



SDI Review Form 1.6

PART 1:

Journal Name:	International Journal of Biochemistry Research & Review
Manuscript Number:	2013_IJBcRR_3777
Title of the Manuscript:	DNA polymerases: An insight into their active sites and catalytic mechanism

General guideline for Peer Review process is available in this link:

(<http://www.sciencedomain.org/page.php?id=sdi-general-editorial-policy#Peer-Review-Guideline>)

- This form has total 7 parts. Kindly note that you should use all the parts of this review form.



SDI Review Form 1.6

PART 2: Review Comments

	Reviewer's comment	Author's comment (if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)
Compulsory REVISION comments	- The manuscript describes the comparison of sequences among different DNA polymerase families and interprets the sequences result mostly based on DNA polymerase I. The purpose of the manuscript is original and it covers enough study for publication. But some changes must be done before acceptance.	
Minor REVISION comments	1- Sequence number in the middle block in Fig 2A is seen wrong. For example, number in this block cover 125-178 for E. coli. This number must be checked and it must be around 400 or 500. The all sequence comparisons must be evaluated at that point in the manuscript. 2- Full name of the microorganisms must be written. 3- For each DNA polymerase family, different microorganisms were selected for comparison in prokaryotes. The reason must be explained well. 4- 5'→3' nuclease activity is written like 5'→3' or 5'-3'. One of them is selected and used in all text. 5-Full name of some abbreviation must be given, such as SDM, IN, etc. 6- There are many comparison from different families and these comparison may be interpreted more in detail.	1) In Fig. 2A, only the conserved blocks are shown. The non conserved blocks are not shown; (mentioned in the legend at the bottom of the figures). Therefore, the numbers are correct and it is only 125-178. After 178 since there are no conserved blocks, there is big jump in the alignment numbers. The full alignment is shown below without any break in the numbers for the Referee's kind perusal. 2) The organism's full name is written when it appears for the first time in the text (<i>Escherichia coli</i> in the abstract and <i>Thermus aquaticus</i> and <i>Pyrococcus furiosus</i> in the introduction part). 3) For each DNA polymerase family, different microorganisms are selected for comparison in prokaryotes. This is



SDI Review Form 1.6

		to show diverse group of microorganisms still have the same conserved set of amino acids in the active sites. Secondly insertion or deletion of even one amino acid is enough to miss the conserved blocks. This is exemplified in my article that appeared in Indian Journal of Biotechnology using invertases and polygalacturonases, as examples. Ref: Palanivelu P. [2007] Multiple sequence analysis of polygalacturonases and invertases and phase shift in conserved motifs. Indian J. Biotechnol. 6: 24-30. 4) Page 33 line 1886 SDM is written completely when it appears for the first time in the text and the abbreviation is given in brackets. The IN should be in the lower case (typo error with caps lock). Correction is made. 5) 5'→3' and 3'→5' exonuclease is corrected in all the places with arrow marks. (Page numbers 32/33/35/37). 6) The main focus of the article is to show that the catalytic amino acid (K/R) and steric gate amino acids (YG/A) are highly conserved in almost all the families of polymerases irrespective of their sources. Their
--	--	--



SDI Review Form 1.6

		absence and deviations, if any, are interpreted in the text.
Optional/General comments	The manuscript is acceptable.	

Figure 2A in the text

CLUSTAL FORMAT for T-COFFEE Version_7.71 [http://www.tcoffee.org] [MODE: regular], CPU=57.71 sec, SCORE=86, Nseq=18, Len=1130

```

sp|P52026|DPO1_BACST  M-----KNKLVLIDGN 11
sp|P00582|DPO1_ECOLI  MVQ-----IPQNPLILVDGS 15
sp|P0A550|DPO1_MYCTU  MVTTAS-----AP-----SEDRAKPTLMLLDGN 23
sp|O34996|DPO1_BACSU  MT-----ERKKLVLVDGN 13
sp|Q9F173|DPO1_SALTY  MVQ-----IPENPLILVDGS 15
sp|P59200|DPO1_STRR6  MD-----KKKLLIDGS 12
sp|O32801|DPO1_LACLM  ME-----DKNRLLIDGS 13
sp|P43741|DPO1_HAEIN  MAQ-----IATNPLVLVDGS 15
sp|Q9ZJE9|DPO1_HELPJ  MEQP-----VIKEGTLALIDTF 17
sp|Q9CDS1|DPO1_LACLA  ME-----NKDRLLIDGS 13
sp|P59199|DPO1_STRPN  MD-----KKKLLIDGS 12

