1as8
Evolutionary trace report by report_maker
March 30, 2010

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1 INTRODUCTION

From the original Protein Data Bank entry (PDB id 1as8):

Title: Structure of nitrite bound to reduced alcaligenes faecalis nitrite reductase at cryo temperature

Compound: Mol id: 1; molecule: nitrite reductase; chain: a, b, c; ec: 1.7.99.3; engineered: yes

Organism, scientific name: Alcaligenes Faecalis;

1as8 contains a single unique chain 1as8A (336 residues long) and its homologues 1as8C and 1as8B.

2 CHAIN 1AS8A

2.1 P38501 overview

From SwissProt, id P38501, 96% identical to 1as8A:

Description: Copper-containing nitrite reductase precursor (EC 1.7.2.1) (Cu-NIR).

Organism, scientific name: Alcaligenes faecalis.

Taxonomy: Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Alcaligenes.

Catalytic activity: Nitric oxide + H(2)O + ferricytochrome c = nitrite + ferrocytochrome c.

Cofactor: Contains 1 cuprous ion, 1 cupric ion and FAD. The cuprous ion is bound within a single monomer, while the cupric ion is held by residues from each of two monomers of the trimer. Nitrite is bound to the cupric ion site. Pseudoazurin is the physiological electron donor for the Cu-NIR in vitro (By similarity).

Pathway: Nitrate assimilation (denitrification).

Subunit: Homotrimer.

Subcellular location: Periplasmic.

Induction: Under anaerobic growth conditions and by nitrite.

Domain: The type I copper site in NIR plays a crucial role for electron transfer from pseudoazurin to the type II copper site of NIR, which comprises the catalytic center of NIR for the reduction of nitrite.

Similarity: Belongs to the multicopper oxidase family.

Similarity: Contains 2 plastocyanin-like domains.

About: This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

Lichtarge lab 2006
2.2 Multiple sequence alignment for 1as8A

For the chain 1as8A, the alignment 1as8A.msf (attached) with 33 sequences was used. The alignment was downloaded from the HSSP database, and fragments shorter than 75% of the query as well as duplicate sequences were removed. It can be found in the attachment to this report, under the name of 1as8A.msf. Its statistics, from the alstat program are the following:

<table>
<thead>
<tr>
<th>Format:</th>
<th>MSF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of sequences:</td>
<td>33</td>
</tr>
<tr>
<td>Total number of residues:</td>
<td>11003</td>
</tr>
<tr>
<td>Smallest:</td>
<td>326</td>
</tr>
<tr>
<td>Largest:</td>
<td>336</td>
</tr>
<tr>
<td>Average length:</td>
<td>333.4</td>
</tr>
<tr>
<td>Alignment length:</td>
<td>336</td>
</tr>
<tr>
<td>Average identity:</td>
<td>68%</td>
</tr>
<tr>
<td>Most related pair:</td>
<td>96%</td>
</tr>
<tr>
<td>Most unrelated pair:</td>
<td>56%</td>
</tr>
<tr>
<td>Most distant seq:</td>
<td>63%</td>
</tr>
</tbody>
</table>

Furthermore, 30% of residues show as conserved in this alignment.

The alignment consists of 39% prokaryotic sequences. (Descriptions of some sequences were not readily available.) The file containing the sequence descriptions can be found in the attachment, under the name 1as8A.descr.

2.3 Residue ranking in 1as8A

The 1as8A sequence is shown in Figs. 1–2, with each residue colored according to its estimated importance. The full listing of residues in 1as8A can be found in the file called 1as8A.ranks_sorted in the attachment.

2.4 Top ranking residues in 1as8A and their position on the structure

In the following we consider residues ranking among top 31% of residues in the protein (the closest this analysis allows us to get to 25%). Figure 3 shows residues in 1as8A colored by their importance: bright red and yellow indicate more conserved/important residues (see Appendix for the coloring scheme). A Pymol script for producing this figure can be found in the attachment.

Table 1.

