	335
B	-----VFDGEGHPTHNRGVTAVPGLYFLGLPWQHTWGS	388
15	LWEKDYDAIEASVPATEQWVEHCRDLAAQTLFPLANSWYMGANIPGKPRVFMF----	YL 518
STMO	LDARGAAGIEGTPEAVADWVEECRNRAEASLLNSANSWYLGANIPGRPRVFMF----	FL 523
9	LDEHNIEIETATDESVDVEAECNEKAAGTLFPTADSWYMGANIPGKPRVFMF----	YI 509
14	LDRRLDVIETPAQAESDVGALTNEIADQTLLEPETNSWYMGANIPGKPRACMV----	YL 512
PAMO	MFKNGLTRSEAVLEKEDEWVEHVNEIADETLYPMTASWYTGANVPGKPRVFMF----	YV 518
24	ARDSGATLVEATPEQNDWVDIETEETVAQTLYATDTSWYRGSNVEGKPNFTMG----	YV 524
CHMO	TVENNVESIATKEAEQWTQTCANIAEMTLFPKAQSWIFGANIPGKKNVTYF----	YL 507
1	MRDNLNRIESEADADAASDVAELTAEALYDKADSWYMGANVPGKPRQLLN----	YP 514
CPMO	LRDNNISRIEQAQEAQEEWKL IADFWDSLFPRAKSWYQGSNIPGKKNVESLN----	FP 525
11	VRDGGYQRFETSEDAEQSWTAHVVEVFHMSLFPRAKSWYHGANIPGKPSQMLN----	YS 521
20	LRDNGITRFENTESEKQWRAHVDEL FVNSMFTKARSWYMGANVPGKPAQMLN----	YS 524
3	MRNNGYTRIEAKPEAQYWGAI AELTSATLFLAKSWYMGANVPGKTVEMLM----	YP 518
4	LRSNGLTRFESTVEADKAWTAH INETDDTALFNRAKSWYNGGNI PGKKNQMLQ----	YL 524
21	MRAHDHTVIEPTLAGEDEWVAHHDETANATLVSKTDSWYNGANVPGKPRRVL S----	YI 522
23	MRAHDHTVIEPTLAGEDEWVAHHDETANATLVSKTDSWYNGANVPGKPRRVL S----	YI 522
ACMO	LRATGKTVIEPTAEGEAWVAHHD ELADANLISKTNSWYVGSNVPKPRRVL S----	YV 509
MEKMO	AAEHGKHVVEASKALEDNVQHHDETAAKTLVVKTD SWYMGSNVDGKPRRLLS----	YI 525
CPDMO	CLDERVDVFEPTEAEAEQAWVDHVMSPAGIKQYDRECTPSYNNEGQVNDVALTRNNF Y	574
CDMO	VLSTGTSSVETTKAEQAWVQLL LDHG--RPLGNPECTPGYNNNEGKPAELKDRLNVGYP	578
7	LDKYD I G K I E V R Q D A D R Y N A E L Q E K L S H S V W N N G G --C A S W Y L D K H G N N T T L ----	WP 481
2	MHSEITAFEVTEEAQRYYNTRI QSELQTTVWVKGG--CSSWYDSEGRNSVQ----	WP 466
12	MNAQGAASIDVRPEIQQAFVDEVDERLQTSVWNTGG--CNSYLSGEGRNF TF----	YP 479
6	ARSNWTRMEPRREVQDAFNAQVQEALATTVYNAGG--CQSYFLDVNGRNSFN----	WP 461
19	AERQGISVLEVRDQPPFRFNDAVQKGLEPTVFNNGG--CSSYLDADGRNF AA----	WP 477
17	MKKRDATAIEVRAGAQRFRN RVVHRKLAGSVWNSGG--CDSWYLDSTGHNR AA----	WP 466
5	VDRRGADSAAVRPAVQSGFNAD IQRKLARGVWSTGG--CVSWYLD SHGVNRTI ----	WP 468
10	LLENGHDAMDVRQDVLDTYNRKVD AALDDTVVWHPGAEVNGYRNSSGRAI V P ----	CP 629
8	LVENDFSAMDVKPEALTVYNEKVEALDQTVVAHPGEGVIGYRNNQGG-----	545
18	MFKKG I K A I D A R P E A N E E Y N E L V D S T H A R T V W T H R G --M S T Y R N S H G R V V F V ----	MP 619
HAPMO	LLEGGHQSMEVKTPVFESYNQRVDEGNALRAWGFSK--VNSWYKNSKGRVTQN----	FP 619
16	MDANGFQCAPER--DSSVEEPP LDF AAGVYLRSVESFPKQGS--KAPWRLRMN----	YF 477
EtaA	MDDNGFDTVVVERPGSDVEERPFMEFTPGYVLRSLDEL PKQGS--RTPWRLNQN----	YL 462
13	MDERGYTTVEPVLTDPGMERVPLLDL TSGYVQRAVAAPPRAGT--SGPWAAMA----	YE 487
F	MWKP T Q Q E A L W F H G G N L H Q S R H Y S Y L A L Q L K A R H E E I P T P V Y G L Q E V H H L S ----	607
G	VWRRSGHPGFWMAGNLHQSRHYSKYLA FQ I K A Q E E -----G L Q P I R -----	595
E	TWRTAQPLWFSSGNFQLCRIYSKVLAMQIRTELDN-----G-----	580
D	GYGPPSSSTIGANRAG--QAAARELTRHLGLSAGSARPT-----	369
grogan	YGDWNGMASATLIGVTRYAREAVRQVTA YCADHQDR-----	357
FM01Ara	MLDQFLKEMEVTNRSSRFYKRHCISTFS--IQHADDMCNDMGLN-----	PWRKSNF 505
FM02Ara	MLDQFLKEMHVMRSSRFYKNCFCSTFS--IQHADDLSKDMNLK-----	P----- 459
FM01dog	MTEEVNARKENKPSGFLGCYCKALQSD--YITYIDELLTINAK--PNLFSLLTDPRLA	460
FM01hum	MIEBINARKENKPSWFLGCYCKALQSD--YITYIDELTTYINAK--PNLFSMLLTDPLHA	460
FM02hum	MMMDI I K R N E K R I D L F G E S Q S T L Q T N --Y V D Y L D L A L E I G A K --P D F C S L L F K D P K L A	460
FM03hum	MMNDINEKMEKRRKWF--KSETIQTD--YIVYMDELSSFIGAK--PNIPWFLFTDPKLA	458
FM05hum	MMABI SKAQEEIDKRYVESQRHTIQGD--YIDTMEELADLVGVR--PNLLSLAFTDPKLA	460
FM04hum	LMMEATEK--EQLIKRGVFKDTSKDKFD--YIAYMDDIAACIGTK--PSIPLFLKDPRLA	458
FM0Fish	MLKAVECDTKMDKNYIVSKLVPLQVD--FVSYMDDIAGEVGVR--PSLAWLFFTDYPLF	461
FM01Dro	MLKDRDRMGLKWAEGLR--KRHAHMLGPKQIDYFTDLSQTAGVKNIKPVMTKLHNESSKC	391
FM02Dro	MIADLEQIEIGRWGCGVRNQQKAHQMGERQFVYVYNELAS IAGIENIKPVIHKLMDCCGKK	400
FM0Yr	MFKQWFYDTHKHTAKEINLIGYSNTES----YMETLLNGTDIPRPPVFTTILRNHIDI	444
H	FFLNAGKLSHG IADPNLSLAWRAATV LNTITETPLYPDLRSSTCSWDVADRAATHPPVD	435
TucD_Lys	FVVNASMQTHGIAEPQLSLMAWRSARILNRVMGRDLF--DLS-----MPPA--	417
PVDA_Orn	YAQGFSAQASHGLSDTL LSVLPVRAEEISGSLYQHLKPG-----TAA	433
SidA_Orn	WLQGCNERTHGLSDLSLVLAVRGEMVQSFGEQLER-----AAV	492
NRho_Orn	YLQGGTEKTHGITSLLSNVAVRAGEIVTSVVTRRRGRNGTL-----ASV	436
FMOMeth	HSYRSLMTGTMAPKHHTPWIDALDSDSLEAYLSDKSEIPVAKEA-----	456
A	AAERLRF IGFVPRPSQIGFAAKQARRAARAIARELR-----	375
C	MLTGGVGRDAAYVAKHIAKRVVRSPEAVA-----	365
B	RFAGVARDAEYLADRIELEAGVLPATATLA-----	418
15	GGFGAYGRICADVAEEGFRG--FEFS--RSRTRLADPVG-----	553
STMO	GGFGVYREIITEVAESGYKG--FAIL--EG-----	549
9	GGFGNYNTICAEVAAAGYKG--FELG--ERRVDVDQ-----	541
14	GGAPTYRATCDEVVAGGYSG--FALT--RAEAAA STVS-----	547
PAMO	GGFHRYRQICDEVAAKGYEG--FVLT-----	542
24	GGVGKYRRMCTEIAKRGYPG--VRIDGETESPHLGPIHREIS-----	564
CHMO	GGLKEYRSALANCKNHAYEG--FDIQLQRSDIKQPANA-----	543
1	GGLPLYLAKWDETVCAGYKG--FTLS-----	538
CPMO	LGLPTYISKFNESAEGYAG--FSLAS-----	550
11	GGLPSYFDHWEENVAAGYKA--FTLS-----	545
20	GGVPQYFARWDKIKANGYAA--FETN-----	548
3	GGLSVYLEILEKAAAGGYQEQFLV-----	543
4	NGVPTYLQFWQEKESGYTDGLTVS-----	549
21	GGVGTYREKTLAAAAAGYKG--FQLS-----	546

