1ag0
Evolutionary trace report by report_maker
September 26, 2008

1 INTRODUCTION

From the original Protein Data Bank entry (PDB id 1ag0):
Title: Structure of cys 112 asp azurin from pseudomonas aeruginosa
Compound: Mol id: 1; molecule: azurin; chain: a, b; engineered: yes; mutation: yes
Organism, scientific name: Pseudomonas Aeruginosa;
1ag0 contains a single unique chain 1ag0A (129 residues long) and its homologue 1ag0B.

2 CHAIN 1AG0A

2.1 P00282 overview
From SwissProt, id P00282, 99% identical to 1ag0A:
Description: Azurin precursor.
Organism, scientific name: Pseudomonas aeruginosa.
Taxonomy: Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
Function: Azurin, found in bacteria, is thought to transfer electrons from cytochrome c551 to cytochrome oxidase.
Subcellular location: Periplasmic.
Similarity: Contains 1 plastocyanin-like domain.
Database: NAME=ProZyme technical fact sheet; WWW="http://www.prozyme.com/technical/".
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.

2.2 Multiple sequence alignment for 1ag0A
For the chain 1ag0A, the alignment 1ag0A.msf (attached) with 22 sequences was used. The alignment was assembled through combination of BLAST searching on the UniProt database and alignment using Muscle program. It can be found in the attachment to this report, under the name of 1ag0A.msf. Its statistics, from the alistat program are the following:

CONTENTS

1 Introduction

2 Chain 1ag0A
  2.1 P00282 overview
  2.2 Multiple sequence alignment for 1ag0A
  2.3 Residue ranking in 1ag0A
  2.4 Top ranking residues in 1ag0A and their position on the structure
    2.4.1 Clustering of residues at 25% coverage.
    2.4.2 Overlap with known functional surfaces at 25% coverage.
    2.4.3 Possible novel functional surfaces at 25% coverage.

3 Notes on using trace results
  3.1 Coverage
  3.2 Known substitutions
  3.3 Surface
  3.4 Number of contacts
  3.5 Annotation
  3.6 Mutation suggestions

4 Appendix
  4.1 File formats
  4.2 Color schemes used
  4.3 Credits

4.3.1 Alistat
4.3.2 CE
4.3.3 DSSP
4.3.4 HSSP
4.3.5 LaTex
4.3.6 Muscle
4.3.7 Pymol
4.4 Note about ET Viewer
4.5 Citing this work
4.6 About report_maker
4.7 Attachments
Fig. 1. Residues 1-129 in 1ag0A colored by their relative importance. (See Appendix, Fig.8, for the coloring scheme.)

Format: MSF
Number of sequences: 22
Total number of residues: 2816
Smallest: 120
Largest: 129
Average length: 128.0
Alignment length: 129
Average identity: 54%
Most related pair: 97%
Most unrelated pair: 36%
Most distant seq: 54%
Furthermore, 10% of residues show as conserved in this alignment.
The alignment consists of 95% 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 1ag0A.descr.

2.3 Residue ranking in 1ag0A

The 1ag0A sequence is shown in Fig. 1, with each residue colored according to its estimated importance. The full listing of residues in 1ag0A can be found in the file called 1ag0A.ranks.sorted in the attachment.

2.4 Top ranking residues in 1ag0A and their position on the structure

In the following we consider residues ranking among top 25% of residues in the protein. Figure 2 shows residues in 1ag0A 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.

2.4.1 Clustering of residues at 25% coverage. Fig. 3 shows the top 25% of all residues, this time colored according to clusters they belong to. The clusters in Fig.3 are composed of the residues listed in Table 1.

![Fig. 2. Residues in 1ag0A, colored by their relative importance. Clockwise: front, back, top and bottom views.](image)

![Fig. 3. Residues in 1ag0A, colored according to the cluster they belong to: red, followed by blue and yellow are the largest clusters (see Appendix for the coloring scheme). Clockwise: front, back, top and bottom views. The corresponding Pymol script is attached.](image)

<table>
<thead>
<tr>
<th>cluster color</th>
<th>size</th>
<th>member residues</th>
</tr>
</thead>
<tbody>
<tr>
<td>red</td>
<td>27</td>
<td>12,14,34,36,38,45,46,47,48</td>
</tr>
<tr>
<td></td>
<td></td>
<td>50,56,64,68,73,78,80,81,83</td>
</tr>
<tr>
<td></td>
<td></td>
<td>85,89,91,112,113,115,116,118</td>
</tr>
<tr>
<td></td>
<td></td>
<td>122</td>
</tr>
</tbody>
</table>