<table>
<thead>
<tr>
<th>cluster color</th>
<th>size</th>
<th>member residues</th>
</tr>
</thead>
</table>

continued in next column
Trace results are commonly expressed in terms of coverage: the residue is important if its “coverage” is small - that is if it belongs to some small top percentage of residues [100% is all of the residues in a chain], according to trace. The ET results are presented in the form of a table, usually limited to top 25% percent of residues (or to some nearby percentage), sorted by the strength of the presumed evolutionary pressure. (I.e., the smaller the coverage, the stronger the pressure on the residue.) Starting from the top of that list, mutating a couple of residues should affect the protein somehow, with the exact effects to be determined experimentally.

### 3.2 Known substitutions

One of the table columns is “substitutions” - other amino acid types seen at the same position in the alignment. These amino acid types may be interchangeable at that position in the protein, so if one wants to affect the protein by a point mutation, they should be avoided. For example if the substitutions are “RVk” and the original protein has an R at that position, it is advisable to try anything, but RVK. Conversely, when looking for substitutions which will not affect the protein, one may try replacing, R with K, or (perhaps more surprisingly), with V. The percentage of times the substitution appears in the alignment is given in the immediately following bracket. No percentage is given in the cases when it is smaller than 1%. This is meant to be a rough guide - due to rounding errors these percentages often do not add up to 100%.

### 3.3 Surface

To detect candidates for novel functional interfaces, first we look for residues that are solvent accessible (according to DSSP program) by at least 10Å², which is roughly the area needed for one water molecule to come in the contact with the residue. Furthermore, we require that these residues form a “cluster” of residues which have neighbor within 5Å from any of their heavy atoms.

Note, however, that, if our picture of protein evolution is correct, the neighboring residues which are not surface accessible might be equally important in maintaining the interaction specificity - they should not be automatically dropped from consideration when choosing the set for mutagenesis. (Especially if they form a cluster with the surface residues.)

### 3.4 Number of contacts

Another column worth noting is denoted “noc/bb”; it tells the number of contacts heavy atoms of the residue in question make across the interface, as well as how many of them are realized through the backbone atoms (if all or most contacts are through the backbone, mutation presumably wont have strong impact). Two heavy atoms are considered to be “in contact” if their centers are closer than 5Å.

### 3.5 Annotation

If the residue annotation is available (either from the pdb file or from other sources), another column, with the header “annotation” appears. Annotations carried over from PDB are the following: site (indicating existence of related site record in PDB ), S-S (disulfide bond forming residue), hb (hydrogen bond forming residue), jb (james bond forming residue), and sb (for salt bridge forming residue).

### 3.6 Mutation suggestions

Mutation suggestions are completely heuristic and based on complementarity with the substitutions found in the alignment. Note that they are meant to be disruptive to the interaction of the protein with its ligand. The attempt is made to complement the following properties: small \{AVGSTC\}, medium \{LPNQDEMIK\}, large \{WFYHR\}, hydrophobic \{LPVAMWFI\}, polar \{GTCY\}; positively \{KHR\}, or negatively \{DE\} charged, aromatic \{WFYH\}, long aliphatic chain \{EKVRQM\}, OH-group possession \{SDETY\}, and NH2 group possession \{NQRK\}. The suggestions are listed according to how different they appear to be from the original amino acid, and they are grouped in round brackets if they appear equally disruptive. From left to right, each bracketed group of amino acid types resembles more strongly the original (i.e. is, presumably, less disruptive) These suggestions are tentative - they might prove disruptive to the fold rather than to the interaction. Many researcher will choose, however, the straightforward alanine mutations, especially in the beginning stages of their investigation.
4 APPENDIX

4.1 File formats

Files with extension “ranks_sorted” are the actual trace results. The fields in the table in this file:

- **alignment#** number of the position in the alignment
- **residue#** residue number in the PDB file
- **type** amino acid type
- **rank** rank of the position according to older version of ET
- **variability** has two subfields:
  1. number of different amino acids appearing in in this column of the alignment
  2. their type
- **rho** ET score - the smaller this value, the lesser variability of this position across the branches of the tree (and, presumably, the greater the importance for the protein)
- **covg** coverage - percentage of the residues on the structure which have this rho or smaller
- **gaps** percentage of gaps in this column