23	GGVGTREKTLAAAAAGYKG-FQLS-----	546
ACMO	GGVGAYRDATLEAAAAAGYKG-FALS-----	533
MEKMO	GGAGDYHRRCAEIAAQYYPG-FEMA-----	549
CPDMO	GGAVAFINILREWREKGDFAQFQQRKR-----	601
CDMO	AGSAAFFRMDHWLAAGSFDGLTFR-----	603
7	GFTFQFRNETKRFDLTAYDSV-ATADLPAPVHVNGKTPGPAIPAQIDLDDDKVTAQ---	537
2	TFTWKFRSQLQRFDQENYVSR-RRAAKETVA-----	496
12	GFNRRFRARTRRVDLHHYIISGAGASAKSIVRTAG-----	514
6	WSTDRMRQLGRFDEAAAYDVS--REPAS---ATATSR-----	493
19	WSTGSLRRRLARFDLENYAIRPYRTEQSPALHPSGKSR-----	515
17	GSSASYWRRMRTPDDRHFELSSLAEREDDEYRGPVLTSGDLTVAVEVFLNGHIEPLDG	526
5	GSTVRYWQTRSVEPADFEFT-----PG-----	491
10	WRLVDYWTMLREPNPDDLTFIGRRAEGRREASAR-----	663
8	-----	-----
18	FLNVEYWQMTTRRPDLENYTAR-----	652
HAPMO	FTAVEFWQRTHSVEPTYQLG-----	640
16	RDLVALRHGKILDDAMTFSRP-----	498
EtaA	RDIRLIRRGKIDDEGLRFKRPAPVGV-----	489
13	KDVERLREGPIEDADLRF TANQPALLAS-----	515
F	-----	-----
G	-----	-----
E	-----	-----
D	-----	-----
grogan	-----	-----
FM01Ara	LLEAFSPYGSQDYRLGQEEKEDMTA-----	530
FM02Ara	-----	-----
FM01dog	LTIFFGPCTPYQFRLTGPWKWGARNAILTQWDRTFKVTKTRIVQ--ESPTPFASLLKLL	518
FM01hum	LTVEFFGPCSPYQFRLTGPWKWEGARNAIMTQWDRTFKVIKARVVQ--ESPSPFESFLKVF	518
FM02hum	VRLYFGPCNSY-----	471
FM03hum	MEVYFGPCSPYQFRLVGPQWPGARNAILTQWDRSLKPMQTRVVGRLQKPCFFHHWLKLF	518
FM05hum	LHLLLGPCPTPIHYRVQGPWKWDGARKAILTDDRIRKPLMTRVVERSSMTSTMTIGKEM	520
FM04hum	WEVFFGPCTPYQYRLMGPGKWDGARNAILTQWDRTLKPLKTRIVPDSSKPSMSHYLKAW	518
FM0fish	KRVLWGPVTAYQYRITGPGKWSGARRAIFTQFERMFQPFKTRQVEEKQGC SVAGRLKLS	521
FM01Dro	FNENLLHFREDNFALDDETFIKLN-----	416
FM02Dro	YIFELDTYRSNKYTLDDENFLKNGEIV-----	429
FM0Tyr	WYTEFLTFRNYQINLLSDTEYEMIIYKPKKVCPLDVQV-----	482
H	SGVDLLTESSRQ-----	447
IucD_Lys	----LIQWRSGT-----	425
PVDA_Orn	RALHEHALAS-----	443
SidA_Orn	QGHQLRAML-----	501
NRho_Orn	NAQDTYATSEAR-----	448
FMOMeth	-----	-----
A	-----	-----
C	-----	-----
B	-----	-----
15	-----	-----
STMO	-----	-----
9	-----	-----
14	-----	-----
PAMO	-----	-----
24	-----	-----
CHMO	-----	-----
1	-----	-----
CPMO	-----	-----
11	-----	-----
20	-----	-----
3	-----	-----
4	-----	-----
21	-----	-----
23	-----	-----
ACMO	-----	-----
MEKMO	-----	-----
CPDMO	-----	-----
CDMO	-----	-----
7	-----	-----
2	-----	-----
12	-----	-----
6	-----	-----
19	-----	-----
17	LYHWYGRVVDGVDAAKGRNRTPLFLTIGDGPEVPAALAERDPWGHFRIAGVGTPTPPFPLA	586
5	-----	-----
10	-----	-----
8	-----	-----
18	-----	-----
HAPMO	-----	-----
16	-----	-----
EtaA	-----	-----
13	-----	-----
F	-----	-----

G -----
E -----
D -----
grogan -----
FM01Ara -----
FM02Ara -----
FM01dog SLLALLMAIFLIFL----- 532
FM01hum SFLALLVAIFLIFL----- 532
FM02hum -----
FM03hum AIPILLIAVFLVLT----- 532
FM05hum LALAFFATIIAYF----- 533
FM04hum GAPVLLASLLICKSSLFLKLVLDKLDQDRMSPYLVSLWRG----- 558
FM0Fish LTAMVGGAAAYFHLQPPSSLT--YLLSKLTPQRV----- 554
FM01Dro -----
FM02Dro -----
FM0Tyr -----
H -----
IucD_Lys -----
PVDA_Orn -----
SidA_Orn -----
NRho_Orn -----
FM0Meth -----
A -----
C -----
B -----