Table 1. Clusters of top ranking residues in 1ag0A.
2.4.2 Overlap with known functional surfaces at 25% coverage. The name of the ligand is composed of the source PDB identifier and the heteroatom name used in that file. Copper (ii) ion binding site. Table 2 lists the top 25% of residues at the interface with 1ag0ACU129 (copper (ii) ion). The following table (Table 3) suggests possible disruptive replacements for these residues (see Section 3.6).

<table>
<thead>
<tr>
<th>res</th>
<th>type</th>
<th>subst's (%</th>
<th>cvg</th>
<th>noc/ bb</th>
<th>dist (Å)</th>
</tr>
</thead>
<tbody>
<tr>
<td>46</td>
<td>G</td>
<td>G (100)</td>
<td>0.11</td>
<td>4/4</td>
<td>2.62</td>
</tr>
<tr>
<td>47</td>
<td>H</td>
<td>H (100)</td>
<td>0.11</td>
<td>9/3</td>
<td>2.07</td>
</tr>
<tr>
<td>48</td>
<td>N</td>
<td>N (100)</td>
<td>0.11</td>
<td>1/1</td>
<td>4.44</td>
</tr>
<tr>
<td>113</td>
<td>D</td>
<td>C (95)</td>
<td>0.12</td>
<td>5/1</td>
<td>1.87</td>
</tr>
<tr>
<td>115</td>
<td>F</td>
<td>F (95)</td>
<td>0.12</td>
<td>3/1</td>
<td>4.01</td>
</tr>
<tr>
<td>118</td>
<td>H</td>
<td>H (95)</td>
<td>0.19</td>
<td>7/1</td>
<td>2.06</td>
</tr>
<tr>
<td>122</td>
<td>M</td>
<td>M (95)</td>
<td>0.19</td>
<td>2/0</td>
<td>3.48</td>
</tr>
</tbody>
</table>

Table 2. The top 25% of residues in 1ag0A at the interface with copper (ii) ion. (Field names: res: residue number in the PDB entry; type: amino acid type; subst's: substitutions seen in the alignment; with the percentage of each type in the bracket; cvg: number of contacts with the ligand, with the number of contacts realized through backbone atoms given in the bracket; noc/ bb: number of contacts with the ligand, with the number of contacts realized through backbone atoms given in the bracket; dist: distance of closest approach to the ligand.)

<table>
<thead>
<tr>
<th>res</th>
<th>type</th>
<th>disruptive mutations</th>
</tr>
</thead>
<tbody>
<tr>
<td>46</td>
<td>G</td>
<td>(KER) (FQMWHD) (NYLPI) (SVA)</td>
</tr>
<tr>
<td>47</td>
<td>H</td>
<td>(E) (TQMMD) (SNKVCLAPIG) (YR)</td>
</tr>
<tr>
<td>48</td>
<td>N</td>
<td>(Y) (FTWH) (SEVCARG) (MD)</td>
</tr>
<tr>
<td>113</td>
<td>D</td>
<td>(R) (FWH) (K) (Y)</td>
</tr>
<tr>
<td>115</td>
<td>F</td>
<td>(K) (E) (Q) (D)</td>
</tr>
<tr>
<td>118</td>
<td>H</td>
<td>(E) (QM) (RD) (NLPI)</td>
</tr>
<tr>
<td>122</td>
<td>M</td>
<td>(Y) (H) (TR) (SCDG)</td>
</tr>
</tbody>
</table>

Table 3. List of disruptive mutations for the top 25% of residues in 1ag0A, that are at the interface with copper (ii) ion.

Figure 4 shows residues in 1ag0A colored by their importance, at the interface with 1ag0ACU129. Interface with 1ag0B. Table 4 lists the top 25% of residues at the interface with 1ag0B. The following table (Table 5) suggests possible disruptive replacements for these residues (see Section 3.6).