```



SDI Review Form 1.6

```

sp|Q9S1G2|DPO1_RHILE  MPNSIW-----TSSDARAIHARMKKGDHFLVDGS  30
sp|Q92GB7|DPO1_RICCN  MT-----QKNTLLLLIDGY  13
sp|P0A551|DPO1_MYCBO  MVTTAS-----AP-----SEDRAKPTLMLLDGN  23
sp|Q9HT80|DPO1_PSEAE  MS-----QAPLVLDVGS  12
sp|Q04957|DPO1_BACCA  M-----KKKLVLIDGS  11
sp|P46835|DPO1_MYCLE  MSAAMT-----AE-----V-CEDHTKPMMLLDGN  24
sp|P52027|DPO1_DEIRA  MVFCGDGGLSCESIDFALCCLRGRSGNYVQSRILPMAD-----ASPDPSKPDTLVLIDGH  55
* *:*

sp|P52026|DPO1_BACST  SVAYRAFFALP----LLHNDKGIHTNAVYGFTMMLNKILAE-----QPTHILVAFDA  60
sp|P00582|DPO1_ECOLI  SYLYRAYHAFPP--T--NSAGEPTGAMYGVNLMLRSLIMQY-----KPTHAAVVFDA  64
sp|P0A550|DPO1_MYCTU  SLAFRAFYALPAE--NFKTRGGLTNAVYGFTAMLINLLRDE-----APTHIAAADFV  74
sp|O34996|DPO1_BACSU  SLAYRAFFALP----LLSNDKGVHTNAVYGFAMILMKMLEDE-----KPTHMLVAFDA  62
sp|Q9F173|DPO1_SALTY  SYLYRAYHAFPP--T--NSAGEPTGAMYGVNLMLRSLIMQY-----QPTHAAVVFDA  64
sp|P59200|DPO1_STRR6  SVAFFRAFFALYQQLDRFKNAAGLHTNAIYGFQMLSHLLERV-----EPHSHILVAFDA  65
sp|O32801|DPO1_LACLM  SVAFFRAFFALYQQLDRFKAPNGLHTNAIFAFHTMLSSLMERI-----QPTHVLIAFDA  66
sp|P43741|DPO1_HAEIN  SYLYRAFHALP--T--NAAGEPTSAMYGVNLMLKSLISQV-----QPTHIAVVFDA  64
sp|Q9ZJE9|DPO1_HELPJ  AYLFRSYMSAK--NKPLTNDKGFPTGLLTGLVGMVKFYKDRK-----NMPFIVFALES  70
sp|Q9CDS1|DPO1_LACLA  SVAFFRAFFALYQQLDRFKAPNGLHTNAIFAFHTMLSSLMERI-----EPHVLIAFDA  66
sp|P59199|DPO1_STRPN  SVAFFRAFFALYQQLDRFKNVAGLHTNAIYGFQMLSHLLERV-----EPHSHILVAFDA  65
sp|Q9S1G2|DPO1_RHILE  GFIFRAFHALP--T--RKTDLGLPIGAVSGFCNMLWKLRLDARNTDVGVTPTHAVIFDY  87
sp|Q92GB7|DPO1_RICCN  GFVFRAYYAQQP----LTSPKGEVPGALYGFTSMLKLLSDF-----KPKHVAVVFD  62
sp|P0A551|DPO1_MYCBO  SLAFRAFYALPAE--NFKTRGGLTNAVYGFTAMLINLLRDE-----APTHIAAADFV  74
sp|Q9HT80|DPO1_PSEAE  SYLYRAFHALP--T--TSTGKPTGAVKGVNLMLLSLRKQY-----PDSPPFAVVFDA  61
sp|Q04957|DPO1_BACCA  SVAYRAFFALP----LLHNDKGIHTNAVYGFTMMLNKILAE-----EPHMLVAFDA  60
sp|P46835|DPO1_MYCLE  SLAFRAFYALPTE--NFKTRGGLTNAVYGFTAMLINLLREE-----APTHIAAADFV  75
sp|P52027|DPO1_DEIRA  ALAFRSYFALP--N--NSKGEMTHAIVGFMKLLRLRLAQ-----KSNQVIVVFD  103
.  :*:..  *  :  :  :  :  :

sp|P52026|DPO1_BACST  GKTTFRHETFQDYKGRQQTPELSEQFPLRLRELLKAYRIPAYELDHYEADDIIGTMAAR  120
sp|P00582|DPO1_ECOLI  KGKTTFRDELFEHYKSHRPPMPDDLRAQIEPLHAMVKAMGLPLLAVSGVEADDVIGTLARE  124
sp|P0A550|DPO1_MYCTU  SRQTFRQLQRYPEYKANRSSTPDEFAGQIDITKEVLGALGITVLSEPGFEADDLIATLATQ  134
sp|O34996|DPO1_BACSU  GKTTFRHGTFKEYKGRQKTPELSEQMPFIRELLDAYQISRYELEQYEADDIIGTLAKS  122
sp|Q9F173|DPO1_SALTY  KGKTTFRDELFEHYKSHRPPMPDDLRAQIEPLHAMVKAMGLPLLAVSGVEADDVIGTLARE  124
sp|P59200|DPO1_STRR6  GKTTFRTEMYADYKGRAKTPDEFREQFPFIRELLDHMGIRHYELAQYEADDIIGTLDKL  125
sp|O32801|DPO1_LACLM  GKTTFRTEMYADYKGRSKTPDEFREQLPFKEMIEKLGIRHYELANYEADDIIGTLDKM  126
sp|P43741|DPO1_HAEIN  KGKTTFRDEMFEQYKSHRPPMPDDLRLKQIQPLHDMIRALGIPLLVVEGIEADDVIGTLALQ  124
sp|Q9ZJE9|DPO1_HELPJ  QTKTKRAEKLGEYKQNRKDAPKEMLLQIPIALEWLQKMGFTCEVGGFEADDVIASLATL  130
sp|Q9CDS1|DPO1_LACLA  GKTTFRTEMYADYKGRSKTPDEFREQLPFKEMIEKLGIRHYELANYEADDIIGTLDKM  126
sp|P59199|DPO1_STRPN  GKTTFRTEMYADYKGRSKTPDEFREQLPFKEMIEKLGIRHYELANYEADDIIGTLDKL  125
sp|Q9S1G2|DPO1_RHILE  SAKTFRKDLYDAYKANRSAPPEELIPQFGLIREATRAFNLPCIETEGFEADDIATYARQ  147
sp|Q92GB7|DPO1_RICCN  GGKNFRHQIYPDYKANRPPPPEDLIQLPLVRDVASNLNFPILKNGYEADDIATFATK  122
sp|P0A551|DPO1_MYCBO  SRQTFRQLQRYPEYKANRSSTPDEFAGQIDITKEVLGALGITVLSEPGFEADDLIATLATQ  134
sp|Q9HT80|DPO1_PSEAE  KGPTFRDELFAEYKANRSPMPDDLRLVQVEPLHASVRALGLPLLCVGEVGEADDVIGTLARS  121
sp|Q04957|DPO1_BACCA  GKTTFRHEAFQEYKGRQQTPELSEQFPLRLRELLRAYRIPAYELENYEADDIIGTLAAR  120
sp|P46835|DPO1_MYCLE  SRKTTFRSECYAGYKANRSSIPAEFHGQIDITKEVLGALGITVFAEAGFEADDLIATLATQ  135

