



STRUCTURAL BIOLOGY  
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**Supporting information for article:**

**Structure of a fungal form of aspartate semialdehyde  
dehydrogenase from *Aspergillus fumigatus***

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**Table S1** Cloning Details

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Source organism	<i>Aspergillus fumigatus</i> (Strain: Af293)
DNA source	Synthetic DNA (codon optimized)
Cloning vector	pET-28a+
Expression vector	pET-28a+
Expression host	<i>E. coli</i> BL21 DE3

Complete amino acid sequence of the construct produced:

MGMASYPKKKCGVLGATGSVGQRFILLADHPFLELHAIGASNRSAGKKYKDA  
VRWKQTTAMSERLSNLVLRDCRADQFSDCDLVFSGLNSDVAGEIEMEFIKAEIPV  
FSNAKNYRKHPLVPLVVPTVNPQHLDLIPHQRKEFGLKKGFLVCNSNCAVIGVVI  
PFAALQAKFGPVEEVEVFTEQAVSGAGYPGVPSMDIMDNVIPYISGEEDKLENEA  
QKILGSLNADATAFDEQKGLTVGATCTRVGVTDGHMAFVSLRFKNRPGPSAEEV  
KQAMREYQSEAQKLGCPSPREAIKVFDEPDRPQPRLDRDISKGYTVSVGRVRE  
AAPGSYFDLRFALSHNTVIGAAGSSILNAEVAVIKGYILEHHHHHH

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**MASCOT Search Results**
**Protein View: gi|71000471**aspartate-senialdehyde dehydrogenase [*Aspergillus fumigatus* Af293]

**Database:** NCBIInr  
**Score:** 191  
**Expect:** 3.3e-13  
**Nominal mass (M<sub>r</sub>):** 39405  
**Calculated pI:** 6.67  
**Taxonomy:** [Aspergillus fumigatus Af293](#)

This protein sequence matches the following other entries:

- [gi|66852560](#) from [Aspergillus fumigatus Af293](#)
- [gi|159127936](#) from [Aspergillus fumigatus A1163](#)
- [gi|666428770](#) from [Aspergillus fumigatus var. RP-2014](#)

Sequence similarity is available as [an NCBI BLAST search of gi|71000471 against nr.](#)**Search parameters**

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Variable modifications:** [Oxidation \(M\)](#)  
**Mass values searched:** 63  
**Mass values matched:** 21

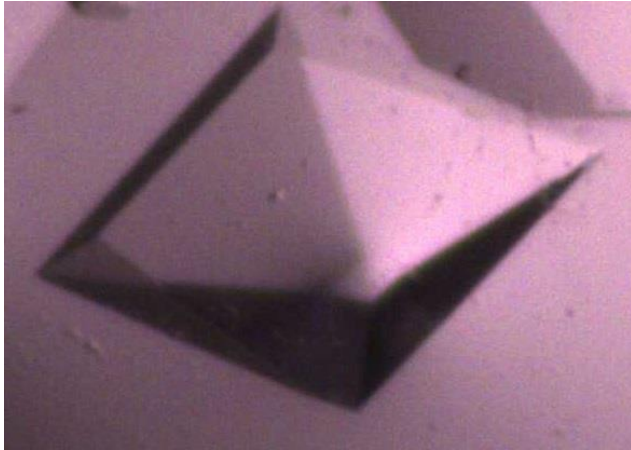
**Protein sequence coverage: 59%**Matched peptides shown in **bold red**.

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1  MASYPKKKCG VLGATGSVGQ RFILLLADHP FLELHAIGAS NRSAGKKYKD
51 AVRWKQTTAM SERLSNLVLR DCRADQFSDC DLVFSGLNSD VAGEIEMEFI
101 KAEIPVFSNA KNYRKHPLVP LVVPTVNPQH LDLIPHQRKE FGLKKGFLVC
151 NSNCAVIGVV IPFAALQAKF GPVEEVEVFT EQAVSGAGYP GVPSMDIMDN
201 VIPYISGEED KLENEAQKIL GSLNADATF DEQKGLTVGA TCTRVGVTDG
251 HMAFVSLRFK NRPGPSAEV KQAMREYQSE AQKLGCPSPAP REAIKVFDEP
301 DRPQPRLDRD ISKGYTVSVG RVREAAPGSY FDLRFAALSH NTVIGAAGSS
351 ILNAEVAVIK GYI
  
```

Unformatted sequence string: [363 residues](#) (for pasting into other applications).

**Figure S1** MASCOT search results of the cleaved peptides by trypsin using MALDI-TOF/TOF spectrophotometer. Protein sequence coverage was found to be 59%



**Figure S2** A typical crystal of *A. fumigatus* ASADH (~40  $\mu\text{m}$  on each edge)