15 -----
STMO -----
9 -----
14 -----
PAMO -----
24 -----
CHMO -----
1 -----
CPMO -----
11 -----
20 -----
3 -----
4 -----
21 -----
23 -----
ACMO -----
MEKMO -----
CPDMO -----
CDMO -----
7 -----
2 -----
12 -----
6 -----
19 -----
17 PVEVEVPISRKLASAE 603
5 -----
10 -----
8 -----
18 -----
HAPMO -----
16 -----
EtaA -----
13 -----
F -----
G -----
E -----
D -----
grogan -----
FM01Ara -----
FM02Ara -----
FM01dog -----
FM01hum -----
FM02hum -----
FM03hum -----
FM05hum -----
FM04hum -----
FM0Fish -----
FM01Dro -----
FM02Dro -----
FM0Tyr -----
H -----
IucD_Lys -----
PVDA_Orn -----
SidA_Orn -----

NRho_Orn	-----
FMOMeth	-----
A	-----
C	-----
B	-----

Sequences used in tree and alignment

Newly cloned *Rhodococcus jostii* RHA1 type II FMO & NMO-H

>a

MSEHQVAIVGAGTSGVAAVALADRGINPLLDIDRADQVGSWSHSRYDRLRLNTGRQFSHLPNRPYPKGTPTFPTREQVIEHLERHARADGIELRLGCPVERLDLTDGHWRLTTAAGSVDAAEVVVATGFDHEPFVPDWPGRGDWRGALVHSSQYRNPSQYNGKRVLVVVGAGCSGMEIAYDLATGGAKVWLSARTPPNIMLRQGGIPGDFIATPLYHAPVPIADAIARFGRERSIGDLREFGLPIPDEGIFARSARLGVAPAIVDKELIAAIRDRSIEVVRGVESLDADSVLVDGVRIDPEAMVCATGFRQLEKLVGHLGVLDERGWPHATGEKPAAERLRFIGFVPRPSQIGFAAKQARRAARAIAARELR

>b

MTEQHTVVVIGGGQAGLSISWHLVQRGIDHVVLERESIAHEWRDSRWDSFTLVTPNWQCTLPGYTYSGGDPDGFMMNREQTYQFVRGYADTFDPPVREGVAVVAVRQSGSGGFVDVDTTEGPMHADHVVAVGGYHTPVVPRFAERLPADITQLHSSQYRSAGALPAGEVLVVGNGQSGAQIAEDLHLAGRTVHLVTGGAPRVARFYRGRDCVAWLHDMGTVDVSIADHPGGLGKRENTNHVVTGRDGGRIDLRAFALAGMRLYGRLLDVVDGTLRFAPTLSSSLDAADAVSESIKDSIDAYIDRAGIDAPREERYVPVWRPEREVTELELPTSGITSVVWSIGFRTDYRMLHAGVFDGEGHPHNRGVTAVPGLYFLGLPWQHTWGSGRFAGVARDAEYLADRIELEAGVLPATATLA

>c

MSTERFETIVIGAGQAGLATGYHLTRCGQRFVILDAHDRVGDVWRERFDSLRLYSPARYDGLPGWGIPAPAWSWPGKDEVADYFEAYAQRFPALPIRTGTTVDGLSRDGDYVVTAGTDRFEADNVVVASGTWQSPVVPDLAERLDPRIRQLHSSDYRNPSQLQDGPVVLVVGCSHSGADIALEASRSHRTTICGPVRGEVFPDIEGRLAHLAVPIMWFMANHVLTERTPVGRKMCTHVRSGGGPLLRVKRADLAAAGVEHFPAKVTGVHDGRPVLDGTAFDVRNVIWCTGFRKDTSWIQIPVTGSDGWPEQSRGVSPDHPGLYFVGLPFLQAFASMLTGGVGRDAAYVAKHIAKRVVVRSPEAVA

>d

MNSEVDVAVIGAGQAGLSAAYYLRRFGVEPESESGFVVLDHAPGPGGAWQFRWPSLTLSTVNGVHDLPLGLGFADTIGVDPNDPEAALVHAASAVPQYFATYEQFELPVHRPVHTRVVCARDERLRIETDRGVVSARGLINATGTWERPFIIPRYPGAESFTGRQVHTKDYSSAQDFAGQHVLVVGGGISAVQLLDEISRVTTTTWVTRRPPEFRDEPFTPEIGRAAVALVEDRVRRLPPLPGSVSVTGLPVTPAIRAARERGVRLARQPMFGEITADGVRWPDGRELKVDVILWCTGFRSSLDHLAPLRLRGPGGGITMTGRLATQVADPRIHLVGYGPSSTIGANRAGQAARELTRHLGLSAGSARPT

>e

MTTTFSDTDLRTDAQAWLDGFSRFLAAELAPTAVFAPQAYWRDVLAFVTGDLRTFSDEIPAELLRRQELTKATNIRIAEDRTPPRLVERAGIPCLEVI FEFDTLAGSAVGVARLVDPERGLLVRSLFTTLDQLADHPERTGEHRPVGQADSSKFGGPNWLDRIIAAQAYENRDPDVLIVGGGQSGLTAAARLGLDVALVVDTHARPGDNWRTRYHALTLHNAVWLNLDLPYMPFPATWPFVQPKDKLAGWFEAYVEAMEINFWGTAFIGGDYDEQSQSWVARVRRGDGTVRTLRPKHVVIATGVSGIPYVPELPLGSLQFAGRTLHSSEYDDANDFAGQRVVIIGTGNSAHDVAQDLHAHGIDVTMVQRSSTTIVSVDPASAAAADASYLTAPTLEDLDCDLLSMATVYPDLYTGSQMITATMKELDKDLVAALNRI GFRTDYGEEDTGQQMKFMRRGGGYLNVGCSDLLISGQVGLVQYADTAGFVAEGLSLTNGDVVEADAVILATGYQTQQEGVRALLGDEIADAVGPIWGYDDEGEVRNTWRRTAQPLWFSNGFQLCRIYSKVLAMQIRTELDNG

>f

MTQTVQPAAVQTSLTPQERVLDLWLASFESALAARDVDRAAGMFAVDSFWRDLVAFWNLKTVTEGRDAVAA MLHARLDDTDPVNFRTTETPDEADGVTSAWIEFETATGRGKGHRLRLKGDEAWFTLTMQELKGHEERRGRNRVKGAVHGSGGDTLSWAEKREIEERELGYTRQPYVLVIGGGGGIALGARLRQLGVPVAVVDKNERPGDQWRNRYKSLCLHDPVWYDHLPYMPFPDNWPFVAPKDKIGDWLEMYTKVMEIPYWSSTICTSATFDDETKEWTVVLDRDGEDVVLHPKQLVLTATGMSGKPNVSPFGQDVFRGEQHSSRHPPGPDAYVGKRVVVGANNSAHDICKALFENGADVMTLQRSSTHIVKSDSLMDLGLGDLYSERAVAAGMTTEKADLTFASLPYKIMHEFQIPIYQKIAERDRDFYDRLEKAGFKLDFGDDGSGFLMKYLRRGSGYYIDVGASELVADGSIHLVSGQVDHLT