```



SDI Review Form 1.6

```

sp|P52027|DPO1_DEIRA  PVKTRFRHEQYEGYKSGRAQTPEDLPGQINRIRALVDALGFPRLEEPGYEADDVIASLTRM 163
      . *      ** *      * :      * .      :      ****:*.:

sp|P52026|DPO1_BACST  AER--EGFAVKVISGDRDLTQLASPVQTVETTKGITDIESYTPETVVEKYGLTPEQIVD 178
sp|P00582|DPO1_ECOLI  AEK--AGRPVLISGDKDMAQLVTPNITLINTMTN----TILGPEEVVVKYGVPPPELIID 178
sp|P0A550|DPO1_MYCTU  AEN--EGYRVLVVTGDRDALQLVSDDVTVLYPRKGVSELTRFTPEAVVEKYGLTPRQYPD 192
sp|O34996|DPO1_BACSU  AEK--DGFEVKVFSGDKDLTQLATDKTTVAITRKGITDVEFYTPPEHVKEKYGLTPEQIID 180
sp|Q9F173|DPO1_SALTY  AEK--VGRPVLISGDKDMAQLVTPNITLINTMTN----TILGPDEVVVKYGVPPPELIID 178
sp|P59200|DPO1_STRR6  AEQ--DGFDTIVSGDKDLIQLTDEHTVVEISKKGVAEFEEFTPDYLMMEEMGLTPAQFID 183
sp|O32801|DPO1_LACLM  AEAPDVNFDVTIVTGDKDMIQLVDGNTRVEISKKGVAEFEEFTPDYLLLEKMGLTPSQFID 186
sp|P43741|DPO1_HAEIN  ASS--LGKKVLISGDKDMAQLVDDNIMLINTMNN----SLLDRKGVIEKYGIPPELIID 178
sp|Q9ZJE9|DPO1_HELPJ  SP-----YKTRIYSKDKDFNQLLSDKIALFDGK-----TEFLAKDCVEKYGILPSQFTD 179
sp|Q9CDS1|DPO1_LACLA  AEAPNVNFDVTIVTGDKDMIQLVDGNTRVEISKKGVAEFEEFTPDYLLLEKMGLTPAQFID 186
sp|P59199|DPO1_STRPN  AEQ--DGFDTIVSGDKDLIQLTDEHTVVEISKKGVAEFEEFTPDYLMMEEMGLTPAQFID 183
sp|Q9S1G2|DPO1_RHILE  AEA--TGADTVIVSSDKDLMLQVSPNVHMYDSMKD---KQIGIPDVIEKWGVPPPEKMIID 201
sp|Q92GB7|DPO1_RICCN  TAA--LGAHVVIISDDKDLLQMLTENIKIYDPLKG---KYITEDDVVKKFGTTSCLKRE 176
sp|P0A551|DPO1_MYCBO  AEN--EGYRVLVVTGDRDALQLVSDDVTVLYPRKGVSELTRFTPEAVVEKYGLTPRQYPD 192
sp|Q9HT80|DPO1_PSEAE  SAA--ADRPVVISGDKDMAQLVDGHITLVNTMTG---SRLDVDGVKEKFGVGPPELIID 175
sp|Q04957|DPO1_BACCA  AEQ--EGFEVKVISGDRDLTQLASPHVTVDITKKGITDIEPYTPPEAVREKYGLTPEQIVD 178
sp|P46835|DPO1_MYCLE  AEN--EGYRVLVVTGDRDALQLVSNVDVTVLYPRKGVSELTRFTPEAVIEKYGVTPAQYPD 193
sp|P52027|DPO1_DEIRA  AEG--KGYEVRIVTSRDAYQLLDEHVKVIAN-----DFSLIGPAQVEEKYGVTVRQWVD 216
      :      : : * *      .      :      :      *      :

sp|P52026|DPO1_BACST  LKGLMGDKSDNIPGVPGIGEKTAVKLLKQFG-TVENVLASIDEIKG-----EKLKENLR 231
sp|P00582|DPO1_ECOLI  FLALMGDSSDNIPGVPGVGEKTAQALLQGLG-GLDTLYAEPEKIAGLSFRGAKTMAAKLE 237
sp|P0A550|DPO1_MYCTU  FAALRGDPSDNLPGIPGVGEKTAAKWIAEYG-SLRSLVDNVDVAVRG-----KVGDALE 244
sp|O34996|DPO1_BACSU  MKGLMGDSSDNIPGVPGVGEKTAIKLLKQFD-SVEKLLESIDEVSG-----KKLKEKLE 233
sp|Q9F173|DPO1_SALTY  FLALMGDSSDNIPGVPGVGEKTAQALLQGLG-GLDTLYAEPEKIAGLTFRGAKTMAAGLA 237
sp|P59200|DPO1_STRR6  LKALMGDKSDNIPGVTKVGEKTGIKLLLEHG-SLEGIYENIDGMKT-----SKMKENLI 236
sp|O32801|DPO1_LACLM  LKALMGDSSDNYPGVTKVGEKTGLKLLQEFQ-SLENLYENVETLKA-----SKMKDNLI 239
sp|P43741|DPO1_HAEIN  YLALMGDSADNIPGVAGVGEKTALGLLQGIG-SMAEIYANLEKVAELPIRGAKKLGEKLL 237
sp|Q9ZJE9|DPO1_HELPJ  YQGIVGDSSDNYPGVTKVGEKTGLKLLQEFQ-SLEKIYENLDLAKNL--L-SPKMYQALI 235
sp|Q9CDS1|DPO1_LACLA  LKALMGDSSDNYPGVTKVGEKTGLKLLQEFQ-SLENLYENVDSLKA-----SKMKENLI 239
sp|P59199|DPO1_STRPN  LKALMGDKSDNIPGVTKVGEKTGIKLLLEHG-SLEGIYENIDGMKT-----SKMKENLI 236
sp|Q9S1G2|DPO1_RHILE  LQAMTGDSVDNVPGIPGIGPKTAAKLLLEYG-DLDTLLERATEIKQ-----VKRRETIL 254
sp|Q92GB7|DPO1_RICCN  VMALIGDRSDNIPGVPSIGPKTASSLITQFG-SVENIFNSLDQVSS-----VKQRETLO 229
sp|P0A551|DPO1_MYCBO  FAALRGDPSDNLPGIPGVGEKTAAKWIAEYG-SLRSLVDNVDVAVRG-----KVGDALE 244
sp|Q9HT80|DPO1_PSEAE  FLALMGDKVDNIPGVPGVGEKTALGLLTGVGGLLEVLYASLDKVPPELPIRGAKGLPAKLE 235
sp|Q04957|DPO1_BACCA  LKGLMGDKSDNIPGVPGIGEKTAVKLLRQFG-TVENVLASIDEIKG-----EKLKETLR 231
sp|P46835|DPO1_MYCLE  LAALRGDPSDNLPGIPGVGEKTAAKWIVDYG-SLQGLVDNVESVRG-----KVGEALR 245
sp|P52027|DPO1_DEIRA  YRALTGDAADNIPGAGIGPKTAAKLLQEYG-TLEKVYEAHAG-TL--K-PDGTTRKKLL 271
      .: **      *      : * *..      :      .      :      :

sp|P52026|DPO1_BACST  QYRDLALLSKQLAAICRDAPVELTLDIVYKGEDR-EKVVALFQELGFQSFQDKMAVQT- 289
sp|P00582|DPO1_ECOLI  QNKEVAYLSYQLATIKTDVELELTCEQLLEVQQPAA-EELLGLFKKYEFKRWTTADVEAGKW 296

```



SDI Review Form 1.6

```

sp|P0A550|DPO1_MYCTU  ANLASVVRNRELTDLVRDVPLAQTPDTRLRLQPWDR-DHIHRLFDDLEFRVLRDRFLDTLA 303
sp|O34996|DPO1_BACSU  EFKDQALMSKELATIMTDAPIEVSVSGLEYQGfNR-EQVIAIFKDLGFNTLLERLGEDS- 291
sp|Q9F173|DPO1_SALTY  QNKDVAYLSYKLATIKTDVELELTCEQLEVQQPIA-DELLGLFKKYEFKRWTDADVESGKW 296
sp|P59200|DPO1_STRR6  NDKEQAFLSKTLATIDTKAPIAIGLEDLVYSGPDV-ENLGKFYDEMGMFKQLKQALNMSS- 294
sp|O32801|DPO1_LACLM  ADKEMAFLSQQLATINTKAPLEIGLEDTLLEKKNV-AELGQFYDEMGMFSQFKSKLLADGG 298
sp|P43741|DPO1_HAEIN  AEKNNADLSYTLATIKTDVELNVTTDQLLLLGESQK-DQLIEYFARYEFKRWLNEVMNGAD 296
sp|Q9ZJE9|DPO1_HELPJ  QDKGS AFLSKELATLERGCIKEFDLSCAFPSENPLLKIKDELKEYGFISTRDLNSPF 295
sp|Q9CDS1|DPO1_LACLA  ADKEMAFLSQQLATINTKAPIEIGLDDTLKGGKV-DELSQFYDEMGMFAQFKSKLLAEAG 298
sp|P59199|DPO1_STRPN  NDKEQAFLSKTLATIDTKAPIAIGLEDLVYSGPDV-ENLGKFYDEMGMFKQLKQALNVSS- 294
sp|Q9S1G2|DPO1_RHILE  ANIDMARLSRDLVRLRDTVDPLDLDLALVLEPQNG-PKLIGFLKTMEFTTLTRRVAEACD 313
sp|Q92GB7|DPO1_RICCN  NSREAA LISWQLIGLSNVDFQLNNLEWSPPNS-DKLTGFLQYGFGRSLYKRVENLLD 288
sp|P0A551|DPO1_MYCBO  ANLASVVRNRELTDLVRDVPLAQTPDTRLRLQPWDR-DHIHRLFDDLEFRVLRDRFLDTLA 303
sp|Q9HT80|DPO1_PSEAE  ENREQAFLSYQLATIKTDVLELDVEIDKLYPGEPQR-EALIALYRELEFKNWLDLLEAK 294
sp|Q04957|DPO1_BACCA  QHREMALLSKKLAAIRDAPVELSLDDIAYQGEDR-EKVVALFKELGFGQSFLEKMESSP- 289
sp|P46835|DPO1_MYCLE  THLASVVRNRELTELKDVPLVQTS DTLRLQPWDR-DRIHRLF DNLEFRVLRDRFLFEALA 304
sp|P52027|DPO1_DEIRA  DSEENVKFSHDLSCMVTDLPLDIEFGVRRLP-DNP-LVTEDLLTELEHLSLRPMILGLNG 329