4.2 Color schemes used

The following color scheme is used in figures with residues colored by the estimated evolutionary pressure they experience can be seen in Fig. 5. A percent pairwise alignment identity is defined as (idents / MIN(len1, len2)) where idents is the number of exact identities and len1, len2 are the unaligned lengths of the two sequences. The “average percent identity”, “most related pair”, and “most unrelated pair” of the alignment are the average, maximum, and minimum of all (N(N-1))/2 pairs, respectively. The “most distant seq” is calculated by finding the maximum pairwise identity (best relative) for all N sequences, then finding the minimum of these N numbers (hence, the most outlying sequence).

![Color scheme used to color residues by their relative importance.]

Fig. 5. Coloring scheme used to color residues by their relative importance.

4.3 Credits

**Alistat** *alistat* reads a multiple sequence alignment from the file and shows a number of simple statistics about it. These statistics include the format, the number of sequences, the total number of residues, the average and range of the sequence lengths, and the alignment length (e.g. including gap characters). Also shown are some percent identities. A percent pairwise alignment identity is defined as (idents / MIN(len1, len2)) where idents is the number of exact identities and len1, len2 are the unaligned lengths of the two sequences. The “average percent identity”, “most related pair”, and “most unrelated pair” of the alignment are the average, maximum, and minimum of all (N(N-1))/2 pairs, respectively. The “most distant seq” is calculated by finding the maximum pairwise identity (best relative) for all N sequences, then finding the minimum of these N numbers (hence, the most outlying sequence).

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4.3.2 **CE** To map ligand binding sites from different source structures, report_maker uses the CE program: http://cl.sdsc.edu/. Shindyalov IN, Bourne PE (1998) “Protein structure alignment by incremental combinatorial extension (CE) of the optimal path.” Protein Engineering 11(9) 739-747.

4.3.3 **DSSP** In this work a residue is considered solvent accessible if the DSSP program finds it exposed to water by at least 10Å², which is roughly the area needed for one water molecule to come in the contact with the residue. DSSP is copyrighted by W. Kabsch, C. Sander and MPI-MF, 1983, 1985, 1988, 1994 1995, CMBI version by Elmar.Krieger@cbmi.kun.nl November 18, 2002, http://www.cmbi.kun.nl/gv/dssp/descrip.html.


4.3.5 **LaTeX** The text for this report was processed using LATEX; Leslie Lamport, “LaTeX: A Document Preparation System Addison-Wesley,” Reading, Mass. (1986).


4.3.7 **Pymol** The figures in this report were produced using Pymol. The scripts can be found in the attachment. Pymol is an open-source application copyrighted by DeLano Scientific LLC (2005). For more information about Pymol see http://pymol.sourceforge.net/. (Note for Windows users: the attached package needs to be unzipped for Pymol to read the scripts and launch the viewer.)

4.4 **Note about ET Viewer**

Dan Morgan from the Lichtarge lab has developed a visualization tool specifically for viewing trace results. If you are interested, please visit:

http://mammoth bcm tmc edu/traceview/
The viewer is self-unpacking and self-installing. Input files to be used with ETV (extension .etvx) can be found in the attachment to the main report.

4.5 Citing this work


4.6 About report_maker

report_maker was written in 2006 by Ivana Mihaela. The 1D ranking visualization program was written by Ivica Reš. report_maker is copyrighted by Lichtarge Lab, Baylor College of Medicine, Houston.

4.7 Attachments

The following files should accompany this report:
- 1as8A.complex.pdb - coordinates of 1as8A with all of its interacting partners
- 1as8A.etvx - ET viewer input file for 1as8A
- 1as8A.cluster_report.summary - Cluster report summary for 1as8A
- 1as8A.ranks - Ranks file in sequence order for 1as8A
- 1as8A.clusters - Cluster descriptions for 1as8A
- 1as8A.msf - the multiple sequence alignment used for the chain 1as8A
- 1as8A.descr - description of sequences used in 1as8A msf
- 1as8A.ranks_sorted - full listing of residues and their ranking for 1as8A