EDAVVLTLDGTELPADLVVYATGYGSMNGWAADLMGQEVADKVGKWCWGLGSDTTKDPGPWEQEQRNMWKPT
QQEALWFHGGNLHQSRHYSLYLALQLKARHEEIPTPVYGLQEVHLLS

>g

MTATLDAPVDNIPQPGDIARRWLAGFGATLERGDARGAAQHFLVDGWWRDLLSFTWDLHTTHGRADIES
RLADSVPVHEPRHLVLSPAHPAEAVADPEGDWIQAFFTFETTLARSRGFVRLRRDDDDGEWRATLISAME
EIKGHEEKKGHRVQGTNHGAHRGKINWLDLRRRTAKGEFETEQPAVVIIVGAGQGGLALAARLQGLVDLTL
VERNDRIGDSWRKRYHSLVLDHPVWYDHLPLNFPDHPVFTPKDKLANWFEFYADAMELNVWTGTEFTG
GSYDDATGEWTVTVARDDGSTRTLHPRHVVLATGMSGVNPRIAGADTFEGTIEHSSWFVGGREMGGKK
ALVVGCCNSGHDIAQELNEQGADVTLQRSSTYVMSKKGIPGLFGGVYEEGGPAVQDADLIFASLPYPL
LAGIHAGATEAIAEKDAEMLDGLRKAGFKVDFGEDGSLFMKYLRGGGYYIDVGASELIASGEVSVKQG
TEIDHFTPDGVVFDGTEMPVDVVVLATGYKNMRESARKFLGDAVADRCQDVWGLDAEGELRTVWRRSGH
PGFWFMAGNLHQSRHYSKYLAFQIKAQEEGLQPIR

>hNMO

MLEHLDLVIGAGPSNLSVAALSAPVGRRLRCKFLDRQPTQRWYPGLMLLSAAVLQVSHLKDVLVLDPTSR
YTFNLFLARTGRHLRFASLHTPLIARREYESYLRWVSDQLDEVQFGCAVEEVTFDQAFRVESTRTGYAA
QHLSIGVGRPRYPVELATGTLDGEDVHFSSDFGYHTDSLGRDVVVVGGGQSGAEVVEHLLQRSGRDAVGS
LWASRRIGFQPLDESPFTNEWFHPDYVRYFHGLSQSRRSQLLDAQQLASDGISKGLLESIRYRLYYNDF
VDSDRIRTTLLPGRELTLGCRGPGGKGRWTTLTHIDTGEIDSVGADIVVLATGYHFPLPEFLHTLGGRIA
RTNCGLPQLAADYSVSWAGPAGNKMFFLNAGKLSHGDIADPNLSLASWRAATVLTITETPLYPDLRSSTC
SWDVADRAATHPPVDSGVDLLTESSRQ

>X (FMO Grogan)

MDSVDVVVIGGGQSGLSAGYFLRRSGLSYVILDAAEASPGGAWQHAWHSLHLFSPAGWSSIPGWMPASQGPYPARAEVLAQYEQKY
ALPVLRLPVRQVSHFGERLRRVARDGRQWLARAVISATGTWGEAYTEPYQGLESFAGIQLHSAHYSTPAPFAGMRAIIGGGNSGAQI
LAEVSTVAETTWITQHEPAFLADDVDGRVLFERATERWKAQQEGREPDLPPGGFGDIVMVPVLDARARGVLAAVPPPAREFSPTGMQWA
DGTERAFDAVIWCTGFRPALSHLKLGLDLVTPQQQVEVDGSGLRALAVPSVWLLGYGDWNGMASATLIGVTRYAREAVRQVTAICADHQD
R

Rhodococcus jostii RHA1 type II BVMO:

>9

MTVQDNDFDAVVVAGISGLYAVYKLRQRGMRVHGFESAEGVGGTWHNRYPGARCDVESIDYSYSFDEELQEQEWTERFATQDEILR
YLEHVADRHLRSAYDFLTRVTSATYDEETTRWSITTDGQNVTRARFCVLTATGVLSATNKPDIPGRDFTGGATYHTGEWPHEPVDVAGK
RVGVI GTGSSG IQSIPVIAEAAEVFVQFORSNPYSIPAGNRPLTGEYIAEVKANYAERRRLSRMSGGTPNSAYPKGALVDAEERRRV
YDEWQRRGGYLFKAFQPDQTIISQAANDTAREYVEAKIREMVTDPDIADQLVPTDHPIGTKRIVTDNGYFKTFNRGNVTLVNLRRTPITE
ITEAGVLTNSFYGLDMLVFATGFDAMTGSLSRIDIRGRAGRNLREWSAGPRTYGLSVAGFPNMFILAGAGSPSVLANMVLMAEQHV
DWISNCLDYLDEHNIEATDESVDWEVAECNEKAAGTLFPATDSWYMGANIPGKPRVFMPIYGGFGNYNTICAEVAAAGYKGFELGE
RRVDVQ

>15

MSARTEVDARANRIGDVAVVVAGFAGLYAVHKLRLSLGLTVQVEAAGVGGTWFVWNRYPGARCDVESVDYSYSFSRELEQEQWVWSEK
YATQPEILAYINHVADRFDLRDRFLFGTRVTSaelDEESLRWEVTRDGDVLSARYCIFATGALSTANMPNIAGRESFTGDTHHTGQWP
HEGVDFTRRRVGIIGTGSSGIQSIPLIAEQAELHYVFORANSYVSPAGNQAWDDEMRAIKAGYEERRRLSRESGGSPYNAHPKSALD
VSDEERREAYETRKLGGVLFKATFPDQTKTEANATAREFAEEKIRLLVDDPAVADKLIPNDHPIGTKRIVTDTHYFETYNRPNVTLV
DLKAAPIESITPSGITADADYALDILVFATGFDAMTGDALDRMIRVGRGGVPLSEYWSEGPNTYLGGLVGPVGNLFFVVTGPGSPVLAN
MVLGAEQHVWDIADCIHLWEKDYDAIEASVPATEQWVEHCRDLAAQTLFPLANSWYMGANIPGKPRVFMPIYGGFGAYGRICADVAEE
GFRGFEFSRSRTRLADPVG

>14

MSKTI SADVDVVVAGFAGLYALRKLDRDMLKSTRVFEAGSEVGGTWFVWNRYPGARCDIESVHYSYSFDEDLQEQWQWSERFAGQPEI
LRYLHVADRFDLRKDIITFDTRVVGWHDDENSVWTVRDTDDGAVVRSRYFISGAGNLSVPKTEPEFGGIDNFRGEVLLTGNWPREGADFT
GKRVAVIGTGASGIQAIPIFAEDAELVVFQRTPNFATPLNGMPMDPNELADIKSNYADVRTAARNHFLGVPFNQVQPSALAVDAEERR
RTFDERWNAAGFRFLDSYQDILFDKANDTIADYIRDRIHERVQDPAKAATLAPTGYAYGTRKRPLETNYEAFNRDSVSVVDVKSTP
IDEITPTGVRVGRVYEVDTIVLATGFDAMTGPLMAMDIRGRGGLPLAEKWEHGPRTYLGIMVNEFPNLFITGQPSPSVLYNMPPLAIE
DHVDFATDAIDYLDLRRDLVIEPTAQAESDWGALTNEIADQTLLEPETNSWYMGANIPGKPRACMVYLGAPTYRATCDEVVAGGYSGFA
LTRAEARAASTVS