```

. . * : : :

```

sp|P52026|DPO1_BACST  DE-G--EKP-----LA----- 297
sp|P00582|DPO1_ECOLI  LQ-AKGAKPAA-KP-----QETSVADEAPEVTA----- 322
sp|P0A550|DPO1_MYCTU  -A-AG-----GPEVD----- 311
sp|O34996|DPO1_BACSU  AE-AEQDQS-----LE----- 301
sp|Q9F173|DPO1_SALTY  LQ-AKGAKPAA-KP-----QETVVIDESPSEPA----- 322
sp|P59200|DPO1_STRR6  AD-V-----AE----- 299
sp|O32801|DPO1_LACLM  GE-VTDETV-----SE----- 308
sp|P43741|DPO1_HAEIN  SITQTTEQPVK-MNQYKATS-----QDQSAVENTPKI----- 327
sp|Q9ZJE9|DPO1_HELPJ  -I-VE-NVPIL-N-----STPILDNTPALD----- 316
sp|Q9CDS1|DPO1_LACLA  GE-VTDEKV-----VD----- 308
sp|P59199|DPO1_STRPN  AD-V-----SE----- 299
sp|Q9S1G2|DPO1_RHILE  CDA-SAIEPAIVRIEWGETARGPDLDAEPEFPVAGGIPEVSGESVMPMPRAKAKSAVEGA 372
sp|Q92GB7|DPO1_RICCN  IKI-NDHKEIA-DS-----KVTE----- 304
sp|P0A551|DPO1_MYCBO  -A-AG-----GPEVD----- 311
sp|Q9HT80|DPO1_PSEAE  -E-AGEN--G-EA-----ETPIQAE----- 309
sp|Q04957|DPO1_BACCA  SE-E--EKP-----LA----- 297
sp|P46835|DPO1_MYCLE  -A-AGER-----VPEVD----- 314
sp|P52027|DPO1_DEIRA  PE-QDGHAPDD-LL-----EREHA-QTPEED----- 352

```

```

sp|P52026|DPO1_BACST  -----GM-D-F-AIA-D-SVTD---EMLADKA----ALVVEVVGDN 326
sp|P00582|DPO1_ECOLI  -----TVISY-DNYVTILDE-ETLKAWIAKLEKAPV-F-AFDTETDSDL 362
sp|P0A550|DPO1_MYCTU  -----EGF-DVRGGALAP-GTVRQWLAEHAGDGRRA-GLTVVGTHL- 349
sp|O34996|DPO1_BACSU  -----DI-N-V-KTV-T-DVTS---DILVSPS---AFVVEQIGDN 330
sp|Q9F173|DPO1_SALTY  -----AALSY-ENYVTILDD-VTLESWIEKLKKAPV-F-AFDTETDSDL 362
sp|P59200|DPO1_STRR6  -----GL-D-F-TIV-D-QISQ---DMLSEES---IFHFELFGEN 328
sp|O32801|DPO1_LACLM  -----EI-K-F-EIVTD-KSSV---ASVNADD---FFYLETLGEN 338
sp|P43741|DPO1_HAEIN  -----QIDR-TKYETLLTQ-ADLTRWIEKLNAAKL-I-AVDTETDSDL 366

```



SDI Review Form 1.6

sp Q9ZJE9 DPO1_HELPJ	-----NAPKKSIRMIVLESAPLSEMFLEKLENPNAR--VFM-RL-VL-	353
sp Q9CDS1 DPO1_LACLA	-----EI-D-F-EIVTD-GSIS---EKNVADD---FFYLETLGEN	338
sp P59199 DPO1_STRPN	-----SL-D-F-TIV-D-QISQ---DMLSEES---IFHFELFGEN	328
sp Q9S1G2 DPO1_RHILE	FSPADLAKARAEAFATLPFDH-SAYVTIRDL-VTLDRWIADARATGL-V-AFDTETTSID	428
sp Q92GB7 DPO1_RICCN	-----IKE-LNNANELADFAKEATKIGIFGIY--LL-	332
sp P0A551 DPO1_MYCBO	-----EGF-DVRGGALAP-GTVRQWLAEHAGDGRRA-GLTVVVGTHL-	349
sp Q9HT80 DPO1_PSEAE	-----VDYDVVLDQ-AGFDAWLKKLEAEAL-I-AFDTETTSID	344
sp Q04957 DPO1_BACCA	-----KM-A-F-TLA-D-RVTE---EMLADKA---ALVVEVVEEN	326
sp P46835 DPO1_MYCLE	-----EGF-DVRGGLLES-GTVGRWLAKHADDGRRS-GLAIVGTHL-	352
sp P52027 DPO1_DEIRA	-----EAA-A--LPAFSA-PELAEWQTPAEG---A-VWGYVLSRED	385
sp P52026 DPO1_BACST	YHHAPIVGIALAN--ER-----GRFFLRPE-----T-A--L---A-----D--- 354	
sp P00582 DPO1_ECOLI	NISANLVGLSFAIEPGV-----AAYIPVAH-----D-Y--L---DAPDQISRERAL 402	
sp P0A550 DPO1_MYCTU	PHGGDATAMAVAAADGE-----GAYLDTAT-----L-----TP---DDD--- 380	
sp O34996 DPO1_BACSU	YHEEPILGFSIVN--ET-----GAYFIPKD-----I-A--V---E-----S--- 358	
sp Q9F173 DPO1_SALTY	NIAANLVGLSFAIEPGV-----AAYVPAH-----D-Y--L---DAPDQISRQAL 402	
sp P59200 DPO1_STRR6	YHTDNLVGFVWSC--GD-----QLYATDKL-----E-L--L---Q-----D--- 356	
sp O32801 DPO1_LACLM	YHREQIVAFWGN--SE-----KIYVSKNL-----D-L--L---T-----E--- 366	
sp P43741 DPO1_HAEIN	YMSANLVGISFALENCE-----AAYLPLQL-----D-Y--L---DAPKTLEKSTAL 406	
sp Q9ZJE9 DPO1_HELPJ	DKDKKILALAPLLQ--D-----QGYFLPLE-----E-A--L---FS----- 381	
sp Q9CDS1 DPO1_LACLA	YHREQIVAFWGN--AE-----KIYVSKNI-----D-L--L---T-----K--- 366	
sp P59199 DPO1_STRPN	YHTDNLVGFVWSC--GD-----KLYATDKL-----E-L--L---Q-----D--- 356	
sp Q9S1G2 DPO1_RHILE	AMQAEVLVGFSLAIADNTADPTGTKIRAAAYVPLVHKNGVGD-L--LGGLADNQIPMRDAL 485	
sp Q92GB7 DPO1_RICCN	QHKGANLAFILSL--QN-----QSYIIKIS-NTSHDL---F---SYNTKSNNWFS 374	
sp P0A551 DPO1_MYCBO	PHGGDATAMAVAAADGE-----GAYLDTAT-----L-----TP---DDD--- 380	
sp Q9HT80 DPO1_PSEAE	AQQAQVVGVSFAVKEGE-----AAYVPLAH-----S-Y--M---GVPEQLDRDAVL 384	
sp Q04957 DPO1_BACCA	YHDAPIVGIAVNV--EH-----GRFFLRPE-----T-A--L---A-----D--- 354	
sp P46835 DPO1_MYCLE	PHGGDATAALAVAAADGN-----GGYIDTAM-----L-----TP---DDD--- 383	
sp P52027 DPO1_DEIRA	DLTAALLAA--ATFEDGV-----ARPAPVSEP---DEWAQA---EAPENLFGE-LL 427	
sp P52026 DPO1_BACST	PKFLAWLGDE--T-----KKKTMFD-----SKR 375	
sp P00582 DPO1_ECOLI	ELLKPILLEDE--K-----ALKVGQN-----LKY 423	
sp P0A550 DPO1_MYCTU	AALAAWLADP--A-----KPKALHE-----AKA 401	
sp O34996 DPO1_BACSU	EVFKWVEND--E-----QKKVVF-----SKR 379	
sp Q9F173 DPO1_SALTY	ELLKPILLEDE--K-----VRKVGQN-----LKY 423	
sp P59200 DPO1_STRR6	PIFKDFLEKT-----SLRVYD-----FKK 375	
sp O32801 DPO1_LACLM	MKFP-----ENTYD-----FKK 378	
sp P43741 DPO1_HAEIN	AAIKPILENP--N-----IHKVGN-----IKF 427	
sp Q9ZJE9 DPO1_HELPJ	PFSLEFLQNA--FSQMLQHACIIGHD-----LKP 408	
sp Q9CDS1 DPO1_LACLA	MKFP-----ENTYD-----FKK 378	
sp P59199 DPO1_STRPN	PIFKDFLEKT-----SLRVYD-----FKK 375	
sp Q9S1G2 DPO1_RHILE	PRLKALLEDE--S-----VLKVAQN-----LKY 506	
sp Q92GB7 DPO1_RICCN	DIIFNLLTDK--S-----IKKITYS-----LKP 395	
sp P0A551 DPO1_MYCBO	AALAAWLADP--A-----KPKALHE-----AKA 401	



