

> [Pdb|1IX1|A](#) S Chain A, Crystal Structure Of P.Aeruginosa Peptide Deformylase Complexed With Antibiotic Actinonin

[Pdb|1IX1|B](#) S Chain B, Crystal Structure Of P.Aeruginosa Peptide Deformylase Complexed With Antibiotic Actinonin
Length=171

Score = 140 bits (354), Expect = 2e-34, Method: Compositional matrix adjust.
Identities = 84/184 (45%), Positives = 115/184 (62%), Gaps = 19/184 (10%)

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Query 1  ALLEIIHYPSKILRTISKEVVSFDAKLHQQLDDMYETMIASEGIGLAATQVGLPLRLMLII 60
          A+L I+ +P LRTI+K V D + Q +DDM+ETM + GIGLAA QV + R+++
Sbjct 2  AILNILEFPDPRRLRTIAKPVEVVDVAVRQLIDDMFETMYEAPGIGLAATQVNVHKRIVVM 61

Query 61  NLPQEDGVQHKEDCLEIINPKFIETGGSM-NYKEGCLSVPGFYEEVERFEKVKIEYQNR- 118
          +L ++ K + INP+F M Y+EGCLSVPGFY V+R +KV+I+ +R
Sbjct 62  DLSQD-----KSEPRVFINPEFEPLTEDMDQYQEGCLSVPGFYENVDRPQKVRKALDRD 116

Query 119 ---FAEVKVLASELLAVAIQHEIDHLNGVLFVDKLSILKRRKFEKELKELOKKQKHKLE 175
          F EV A LLAV IGHEDHLNG LEVD LS LKR + K+L +++H+ +
Sbjct 117 GNPFEV-----AEGLLAVCIQHEIDHLNGKLFVDYLSTLKRDRIRKLI-----EKQHRQQ 167

Query 176 HHHH 179
          HHH
Sbjct 168 AHHH 171

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Inferred conserved binding residues		
Inferred binding site of Peptide deformylase of <i>P.aeruginosa</i> (PDB:1IX1)	<i>Helicobacter pylori</i> Peptide deformylase residues mapped from 1IX1	Observed binding site of <i>Helicobacter pylori</i> Peptide deformylase (PDB-1EW5)
P43 G44 I45 G46	E G I G	E42 G43 I44 G45
Q51	Q	Q50
Y88 Q89 E90 G91 C92 L93	Y K E G C L	Y91 K92 E93 G94 C95 L96
Y99	Y	Y102
V130 C131	V A	V133 A134
H134 E135	H E	H137 E138
H138	H	H141