>24

MTTSMKAANPMNFPSTSDTGIVDVLGVGAGFSGLYLSHRLTTAGWTFAGFEAGPSVGGTWFVWNTYPGARCDVESIYYSYSFDEALQEQW
TWSQRFAPQAEILSYINHVADRFDLRKHFNFNTRVVGATWNAERLWVQLDNGETRRGRYLI SGAGGLSTPKDFVPLGNFTGLQVS
TSRWNISLDDLAKRVAVIGTGSSGVQAIPIIAEVAEHVTVFQRTPNYVMPARNAELPLERVDSIKDDYPATREECRHSPPGGIPDRPV
DKAFDVAEERQRRYEAAEYERSGFNGVGGEFADLLTDVEANRTASEFIHDKIREIVEDPATAEALLVPRYHPLGAKRSVFGTDYYETYNR
PNVSLVSLRDEPIETMTANAIVTSKGTYEADAVLAIGFDAFTGLYGLGLTGASGRKLQETWQDGI RTYLGMMTDFPNFVWVAGPQS

PALASNVMVTIEQAVDWIADLIEHARDSGATLVEATPEGQNDWVDITEETVAQTLTYATTDWSYRGSNVEGKPNTFMGYVGGVGYKYYRMC
TEIAKRGYPGVRIDGETESPHLGPIHREIS

>1

MSTAAPAVTEVLDVLLVVGAGFAGLYQLENLRSRGYSVKVVEAGEGLGGIWHWNRYPGARVDSEGPYQFTRPDLWDEFASFSELYPGGDE
LRRYFKYVDAKLDLSDKIYYNTRIISAFFDDTANTWVTAENGSSVFCYFVLCTGFAAKP IFPKLPGMDSFTGINHHTGLWPEGGIEF
AGKRIA IGTGASGVQVAQEASKKAAQLTVFQRTFPVQALPMRQRLTDEDNAKIKFDLADRFRRRSASFSGFDFDFIPKSA LGVSDEER
ITTYERLWECGFEFWLGTYQDVFDVDDANDTAYEFWRDRTRARIKDPVIAEKLAPTKKAYPFVVKRPSLEQTYDIFNQDNVRVVDLHE
DPIETITPTGLKTTSEQHEFDIIVYATGFDAVGTGLTAMDIRGTDGTLRLDRKWSNGVRANLGVATAGFPNLLFLYGLSPSGFCNGPSC
AEIQGDLIVNTIDYMRDNGLNRIESEADADAASDHWAEALTAELYDKADSWYMGANVPGKPRQLLNYPGGGLPLYLAKWDETVACAGYK
FTLS

>11

MTASIDTRELDEANGVLDVLLVVGAGFAGLYQDLQRLSRGF SVKVVEAGDSLGGIWIWNCYPGARTDSTGQIYQYSREDLWKDWSYDEL
YPSWSGVRDYFVYDRKLDLSDRIIFSTRVTSADFDGERNQWTVRDTGRMLRARSVVICTFGAKPHIPSINGLNSFAGESHHTALW
QEGLDMAGKRVG IGTGSSGVQVTEAAADAEQITTFQRTPNLALPMRQQQLTGQLKEKLENLPERFAQRRRSFAGFDMDFIPKSVFE
VSDEERADTYERMWATGGFELWLANYQDILLDERANRIMYDFWRDKVQRVTDPVKAEKLAPMDPPHFGTKRPSLEQNFYDVVNQENV
DIVDVNEDPIERITPAGVQTKSGLHEFDILVFATGF DANRGGITSIDIRGTNDQLLSHKWSERLDTFMGLT TAGFPNLMFYVGPQSPAG
FCNGPTCAEVQGEIIVDFLTHVRDGGYQRFETSEDAEQSWTAHVEEVFHMSLFPRAKSWYHGANI PGKPSQMLNYSGGLP SYFDHWEEN
VAAGYKAFTLS

>20

MTASQADATARTGKHSNNDVLDVLIIGGGFSGLYALDRIRD LGFTAKVWDAAGGLGGIWWWNCYPGARTDSTGQIYQFSHKDLWKYDF
AELYPGHDGVRNYFEYVDSQLDLTRDVVFDTFAESCTWDEETRQWARSADGKVQNAQVIIVATGFAKPLYPNLEGLDLFAGDCYHTA
RWPQEGVDMTGRKVVMTGSSGVQVQVQEAAGHVAEHVTVFQRTPNLAIPMQQRALTHDDNEQFRKGLPERFEARYKAFAGFDFDFLPQN
AADLSMEERDAIYEMWAEAGGFEMWLGNFQDILVDE DANRTFYDFWRNKVLEVRTDPKKAIAVAPETPPHYGVKRPSELDYDFVINQ
SNVEVIDSNLTPIRRVLPHEG IETDDGVIECDLLVLATGF DNNSGGIMADITGVDGLSIQDKWKSVDTCMGLSTRGFNMMFLYGPQS
PSGFCNGPTSAEYQGEIIVDFLTHVRDGGYQRFETSEDAEQSWTAHVEEVFHMSLFPRAKSWYHGANI PGKPSQMLNYSGGLP SYFDHWEEN
DKIKANGYAAFETN

>4

MTA IHAPKNDLAQS AETPTDYVIVVGGGGIYQLRHLRDRGFSVILLEASGGFGGAWSLNRYPGARVDSHAPVYQFTDEYLWKDWDFS
QMYPDHEEMRSYFNVD SKLDSLKDSRFNTKVVGATFDEEQRMWSLETQDGATFRARFVVFATGSTEPTPTSPMDAYQGELVHTAR
WRSDLDMTGKRVAVIIGTGASAVQVQVQEAAGPVVENVLTVFQRTPNISLPMQKYLDDDEQAALKNKMPDVAACKRETHAAIDYDFDRSGF
ETPEDERNAVFERLWNQGGFAFWLGNFSDYLFNDKTNALTYEFWKNKIKPQIKDPVKAELLVPEIAPHPF GAKRPAALHQNYYEVMNQTN
VSLVSTKETPIVGFTEGTGIRTADGVEHGEFDIIVLATGFNNNTGALTSIDVQANANGVTLRDKWSQGVDAYLGAVTAGFPNAIFVYGPQS
PAAFANGSTNAELQGEVMVDFEFELRSNGLTRFESTVEADKAWTAHINETDDTALFNRAKSWYNGNIPGKKMQMLQYLNQVPTYLQFV
QKEKESGYTDLTVS

>7

MVSYMSLPVTDTSAPPAGVRHIDTLIIGSGFAGLGAAIKLTQAGKTD FVLVLEGRSDVGGTWRDNTYPGAACDVPSHLYSYSFALNPEWT
RSFSTQPEIQKYIQSVADKYKVRNKHFGCDVQSAHWNESSTRWEVTTTKGNFVAKVLSAVGALCEPSLPDIKIGIEGFEGEIFHSARW
NHDADLTGKRVAVIIGTGASAVQVQVQEAAGPVVENVLTVFQRTPNISLPMQKYLDDDEQAALKNKMPDVAACKRETHAAIDYDFDRSGF
VFMKPLQFAAERHLRRIKDKALRKKVTPNFQIGCKRMLISNNYPTLAQDNVDLVDGIAEVTADS SVSKDGTVREVD AIVVATGFHV
TDSPTFEGIFGKDGSLADVFDEGGQGYKGAAILANFPNMFLVGPNTGLGHSTMVFMIESQLNLYLVDALQTLDDKYDIPKIEVYQDAQD
RYNAELQEKLSHSVWNNGGCASWYLDKHKGNNTLWPGFTFQFRNETKRFDLTAYDSVATADLPAPVHVNGKTPGPAIPAQIDLDDDKV
TAQ