SDI Review Form 1.6

```
sp|Q9HT80|DPO1_PSEAE  RALKPLLEDP--K-----KLKVGQH-----AKY 405
sp|Q04957|DPO1_BACCA  PQFVAWLGD--T-----KKKSMFD-----SKR 375
sp|P46835|DPO1_MYCLE  DALAAWLADP--D-----NPKALHE-----AKL 404
sp|P52027|DPO1_DEIRA  PSDKPLTKKEQKA-----LEKAQKDAEKARAKLREQFPATVDEAEFVGQRTVTAAAKA 481
*
```

```
sp|P52026|DPO1_BACST  AAVALKW--KGIELRGVV-FDLLLAAYLLDPAQAAGDVA AVAKMHQYEAVRSDEAVYGGK 432
sp|P00582|DPO1_ECOLI  DRGILAN--YGIELRGIA-FDTMLESYILNSVAGRHDMSLAERWLKHKTTITFEEIAGKG 480
sp|P0A550|DPO1_MYCTU  AVHDLAG--RGWTLGVT-SDTALAAYLVPRGQRSFTLDDLRLYLRLRELRAE-TPQQQ- 456
sp|O34996|DPO1_BACSU  AVVALRW--QGIELKGAE-FDTLLAAYIINPGNSYDDVASVAKDYGLHIVSSDESUYGKG 436
sp|Q9F173|DPO1_SALTY  DRGVLQN--YGIELRGIA-FDTMLESYILNSVAGRHDMSLSDRWLKHKTITFEDIAGKG 480
sp|P59200|DPO1_STRR6  VKVLLQR--FGVDLQAPA-FDIRLAKYLLSTVE-DNEIATIASLYGQTYLVDDTFYGGK 431
sp|O32801|DPO1_LACLM  NRVLLSH--LNIELPLVK-FDAMLAKYLLISTE-DNKISTARLFDVGHATDEEIFGKG 434
sp|P43741|DPO1_HAEIN  DESIFAR--HGIELQGVF-FDTMLLSYTLNSTG-RHNMDLAKRYLGHETIAFESLAGKG 483
sp|Q9ZJE9|DPO1_HELPJ  LLSFLKA-KYQVPLENIRIQDTQILAFKLNPEKV--GFDEVLYKEYLKEDLPHEKIKDFK 465
sp|Q9CDS1|DPO1_LACLA  NRVLLSH--LDIELPLVK-FDAMLAKYLLISTE-DNKISTARLFNSGHLATDEEIFGKG 434
sp|P59199|DPO1_STRPN  VKVLLQR--FGVDLQAPA-FDIRLAKYLLSTVE-DNEIATIASLYGQTYLVDDTFYGGK 431
sp|Q9S1G2|DPO1_RHILE  DYLLLR--YGIETRSF--DDTMLISYVLDAGTGAGHMDPLSEKFLGHTPIPYKDVAGSG 562
sp|Q92GB7|DPO1_RICCN  LLKFYAN--QSHDITAI--EDLELMQYALSAGLSQKNL-----F--- 430
sp|P0A551|DPO1_MYCBO  AVHDLAG--RGWTLGVT-SDTALAAYLVPRGQRSFTLDDLRLYLRLRELRAE-TPQQQ- 456
sp|Q9HT80|DPO1_PSEAE  DINVLANASTPIALRGVA-YDTMLESYVLDSTATRHDMSLALRYLGHSTIRFEDIAGKG 464
sp|Q04957|DPO1_BACCA  AAVALKW--KGIELCGVS-FDLLLAAYLLDPAQGVDDVAAAKMKQYEAVRPDEAVYGGK 432
sp|P46835|DPO1_MYCLE  AMHDLAG--RGWTLGGIT-SDTALAAYLVPRGQRSFTLDDLRLYLRLRELRAE-TPEQE- 459
sp|P52027|DPO1_DEIRA  LAHLSVR--GTVVE-PG-DDPLLYAYLLDPANT--NMPVVAKRYLDREWPAD-AP---- 530
* : : . .
```

```
sp|P52026|DPO1_BACST  AKRTVPD-EPT----LAEHLVRKAAAIWALEEPLMDELRRN-EQDRLLTELEQPLAGILA 486
sp|P00582|DPO1_ECOLI  KNQLTFN-QIALEE-AGRYAEDADVTLQLHLKMWPDQLKHKGPLNVFENIEMPLVPVLS 538
sp|P0A550|DPO1_MYCTU  QLSLLDD-DDTDAE-TIQTTLIRARVIDLADALDAELARI-DSTALLGEMELPVQVLA 513
sp|O34996|DPO1_BACSU  AKRAVPS-EDV----LSEHLGRKALAIQSLREKLQVELENN-DQLELFEELEMPALILG 490
sp|Q9F173|DPO1_SALTY  KNQLTFN-QIALEE-AGRYAEDADVTLQLHLKMWPELQKHKGPLNVFENIEMPLVPVLS 538
sp|P59200|DPO1_STRR6  VKKAIPE-REK----FLEHLACKLAVLVETEPILLEKLSN-GQLELLYDMEQPLAFVLA 485
sp|O32801|DPO1_LACLM  TKLALPD-DEI----LFDHLARKIRVLARAKEKMAELIEN-EQEHLSDMELPLAEVLA 488
sp|P43741|DPO1_HAEIN  KSQLTFN-QIPLEQ-ATEYAAEDADVTKLQALWLKLQEEPTLVELYKTMELPLLVLS 541
sp|Q9ZJE9|DPO1_HELPJ  TKS-----KAE-KSELLSMELNALKRCEYFEKGGLEE-DLLTLARDIETPFVKVLM 515
sp|Q9CDS1|DPO1_LACLA  TKIALPD-DAV----LFEHLARKIKVLALAKEKMAELLEN-EQEHLSDMELPLAEVLA 488
sp|P59199|DPO1_STRPN  VKKAIPE-REK----FLEHLACKLAVLVETEPILLEKLSN-GQLELLYDMEQPLAFVLA 485
sp|Q9S1G2|DPO1_RHILE  KANVTFD-LVDIDR-ATHYAAEDADVTLRLWLVLKPLRLAA-GLTSVYERLERPLPVLA 619
sp|Q92GB7|DPO1_RICCN  --KEVLK-ETWIENIIIESAKIVIN-FIALYKQTIWELKDN-KTFRLYSNIDLPICFILD 485
sp|P0A551|DPO1_MYCBO  QLSLLDD-DDTDAE-TIQTTLIRARVIDLADALDAELARI-DSTALLGEMELPVQVLA 513
sp|Q9HT80|DPO1_PSEAE  AKQLTFD-QIAIEQ-AGPYAEDADVTLRLHQALWQKLEAIPSLARVLTDIEMPLVPVLA 522
sp|Q04957|DPO1_BACCA  AKRAVPD-EPV----LAEHLVRKAAAIWALERPFLDELRRN-EQDRLLVELEQPLSSILA 486
sp|P46835|DPO1_MYCLE  QFSLLDNVDEVKQ-AIQTLILRARAVVDLAAALDAELDLI-DSTSLGEMELPVQVLA 517
sp|P52027|DPO1_DEIRA  -----TRAATGHLLREL-PPLDD-ARRKMYDEMEKPLSGVLG 567
: : : *
```



SDI Review Form 1.6

```

sp|P52026|DPO1_BACST  NMEFTGVKVDTKRLEQMGAELTEQLQAVERRIYELAGQEFNINSPKQLGTVLFDKLQLPV 546
sp|P00582|DPO1_ECOLI  RIERNGVKIDPKVLHNSSEELTLRLAELEKKAHEIAGEEFNLSSTKQLQTILFEKQGIKP 598
sp|P0A550|DPO1_MYCTU  KMESAGIAVDLPMTELQSQFGDQIRDAEEAAYGVIGKQINLGSPPQLQVVLFDLGMMPK 573
sp|O34996|DPO1_BACSU  EMESTGVKVDVDRLEKRMGEEELGAKLKEYEKKIHEIAGEFPFNINSPKQLGVILFEKIGLPV 550
sp|Q9F173|DPO1_SALTY  RVERNGVKIDPAVLHKKHSEETLRLAELEKKAHDIAAGEAFNLSSTKQLQTILFEKQGIKP 598
sp|P59200|DPO1_STRR6  KMEIAGIVVKETLLEMQAENELVIEKLTQEIYELAGEEFNVNNSPKQLGVLLFEKLGPL 545
sp|O32801|DPO1_LACLM  KMEITGISVSQNTLEEIGAENEEKLASLTREIYDLAGEEFNINSPKQLGVILFEKLGPLV 548
sp|P43741|DPO1_HAEIN  RMERTGVLDSDALFMSNEIASRLTALEKQAYALAGQPPFNLASTKQLQEILFDKLELPV 601
sp|Q9ZJE9|DPO1_HELPJ  GMEFQGFKIDAPYFKRLEQEFKNELNVLERQILDIGVDFNLNNSPKQLGEVLYDKLGLPK 575
sp|Q9CDS1|DPO1_LACLA  KMEITGIAVSQNTLEEIGAENEEKLASLTREIYDLAGEEFNINSPKQLGVILFEKLGPLV 548
sp|P59199|DPO1_STRPN  KMEIAGIMVKKETLLEMQAENELVIEKLTQEIYELAGEEFNVNNSPKQLGVLLFEKLGPL 545
sp|Q9S1G2|DPO1_RHILE  RMEARGITVDRQILSRLSGELAQGAARLEDEIYVLAGERFNIGSPKQLGDLIFGKMGLSG 679
sp|Q92GB7|DPO1_RICCN  KMEKVGITVDANYLKQLSAEFGTEILKLEEBIFALSGTKFNIGSPKQLGEILFEKMLPF 545
sp|P0A551|DPO1_MYCBO  KMESAGIAVDLPMTELQSQFGDQIRDAEEAAYGVIGKQINLGSPPQLQVVLFDLGMMPK 573
sp|Q9HT80|DPO1_PSEAE  RIERNGALVDANLLGQSRELGKEMVALERQAYDLAGEEFNINSPKQLGAILYDKLGLPV 582
sp|Q04957|DPO1_BACCA  EMEFAGVKVDTKRLEQMGEEELAEQLRTVEQRIYELAGQEFNINSPKQLGVILFEKLGPLV 546
sp|P46835|DPO1_MYCLE  DMEKAGIAADRLRLTELQSQFGDQIRDAEEAAYAVIGKQINLSSPKQLQVVLFEELGMMPK 577
sp|P52027|DPO1_DEIRA  RMEVRGVQVDSDFLQTLISIQAGVRLADLESQIHEYAGEEFHIRSPKQLETVLYDKLELAS 627

: * . : : * : : * . * * : : :

sp|P52026|DPO1_BACST  --LKKTK--TG-YSTSADVLEKLAPH--HEIVEHIL-HYRQLGKLQSTYIEGLLKVVHPV 598
sp|P00582|DPO1_ECOLI  --LKKTP--GGAPSTSEEVLEELALD--YPLPKVIL-EYRGLAKLKSTYTDKPLPLMINPK 651
sp|P0A550|DPO1_MYCTU  --TKRTK--TG-YTTDADALQSLFDKTGHPFLQHLL-AHRDVTRLKVT-VDGLLQAVA-A 625
sp|O34996|DPO1_BACSU  --VKKTK--TG-YSTSADVLEKLADK--HDIVDYIL-QYRQIGKLQSTYIEGLLKVTRPD 602
sp|Q9F173|DPO1_SALTY  --LKKTP--GGAPSTSEEVLEELALD--YPLPKVIL-EYRGLAKLKSTYTDKPLPLMINPK 651
sp|P59200|DPO1_STRR6  EYTKKTK--TG-YSTAVDVLERLAPI--APIVKKIL-DYRQIAKIQSTYVIGLQDWILA- 598
sp|O32801|DPO1_LACLM  --GKKTK--TG-YSTAVDVLEDLAAL--SPVVAKIL-EYRQINKVQSTYVKGILPQIAD- 599
sp|P43741|DPO1_HAEIN  --LQKTP--KGAPSTNEEVLEELSYS--HELPKILV-KHRGLSKLKSTYTDKLPQMVNSQ 654
sp|Q9ZJE9|DPO1_HELPJ  --NKS-----HSTDEKNLLKILDK--HPSIPLIL-EYRELNKLFTNTYTPLLRLKD-K 622
sp|Q9CDS1|DPO1_LACLA  --GKKTK--TG-YSTAVDVLEDLAAL--SPVVAKIL-EYRQINKVQSTYVKGILPQIAD- 599
sp|P59199|DPO1_STRPN  EYTKKTK--TG-YSTAVDVLERLAPI--APIVKKIL-DYRQIAKIQSTYVIGLQDWILA- 598
sp|Q9S1G2|DPO1_RHILE  --GSKTK--TGQWSTSAQVLEDLAAA-GFELPRKIV-DWRQVTKLKSTYTDALPGYVHPE 733
sp|Q92GB7|DPO1_RICCN  --GKASAKASS-YSTGAIELEKLSEH-GYNIADLLL-RWRQLTKLKNTYTDSPKQIDNI 600
sp|P0A551|DPO1_MYCBO  --TKRTK--TG-YTTDADALQSLFDKTGHPFLQHLL-AHRDVTRLKVT-VDGLLQAVA-A 625
sp|Q9HT80|DPO1_PSEAE  --LSKTA--TGQPTAEAVLAELAEQ-DFELPKVIM-QYRSMKSLKSTYTDRLPEQINPR 636
sp|Q04957|DPO1_BACCA  --LKKSK--TG-YSTSADVLEKLAPY--HEIVENILQHYRQLGKLQSTYIEGLLKVVRPD 599
sp|P46835|DPO1_MYCLE  --TKRTK--TG-YTTDADALQSLFCKTEHPFLQHLL-THRDVTRLKVT-VDGLLNAVA-A 629
sp|P52027|DPO1_DEIRA  --SKTKL-TGQRSTAVSALEPLRDA--HPIIPLVL-EFRELDKLRGTYLDPIPNLVNPH 681

. : * * : : : * : : * :

sp|P52026|DPO1_BACST  TGVHMTMFNQALTQTGRLSSVEPNLQNIPIRLEEGRKIRQAFVFPSEP--DW-LIFAADYS 655
sp|P00582|DPO1_ECOLI  TGRVHTSYHQAVTATGRLSSDTPNLQNIPIRNEEGRRIRQAFIAPE---DY-VIVSADYS 707
sp|P0A550|DPO1_MYCTU  DGRIHTTFNQATIAATGRLSSSTEPNLQNIPIRTDAGRRIIRDAFVVGDD---GYAELMTADYS 682
sp|O34996|DPO1_BACSU  SHKVHTRFNQALTQTGRLSSDTPNLQNIPIRLEEGRKIRQAFVFPSEK--DW-LIFAADYS 659
sp|Q9F173|DPO1_SALTY  TGRVHTSYHQAVTATGRLSSDTPNLQNIPIRNEEGRRIRQAFIAPE---DY-LIVSADYS 707
sp|P59200|DPO1_STRR6  DGKIHTRYVQDLTQTGRLSSVDPNLQNIPIRLEEGRKIRQAFVPEWE--DS-VLLSSDYS 655