>10

MTETIAAGLAVPSDRDAQLYNAIAESDPAPLLMALVHATGDTGLLDEFGARLTIEEPGNHYRTGIRPTAPPGIYPEDVAEDIRIRAREI
LTPDVVAELGVPDDELFRMATVCTSQRVDAEFAPILLEQAGFTKNRRHVPVTVAPPADFDVIVIGAGIVGINAGIKLGEAGFRYTIIE
EREDVGGTWRNTYPGAAVDTPSHYYSYFELNPNWSKYPTGPEYQNYLLDVEKYRLREHIFRTRVLSARWLDDEHRWEVVTEDGE
GSVVRHRARAVITAMGMLNAANIPEVDGLDSFAGRVVHTAEWSDLDL SGKRVVVLGTGCTSVQVANIIVDQVEALD VVVRSPHWLVE
KAVSGDVTEGEKVALANLPFYDRWRFLRSYWFASDNLYLPRIDKEWAATHLSASPANDMVLRTAQEYLTQTSFTDRPDLIAKLTDFRFR
YAKRIKDPGFFAALNREHVS LHRASF EKVTPEGVYTTGAFIPADVILATGFKLQFTTSIEIEGRDGRTLSEVWNGGDDPRAYLGVQ
VAGFPNLFITAGPNSAPNHGAGHNLSEEHVHYIVECLQYLLENGHDAMDVRQDVLDTYNRKVDAALDDTVVWHPGAEVNGYRNSSGR
AIVPCPWRLVDYWTMLREPNPDDLTFIGRRAEGRREASAR

>2

MNLPOHVHTLIVGAGFAGMGLAARILQTPQADVLI IERGDDVGGTWRDNTYPGCACDVPTSLYSYFAPSADWSHTFARQPEIHRYLK
KVAADTGVRSRVVTDCELQEAHWDAEAVWTVRTRSGTADVVVAATGALSTPSVPDMPGLETFGGTTFHSATWNHDHDLTGERVAVI
GTGASAVQFVPEIAPVAEHLTVFQRTPAWV IPRLDRELSGSEKRLYRRLPLVQKAVRGTVYGFREALGGVLAHATGLLPVEMVAKAHL
RRQVRDPELRRKLTNPNTIGCKRMLLSNDWLRLTDRPDVTLVDAGLAGVTPDGVVDALGNEHKVDTIIFATGFTPEPPVAHALRGANG
RTLAEHWDGSPSAYKGTTVAGFPNLFMLYGPNTNLGHS SIVYMLSESQAYIADALNMHHS EITAFEVTEEAQRRYNTRIQSELQTTVW
NKGCCSSWYDSEGRNSVQWPTFTWKFRS QLQRFQDENYVSRRAAKETVA

>17

MTTGTTEPDVLLVVGTFAGLCMAIKLKEAGEENVVLEKADRGGTWRNTYPGCGCDVMSLMYSFSFAPNRKWRMYARQPEILDYIE
RVVRDYDLAPHIRFGAEV I SYEFDETTDRWRVETRSGSVYHPRIVVAGPGPLHKPSVPDLPGRKFSFSGVAFHSAEWDHSDVLTGKRVAV
VGTGASAVQFVPEIAPVAEHLTVFQRTPAWV IPRLDRELSGSEKRLYRRLPLVQKAVRGTVYGFREALGGVLAHATGLLPVEMVAKAHL
RRQVRDPELRRKLTNPNTIGCKRMLLSNDWLRLTDRPDVTLVDAGLAGVTPDGVVDALGNEHKVDTIIFATGFTPEPPVAHALRGANG
LTIQRAWRDGMEAYLGVAVAGFPNFFLMMGPNSSGGNQSVFVIEAQAHYITRCLALMKKRDRATR IEVRAGA QREFNRVVRHKLKAGSVW
NSGGCDSWYLDSTGHNRAAWPGSSASYWRRMRTPDRHFELSSLAEREDDTEYRGPVLTSGDLTVAVEVFLNGHIEPLDGLYHWYGRV
VGDGVDAAKGRNRTPLFLTIGDGEVPAALAEERDFWGHFR IAGVGTPTFPPLAPVEVEVPI SRAKLASAE

>18

MKAAQQVQEA GAATDDRINPDRLTESEIRTAVARANVPSLLMVVFQTTGDEKWLAAAPYRPRTRGKGLGDHDSGGLEEPIQDEIREAAVKA
ILDQLNGALPAVETPSPELTVRMI SVCTGEEVGEYGPMLSLELARRAAPDAPSLALEPVD APEGYSVVVIGTG VAGIAAAQQLED MGI
VLDILEKQPEAGGNWQNTY PGAGVDTPSHL YSF AKNDWTTHEL RNELOQYF GAVLKD LGAGERVRYGTVEVRS TRYGTVEVRSVYD
MINPDDGSSSTLRADV I SAVGLNRPKTPNVPGMDSFTGTSFHSAAWPDLDL DGKRVAVIGTGASSMQIAPAIADRVAHLSIYQSRSPQ

WVAPFEKFRAPIPMELRRLMQTCPYHSHWYWRIFWQFGDKVIESLRVDPWEHHPERSVNRNDAHREYFTRYITSQVGDRTDLLDKVM
PDYPPFGKRIILLDNQWYSTRKDNVDLDRSVTAVRPEGLVDQGAENDVDVIVWATGFEEARFVSSMDVVGMDGRTLREVWDDDPKA
YLGVSVPFPPNFMLGGPNSFPGSGSFMFMEVQMRIRGLLTEMFKKGIKAI DARPEANEYNELVDSTHARTVWTHRGMSTYYRNSH
GRVVFVMPFLNVEYWQMRPDLNENYAR

>12

MVRSAPVELPVDSVDHPPEVVDVLLVVGAGFGLGTAIRLKQAGIDDFVVLDRADIEDGGTWRVNTYPGAQCDIPSIILYSFSAFNPNNWT
RLYPLQOEIHDYLRSCAENFIVPHLRMGHDVQDAAWDDSDQVHVHTSRGTWEARILVGMGPFSEPAVNPALPAESFRGAVFHSAAW
DHEHDLAGERAVVIGTGASAVQIIPRIQPIVGSMTVFQRTPTWILPHDPQPMGTGWPRKLFARVPAVQRLARSLDLVQEAAMPVGFVYKP
ALLKGLAALGRAHLRRQVHDPELRKLTPTYAFGCKRPTFSNSFYPALAQPNVDVI TDGIREVRSNGIVTEDEGLVHEVDITVMGTGFRL
TDNPAFDVVRGRDGRTLAEAWNGNARAYLGTIISGFPPNFMLLGPNSVYVTSQVVTIEAQIAYILSCLQEMNAQGAASIDVRPEIQQAF
VDEVDRLQTSVWNTGGCNSYLLSGEGRNFTFPYGFNRRFRARTRRVDLHYYIISGAGASAKSIVRTAG