```

SDI Review Form 1.6

sp O32801 DPO1_LACLM	DGKIHTRYVQDLTQTGRLLSSVDPLNQNPVRLEEGRKIRKAFVPS-Q--DS-LLSSDYS	655
sp P43741 DPO1_HAEIN	TGRVHTSYHQAVTATGRLSSSDPLNQNPIRNEEGRHIRQAFIARE---GY-SIVAADYS	710
sp Q9ZJE9 DPO1_HELPJ	DDKIHTTFIQGTATGRLSSHSPPLNQNPVRSPKGLLRKGFIASSK---EY-CLLGVDS	679
sp Q9CDS1 DPO1_LACLA	DGKIHTRYVQDLTQTGRLLSSVDPLNQNPVRLEEGRKIRKAFVPS-K--DS-LLSSDYS	655
sp P59199 DPO1_STRPN	DGKIHTRYVQDLTQTGRLLSSVDPLNQNP1PARLEQGRLIRKAFVPEWE--DS-VLLSSDYS	655
sp Q9S1G2 DPO1_RHILE	TKRVHTSYSLASTTTTGRLLSSEPPLNQNPVRTAEGRKIRTAFASTP---GH-KLISADYS	789
sp Q9ZGB7 DPO1_RICCN	THRVTHTFLQSTTTTGRLLSQEPPLNQNPVIRSEGNQIRKAFIAE---GY-KLISADYS	656
sp P0A551 DPO1_PYCOB	DGRHHTTFNQTTAATGRLLSTEPPLNQNP1RTDAGRRIRDAFVVDG---GYAELMTADYS	682
sp Q9HT80 DPO1_PSEAE	TGRIHTSYHQAAATGRLLSSDPLNQNP1RTAEGRRIRQAFVAPQ---GY-KLLAADYS	692
sp Q04957 DPO1_BACCA	TKKVHTIFNQALTQTGRLLSTEPPLNQNP1RLEEGRKIRKAFVPS--DW-LIFAADYS	656
sp P46835 DPO1_MYCLE	DGRHHTTFNQTTAATGRLLSTEPPLNQNP1RTNAGRQIRDAFVVGSENNGYTELMTADYS	689
sp P52027 DPO1_DEIRA	TGRLHTTFAQTAVATGRLLSNPLNQNP1RSELGREIRKGFIAED---GF-TLIAADYS	737

sp P52026	DPO1_BACST	QIELRVLAHIAEDDNLIEAFRRGLDIHTKTAMDIFHVSE-EDVTANMRRQAKAVNFGIVY	714
sp P00582	DPO1_ECOLI	QIELRIMAHLSRDKGLLTAFAGGKDIHRATAAEVFGPLP-ETVTSQRRSAKAINFGLIY	766
sp P0A550	DPO1_MYCTU	QIEMRIMAHLSGDEGLIEAFNTGEDLHSFVASRAFQVPI-DEVTGELRRRVKAMSYGLAY	741
sp O34996	DPO1_BACSU	QIELRVLAHISKDENLIEAFNTMDIHTKTAMDVFHVAK-DEVTSAMRRQAKAVNFGIVY	718
sp Q9F173	DPO1_SALTY	QIELRIMAHLSRDKGLLTAFAGGKDIHRATAAEVFGPLP-DSVTGEQRRSAKAINFGLIY	766
sp P59200	DPO1_STRR6	QIELRVLAHISKDEHLIKAFQEGADITHSTAMRVFGIEKPDVNTANDRRNAKAVNFGVVY	715
sp O32801	DPO1_LACLM	QIELRVLAHISADEHLIDAFKHGADIHTSTAMRVFGIEKAEDVTANDRRNAKAVNFGVVY	715
sp P43741	DPO1_HAEIN	QIELRIMAHLSGDEGLINAFSQGKDIHRSTAAEIFGVSL-DEVTSQRRNAKAINFGLIY	769
sp Q9ZJE9	DPO1_HELPJ	QIELRLLAHFSQDKDLMEAFLKGRDIHLETSKALFG---EDLAKEKRISIAKSINFGLVY	735
sp Q9CDS1	DPO1_LACLA	QIELRVLAHISGDEHLIDAFKHGADIHTSTAMRVFGIEKAEDVTANDRRNAKAVNFGVVY	715
sp P59199	DPO1_STRPN	QIELRVLAHISKDEHLIKAFQEGADITHSTAMRVFGIEKPDVNTANDRRNAKAVNFGVVY	715
sp Q9S1G2	DPO1_RHILE	QIELRVLAHVAEIPQLTKAFEDGVDIHMTASEMFGVPV-EGMPGEVRRRAKAINFGLIY	848
sp Q92GB7	DPO1_RICCN	QIELRLILSHIANIDALKQAFINCKDDIHTQTACQIFNLQK-HELTSEHRRKAKAINFGLIY	715
sp P0A551	DPO1_MYCBO	QIEMRIMAHLSGDEGLIEAFNTGEDLHSFVASRAFQVPI-DEVTGELRRRVKAMSYGLAY	741
sp Q9HT80	DPO1_PSEAE	QIELRIMAHLLAKDGLLDFAFRHLDVHRTAAAEVFGVPL-EDVSGDQRRSAKAINFGLIY	751
sp Q04957	DPO1_BACCA	QIELRVLAHIAEDDNLIEAFRRGLDIHTKTAMDIFQVSE-DEVTNPMRRQAKAVNFGIVY	715
sp P46835	DPO1_MYCLE	QIEMRIMAHLSRDEGLIEAFNTGEDLHSFVASRAFQIPI-EDITPELRRRVKAMSYGLAY	748
sp P52027	DPO1_DEIRA	QIELRLLAHIAADDPLMQQAFVEGADIHRRATAAQVIGLDE-ATVDANQRRRAKTVNFGVLY	796

sp P52026	DPO1_BACST	GISDYGLAQNLNITRKEAAEFIERYFASFGVKQYMDNIVQEAQKQGVVTTLLHRRRYLP	774
sp P00582	DPO1_ECOLI	GMSAFGLARQLNIPRKEAQKQYMDLYFERYPGVLEYMERTRAQAKEQGYVETLDGRRLYLP	826
sp P0A550	DPO1_MYCTU	GLSAYGLSQQLKISTEEEAQMDYAFARFGGVRDYLRVAVRAREKQGYVETLVGRRLYLP	801
sp Q34996	DPO1_BACSU	GISDYGLSNLNGITRKEAGAFIDRYLESFGVKVAYMEDSVQEAQKQGVVTLMHRRRYLP	778
sp Q9F173	DPO1_SALTY	GMSAFGLSRQLNIPRKEAQKQYMDLYFERYPGVLEYMERTRAQAKEQGYVETLEGRRLYLP	826
sp P59200	DPO1_STRR6	GISDFGLSNNLGISRKEAKAYIDTYFERFPGIKNYMEDVVRAREKQGYVETLTKRRREL	775
sp Q32801	DPO1_LACLM	GISDFGLARNLGITRKDAKNYIETFYERFPGIKNYMENIVREARDKGFVETMSHRRRKIP	775
sp P43741	DPO1_HAEIN	GMSAFGLSRQLGISRADAQKQYMDLYFQRPYSQVFQMTDIREKAKAQGVVETLFGRRLYLP	829
sp Q9ZJE9	DPO1_HELPJ	GMGSKKLSSETLSIPLSEAKSYIEAYFKRFPISKDYLNGMREEILKTSKAFTLLGRYRV-F	794
sp Q9CDS1	DPO1_LACLA	GISDFGLARNLGITRKDAKNYIETFYERFPGIKNYMENIVREARDKGFVETMSHRRRKIP	775
sp P59199	DPO1_STRPN	GISDFGLSNNLGISRKEAKAYIDTYFERFPGIKNYMEDVVRAREKQGYVETLTKRRREL	775
sp Q981G2	DPO1_RHILE	GISAFGLANQLSIERSEAGDYIKKYFERFPGIRDYMSKAMARDKGVVETIFGRRIINYP	908