>6

MTHYDILIVGAGISGIGAAIRLKQSGIDNFAILEKGDALGGTWRDNTYPGCACDVP SALYSYSAFNPNEWSRLFAGQDEIRRYIERTAA
EHGVP AHVKFGTEMQRAQWSEQSRRTVDT SAGTF TANAVIAAAGPWNEPLVPTVPLGLDTFTGEVFSRRWNHTYDLTGKRVAVVGTGA
SAVQFVPAIQPTVESLHLYQRTAQWVLPKPDHTLPGVERAILRRVPGAIRALRRVEYAIMESLGLGFRHPWILRVIQQVGAQLRAQVR
DPKLRKALTPDYTLGCKRLLSNTYYPALTRPNVEVHANAVESVRGNVVVSGDGAEREVDIAIFGTGFHILDMPIGSKVFDGDRSLDD
HWKGSPOAYLGTTVAGFPNAFVLLGPALGTGHTSAFMILEAQLDYLIQAVTAARSNGWTRMEPRREVQDAFNAQVQEALATTVYNAGGC
QSYFLDVNGRNSFNWPFSTDRMRQLGRFDEAAVDVSREPASATATS

>5

MGGEVHRCRVLVIGTGFSGLGTAIQLRRRGRDDFILLEKAREVGGTWRNTYPGCACDVP SHLYSFSFEPNPDWTRMWSGQEEIFDYLR
GLADKYDLRRNIHFGRMTGGHWAERRRWHVHTESGDEYVAQFVVSIGI GALHIPNVDPDLPADTFDGTGFHSARWNHDYDLRGKKVAV
IGTGASAVQFVPEIVGDVAELHLYQRTPPWVPLGNFIPPEARRLFRVPLARRMVAAYWYTESLALGFNGHSRLMRPIESMARKN
LNRTVADPELRRKLTSPYRIIGCKRILGSDVYYPALISPKTVVITEGIAEVRPHSIVAGDGAERVDAI IYATGFHVTDGFDNVELTGVG
GRRLADEWEHEGIRTHLGI TVAGYPAFFLFGPNTGLGHNSVVFMIESQIRYALELMDLVDRRGADSAAVRPAVQSGFNADIQRLKARG
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>19

MTATTQHA AAPDGGGDERHLRVVVGAGLSGIAAAVKLERAGITDFVLEKSDRVGGVWRENTYPGCGVDIPAPVYSFSFHPNPRWRS
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HDVDLTGKRVAVVGTGASAVQF IPEIQPDVEELYVFORTPAWVVRDLDFPPFRIAQWAFARVPAVQALRRLLDVILRLTLTWVMRCERT
ARLLNPIGTRWLRQVDPALRAALTPNFTLGCKRLLSNTYLPALTKSNVELIPHALAEVDGRVVVGADGTRREVDVIFGTGFDVSH
PPIASRIRGRDGTLLSEKWSKSPAYLATTPGAPNAYIMLGNILVYNSFLGLAETQLDYVIDGLTTAERQGI EIVLEVRDQPPFRFND
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>16

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VHPQQWPEDDLDEYEGKRVVIGSGATAVTLAP SMAADAHVHTMQRSPYIISMPAKDKLANLKRRLHLPAGLAYGLTRLNKASVATAIYQ
LCQRYPEFMKGRIRQLQEKWLPKGYDIDHTFTPRYNPDQRLCLVPNGDLFRAIRNDEVSI VTDHIDTFTETGITLKSGEELHADVVVT
ATGLNLLAFGGMTLAVDGHDI DLTETMAYKGMMLSGVNFVAFVIGYTNASWTLKADLVCEYVCRLLAHMDANGFTQCAPERDSSVEEPE
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>13

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GIEDFTGQVHPQHWPPEELDYSGKKVVVIGSGATAATLIPAMAGTAAHITMLQRSPSYVLSLPAEDA IANTLNKLI GPKRAYPIIRKKN
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ELEADIVVTATGLNMLAFGAIQLSVDGEPVNPDDTTVYKSMMLSGLPNFVVALGYTNI SWTLKVDLI SEHFRLLDHMDERGYTTVEPV
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>3

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TSANPIREVASDAIITADGTRHEVDVIVLATGFDVSTGGLTAIDIRGTNETFEVFRGGSRTALGKATVGFNNLVYVGPQSPNAFCN
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GYEQFELV

>21

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AAAAGYKGFQLS

>23

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DLTPEQRNDVLEEIYENGLKWLWASFGEMFYDEEISEEISEFVRRKMRARLQDPHLCDLLIPTDYGFGTHRVPLETNYLETYHRPNVE
AIGVRDNPITRIVPQGLVLDAGTLHEVDVIVMATGFDAGTGSLTRIDIRGRGGRALKDDWNRDIRTMGLMVHGYPNMLTTGAPLAPSA
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>8

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Type II BVMO

>PAMO

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HEPVDFSGQVGVIGTGSSGIQVSPQIAKQAAELFVVFQRTPHFAVPARNAPLDPEFLADLKKRYAEFREESRNTPGGTHRYQGGPKSALE
VSDEELVETLERYWQEGGPDILAAYRDIRLDRDANERVAEFIRNKIRNTVRDPEVAERLVPKGYPFGTKRLILEIDYEMFNDRNVHLV
DTLSAPIETITPRGVRTSERYELDSLVLATGFDALGTALFKDIDIRGVGNVALKEKWAAGPRTYGLSTAGFPNLFPIAGPGSPSALS
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GYEGFVLT

>CPMO

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ALWPEQEGVNMAGKRAVAIGTGSSGVQVAQEAALDAKQVTVYQRTPNLALPMHQKQLSAEDNLRMKPELPAFAFERRGKCFAGDFDFIAK
NATELSAAERTEILEELWNAGGFYWLANFQDYLFDDKANDYVYEFWRDKVRARIKDPKVAEKLAPMKKPHYPYGAKRPSLEQWYEIFN
QNNVTLVDVNETPVLRI TEKGIVTAEGEAEFDLIVFATGFDVATGGLTSIDFRNNQGGSFKDVWSDGIRTQLGVATAGFPNLLFGYGPQ
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FNESAEGYAGFSLAS

>HAPMO

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TWRENTYPGCRVDINSFWYSFSFARGIWDCCFAPAPQVFA YMQAVAREHGLYEHIRFNTEVSDAHWDESTQRWQLLYRDSEGGTQVDSN
VVVFAVGLNRPMIPAIPIGIEFTFKGPMFHSAQWDHDVDWVSGKRVVIGTGASATQFIPQLAQTAELKVFARTTNWLLPTPDLHEKISD
SCKWLLAHVPHYSWYRVAMAMPQSVGFLEDVMVDVGYPPTELAVSARNDRLRQDISAWMEPQFADRPDLREVLIPDSPVGGKRIVRDN
GTWISTLKRDNVSMIRQPIEVITPKGICCVDGTGEHEFDLIVYGTGFHASKFLMPINVTGRDGVALHDVWKGDDARAYLGMTVPQFPNMF
CMYGPNTGLVYVSTVIEQSEMTASYIVDAVRLLLLEGGHQSMEVKTPVFESYNQRVDEGNALRAWGFSKVNWSYKNSKGRVTONPFTAV
EFWQRTHSVEPTDYQLG

>CHMO

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VGVIGTGSTGVQVITAVAPLAKHLTVFQRSAQYSVPIGNDPLSEEDVKKIKDNYDKIWDGVWNSALAFGLNESTVPAMSVSAEERKAVF
EKAWQTGGGFRFMFETFGDIATNMEANIEAQNF IKGKIAEIVKDP AIAQKLMPODLYAKRPLCDSGYNTFNDRDNVRLEDVKANPIVEI
TENGVKLENGDFVELDM LICATGFDVADGNYVRMDIQGKNGLAMKDYWKEGPPSSYMGVTVNNYPNMFVLPNGPFTNLPPSIESQVVE
ISDTIQYTVENNVESI EATKEAEEQWTOQT CANIAEMTLFPAQSWIFGANIPGKKNVYFYLGGLKEYRSALANCKNHAYEGFDIQLQR
SDIKQPANA