sp Q92GB7 DPO1_RICCN	GISAFGLAKQLNVTNGEASEYIKKYFAEYKGVQEYMEQTKAFASSNGVITNCFGRKCFVP	775
sp Q0A551 DPO1_MYCBO	GLSAYGLSQQLKISTEEANEQMDYAFARFGGVDRYLAVMERARQDQYSTVLGRRRYL	801
sp PH87H0 DPO1_PSEAE	GMSAFGLAKQIGVERKEAQAYIDRYFARYPGVLVAMERTRAQAEQGFVETLFGRRLYL	811
sp Q04957 DPO1_BACCA	GISDYGLAQLNLNISRKEAAEFIERYFESFPGVKRYMENIVQEAKQKGYVTTLLHRRRYL	775
sp P46835 DPO1_MYCLE	GLSAYGLATLQKISTEEAKLMQIEYFARFGGVDRYLDVMEQARQDQYSTVLGRRRYL	808
sp P52027 DPO1_DEIRA	GMSAHRLSNDLGIPYAEAAQTFEIFYATPYGRIYRINMHTDVGTHGVETLGGRRRYVP	856

[illegible]

sp P52026	DP01_BACST	DITSRNFNVRSFAERTAMNTPIQGSAAIDIKKAMIDLSVRLREERL--QARLLLQVHDEL	832
sp P00582	DP01_ECOLI	DIKSSNGARRAAEAERAINAPMQGTAAIDIKRAMTAVDAWLQAQBP--RVRMTMQVHDEL	884
sp P0A550	DP01_MYCTU	ELDSSNRQVREAAEAERALNAPIQGSAAIDIKVAMIQVDKALNEAQL--ASRMLLQVHDEL	859
sp Q34996	DP01_BACSU	ELTSRNFVIRSAERTAMNTPIQGSAAIDIKKAMIDMAKLEKQL--KARLLQVHDEL	836
sp Q9F173	DP01_SALTY	DIKSSNAARRAGAERAAINAPMQGTAAIDIKRAMTAVDAWLQAQBP--RVRMTMQVHDEL	884
sp P59200	DP01_STRR6	DINSRNFNIRGFAERTAINSPIQGSAADILKIAMIQLDKALVAGGY--QTKMLLQVHDEI	833
sp Q32801	DP01_LACLM	DINARNFNVRGFAERTAINSPIQGSAADILKIAMINLKDALTERQP--KSKLLLQVHDEI	833
sp P34741	DP01_HAEIN	DINSSNAMRRKAERAINAPMQGTAAIDIKRAMIKLDEVIHRDS--DIEMTMQVHDEL	886
sp Q9ZJE9	DP01_HELPJ	DFTGVNDYVKGNYLREGVNAIFQGSADLLKLGLMKVSERFKN-NP--SVRLLLQVHDEL	851
sp Q9CDS1	DP01_LACLA	DINARNFNVRGFAERTAINSPIQGSAADILKIAMINLKDALSARDF--KSKLLLQVHDEI	833
sp P59199	DP01_STRPN	DINSRNFNIRGFAERTAINSPIQGSAADILKIAMIQLDKALVAGGY--QTKMLLQVHDEI	833
sp Q9S1G2	DP01_RHILE	EIRSSNPVSRAFNERAAINAPIQGSAAADVIRRAMIKIEPALVEVGLADVRMLLQVHDEL	968
sp Q92GB7	DP01_RICCN	L1HDK--KLKQFAERAARAINPIGTNTDIIKIAMINLDQIEKRKL--KTRVLVQIHDEL	831
sp P0A551	DP01_MYCBO	ELDSSNRQVREAAEAERALNAPIQGSAAIDIKVAMIQVDKALNEAQL--ASRMLLQVHDEL	859
sp Q9HT80	DP01_PSEAE	EIHSKNGAMRKAERTAINAPMQGTAAIDIMKRAMVAVDNWLQESGL--DARVILQVHDEL	869
sp Q04957	DP01_BACCA	DITSRNFVIRSAERAMALNAPIQGSAAIDIKKAMIDLNARLKKEERL--QARLLLQVHDEL	833
sp P46835	DP01_MYCLE	ELDSSNRQIREAAERAAALNAPIQGSAAIDIKVAMTAVDKSLKQAKL--ASRMLLQVHDEL	866
sp P52027	DP01_DEIRA	GLSSNRNVORAEERLAYNMPIOGTAAIDIMKLAMVOLDPOLDA--I--GARMLOVHDEL	912

* * *

sp P52026 DP01_BACST	ILEAPKEEIERLCRLVPEVME-QA----	VTLRVPLKVDYHYGPTWYD-AK	876
sp P00582 DP01_ECOLI	VFEVHKDDVDAVAQIHLQME-NC----	TRLDPVLLVEVGSGENWDQ-AH	928
sp P0A550 DP01_MYCTU	LFEIAPGERERVEALVRDKMG-GA----	YPLDVPLEVSVMGVGRSWDAAA	904
sp Q34996 DP01_BACSU	IFEAPKEEIEILEKLVPEVME-HA----	LALDVLKVDVFASGSPWYD-AK	880
sp Q9F173 DP01_SALTY	VFEVHKDDLDAVAKRIHQLME-NC----	TRIDVPLLVVEVGSGENWDQ-AH	928
sp P59200 DP01_STRR6	VLEVPKSELVEMKKLVKQTM-EA----	IQLSVPLIADENEGATWYE-AK	877
sp Q32801 DP01_LACLM	ILDVPLEELEDIKALVQTM-EA----	IELAVPLKVDVNTGKTWYE-AK	877
sp P43741 DP01_HAEIN	VFEVRSKEKVAFFREQIKQHME-AA----	AELVPLLVKVDVNTGQNWDE-AH	930
sp Q9ZJE9 DP01_HELPJ	IFEETENAPELQEQEIQRILNDEV----	YPLRVPLETSAFIAKRWNLKG	897
sp Q9CDS1 DP01_LACLA	ILDVPLEELEDIKVLVKQTM-EA----	IELAVPLKVDENTGKTWYE-AK	877
sp P59199 DP01_STRPN	VLEVPKSELVEMKKLVKQTM-EA----	IQLSVPLIADENEGATWYE-AK	877
sp Q9S1G2 DP01_RHILE	IFEVEDQVKEKMPVIVSVM-EA----	NATPALEMRVPLRDVARAATNWDE-AH	1016
sp Q92GB7 DP01_RICCN	LFEAPIDEVEIITPIIKKIME-NS----	TNMAVPIITEIRAGNNWME-IH	875
sp P0A551 DP01_MYCBO	LFEIAPGERERVEALVRDKMG-GA----	YPLDVPLEVSVMGVGRSWDAAA	904
sp Q9HT80 DP01_PSEAE	VLEVREDLVQVCEGIRPLMS-GA----	ATLDVPLVVEAGVGSNWDE-AH	913
sp Q04957 DP01_BACCA	ILEAPKEEIERLCRLVPEVME-QA----	VTLRVPLKVDYHYGSTWYD-AK	877
sp P46835 DP01_MYCLE	LFEVAIGEREQIEAMVQMG-SA----	YPLDVPLEVSVMGVGRSWGAAA	911
sp P52027 DP01_DEIRA	LIEAPLDKAEQVAALTKVME-NV----	VQLKVLAVEVGTGPNWFD-TK	956

SDI Review Form 1.6

SCIENCEDOMAIN international
www.sciencedomain.org



:::

:

: **: . . . *