>Et aA

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VVI GSGATAVTLV PALADSGAKHVTMLQRSPITYIVSQPDRD GIAEKLNRWLPETMAYTAVRWKNVLRQA AVVSACQKWPRRMRKMFLSL
IQRQLPEGYDVRKHFPHYNPWDQRLCLVPNGDLFRAIRHGKVEVVDTI IERFTATGIRLNSGRELPADIIITATGLNLQFLGGATATI
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LPKQGSRTPLNQNLYLRDIRLIRRGKIDDEGLRF AKRPAPVGV

>CPDMO

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DDEAARWRIITDRGDKFSARFVCMSTGQLRQPKLPGIPGITSFKGHSFHTSRWDYSYTGDDQTNLEGLKDKRVAIIGTGATSIQAVPH
LAAAYQELYVIQRTPI SVGFRGNKPTDPEWAKSLQPGWQQARMDFNAITHGMPVDVLDVQDSWTKIFGEIGVFLGSDGSAQMVDFQL
MEQIRARVDQEVKDPATAESLKYNYMCKRPGFHD SYLPSFNKPNVTLVDTQGAGVERITEKGLVNGREYEVDCLIYATGFYEQTKL
SRRNGYIEHGRNGQPLSDKWKDGLSTLWGYHIRDFPNCFILGNGQSAVTPNF THMLNEAGKHVAYVVKHCLDERVDVFEPTAEAEQAWV
DHVMSFAGIKQQYDRECTPSYNNEGQVNDVALTRNNFYPGGAVAFINILREWREKGDFAQFQQRKR

>STMO

MNGQHPRSVVTAPDATTGTTSYDVVVVAGIAGLYAIHRFRSQGLTVRAFEAASGVGGVWYWNRYPGARCDVESIDYSYSFSPELEQEW
NWSEKYATQPEILAYLEHVADRFLRRDIRFDTRVTSVLDDEGLRWVTRDRGDEVSARFLVVAAGPLSNANTPAFDGLDRFTGDIVH
TARWPHDGVDFTGKRVGVI GTGSSGIQSIP IIAEQAEQLFVFORSANYSIPAGNVP LDDATRAEQKANYAERRRSLRESGGSPHRPH
KSALEVSEEEERRAVYERWKLGGVLF SKAFPQDLTDP AANDTARAFWEEKIRAVVDDPAVAELLPKDHAIGAKRIVTDSGYEYETYNRD
NVELVDLRSTPIVGMDETGI VTTGAHYDLDMIVLATGFDAMTGLDKLEIVGRGRTLKETWAAGPRTYGLGIDGFPNLFNLTPGSP
SVLANMVLHSELHVDWADAIA YLDARGAAGEIEGTPEAVADVVEECRNRAEASLLNSANSWYLGANIPGRPRVFMPLGGFVYREIIT
EVAESGYKGFALILEG

>ACMO

MSTTTLDAAVIGTGAVGLYELHMLREQGLEVRAYDKASGVGGTWWYNNRYPGARFDSEAYIYQYLFDEDLKYGKWSWSQRFPQGEETIERWL
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GVIENGATGIQVIQSIAADVDELKVFIRTPQYALPMKNPSYGPDEVAWYKSRFGELKDTLPHTFTGFYDFTDAWEDLTPQRARRLED
DYENGLKWLWASFAEIFSDEQVSEEVSEFVREKMRARLVDPLECDLLIPSDYGFGRVPLETNYLEVYHRDNVAVLVRDNPITRIR
ENGLIADGTVHELVDVIMATGFDAGTGALTRIDIRGRDGRTLADDWSRDIRTMMGLMVHGYPNMLTAVPLAPSAALCNMTTCLQQQT
EWI SEAIRHLRATGKTVIEPTAEEGEEAWVAHHDELADANLISKTNWSYVGSNVPKPRRVL SYVGGVGAYRDATLEAAAAGYKGFALS
>CDMO
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DDEQMERIRARVDEIVTDPATAAQLKAWFRQMCKRPFHDDYLPANRPNTHLVDTGGKGVERTENGVVVAGVEYEVDCIVYASGFEEF
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>MEKMO
MSAQSCLAAGSCAYGNVTS LDAMVIGAGVAGLYQLYRLREMGTLVRA YDTASGVGGTWWYNNRYPGARFDSQAEIYQYWFSEELYKSWQP
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WAEKTPDERQAVLEQLWKDGLAMWLASPEMFFDEQVNEVVQFVRIKMRERLRSRDLCDLLIPTDYGFGRVPLENNYLEVYLQS
NVKAVDCKQSPERIVPQGIQTADGKIHEVDIIVLAVGFDAGSGALSRI DIRGRDSRSLKEQWQOEIRTAMGLQIHGYPNLF TTGAPLA
PSAALCNMTTCLQQQVDWI TGCIEFAAEHGKHVVVEASKALEDNWNVQHHDETA AKTLVVKTD SWYMGSNVDGKPRRLLSYIGGAGDYHRR
CAEIAAQGYPGFEMA

Type I FMO

>FMO1Ara

MASNKYDKLTSRVAII GAGVSGLAAAKNLVHNNPTVFEASDSVGGVWRSCYETTKLQ SARVDYEFSDFPWPNRRDDTTFPPYLEILDY
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KGPMPFQGGKVMHSMYCKLEKEEASTLLSGKKVAVIGFKKSAIDLALLESALANQGEKKACTMVVTRTHWGI PHYVWVWGLPFFLFYSSR
ASQFLHDRPNQSFRLTLFCLLFLSLRAVVSFKIESYVLWKLPLEKYGLKPNHSEEDYASCQMAI IPENFFEEADKGMIRFKKSSKWWF
YEEGIVFEDGTTLEADVVI LATGYDGKKLKAIVPEPFRTWLEFP SGVMPLYRGTIHLIPNMGFVGYVQSSNLHTSELRSMWLSRLV
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>FMO1dog

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PDIFDKRVLVIGMNSGTDIAVETSRLAKKVFLSTTGAWMSRVFDSGYPWDMVMTRFQNMFRNSLPTP IVTWLMARKMNSWFNHA
NYGLVPEDRTQLREPVNLDELPGCIITGKVLIKP SIKEVKENS VVFNNTKPEEIDIVFATGYTFAPFLDETVKVENQASLYKYI
FPVHLQKPTLAIIGLTKPLGSMIPTGETQARWAVRVLKGVNKLPPSPVMIEEINARKENKPSWFGLCYCKALQSDYITYIDELLTYINA
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>FMO1hum

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FPAHLQKPTLAIIGLTKPLGSMIPTGETQARWAVRVLKGVNKLPPSPVMIEEINARKENKPSWFGLCYCKALQSDYITYIDELLTYINA
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>FMO2Ara

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>FMO2hum

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FPAHLKSTLACIGLIQPLGSIFPTAELQARWVTRVFKGLCSLPSERTMMDI I KRNEKRIDLFGESQSQTQTNYVDYLDLALALEIGA
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>FMO3hum

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FPPLLEKSTIAVIGFVQSLGAAIPTVDLQSRWAAQVIKGTCTLPSMEDMMNDINEKMEKKRWFVKSETIQTDYIVYMDLSSFTGAKP
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>FMO4hum

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>FM05hum
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