<table>
<thead>
<tr>
<th>res</th>
<th>type</th>
<th>subst's (%</th>
<th>cvg</th>
<th>noc/ bb</th>
<th>dist (Å)</th>
</tr>
</thead>
<tbody>
<tr>
<td>14</td>
<td>M</td>
<td>M (95)</td>
<td>0.19</td>
<td>1/0</td>
<td>4.25</td>
</tr>
<tr>
<td>45</td>
<td>M</td>
<td>M (95)</td>
<td>0.19</td>
<td>1/0</td>
<td>4.86</td>
</tr>
</tbody>
</table>

Table 4. continued

<table>
<thead>
<tr>
<th>res</th>
<th>type</th>
<th>subst's (%</th>
<th>cvg</th>
<th>noc/ bb</th>
<th>dist (Å)</th>
</tr>
</thead>
<tbody>
<tr>
<td>73</td>
<td>Y</td>
<td>L (4)</td>
<td>0.21</td>
<td>1/0</td>
<td>4.40</td>
</tr>
<tr>
<td>116</td>
<td>P</td>
<td>P (90)</td>
<td>0.22</td>
<td>25/12</td>
<td>3.43</td>
</tr>
</tbody>
</table>

Table 4. The top 25% of residues in 1ag0A at the interface with 1ag0B. (Field names: res: residue number in the PDB entry; type: amino acid type; subst's: substitutions seen in the alignment; with the percentage of each type in the bracket; cvg: number of contacts with the ligand, with the number of contacts realized through backbone atoms given in the bracket; noc/ bb: number of contacts with the ligand, with the number of contacts realized through backbone atoms given in the bracket; dist: distance of closest approach to the ligand.)

<table>
<thead>
<tr>
<th>res</th>
<th>type</th>
<th>disruptive mutations</th>
</tr>
</thead>
<tbody>
<tr>
<td>14</td>
<td>M</td>
<td>(TY) (SCHRGR) (D) (RE)</td>
</tr>
<tr>
<td>45</td>
<td>M</td>
<td>(Y) (TH) (R) (SCG)</td>
</tr>
<tr>
<td>73</td>
<td>Y</td>
<td>(K) (Q) (EM) (NR)</td>
</tr>
<tr>
<td>116</td>
<td>P</td>
<td>(YR) (H) (TKE) (SCDG)</td>
</tr>
</tbody>
</table>

Table 5. List of disruptive mutations for the top 25% of residues in 1ag0A, that are at the interface with 1ag0B.

Figure 5 shows residues in 1ag0A colored by their importance, at the interface with 1ag0B.
2.4.3 Possible novel functional surfaces at 25% coverage. One group of residues is conserved on the 1ag0A surface, away from (or substantially larger than) other functional sites and interfaces recognizable in PDB entry 1ag0. It is shown in Fig. 6. The right panel shows (in blue) the rest of the larger cluster this surface belongs to.

Another group of surface residues is shown in Fig. 7. The right panel shows (in blue) the rest of the larger cluster this surface belongs to.

The residues belonging to this surface "patch" are listed in Table 8, while Table 9 suggests possible disruptive replacements for these residues (see Section 3.6).

![Fig. 5](image1.png)

**Fig. 5.** Residues in 1ag0A, at the interface with 1ag0B, colored by their relative importance. 1ag0B is shown in backbone representation (See Appendix for the coloring scheme for the protein chain 1ag0A.)

![Fig. 6](image2.png)

**Fig. 6.** A possible active surface on the chain 1ag0A. The larger cluster it belongs to is shown in blue.

<table>
<thead>
<tr>
<th>Table 6. continued</th>
</tr>
</thead>
<tbody>
<tr>
<td>res</td>
</tr>
<tr>
<td>------</td>
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<tr>
<td>81</td>
</tr>
<tr>
<td>80</td>
</tr>
</tbody>
</table>

**Table 6.** Residues forming surface "patch" in 1ag0A.

<table>
<thead>
<tr>
<th>Table 7.</th>
</tr>
</thead>
<tbody>
<tr>
<td>res</td>
</tr>
<tr>
<td>------</td>
</tr>
<tr>
<td>56</td>
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<tr>
<td>83</td>
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<tr>
<td>78</td>
</tr>
<tr>
<td>81</td>
</tr>
<tr>
<td>80</td>
</tr>
</tbody>
</table>

**Table 7.** Disruptive mutations for the surface patch in 1ag0A.

<table>
<thead>
<tr>
<th>Table 8.</th>
</tr>
</thead>
<tbody>
<tr>
<td>res</td>
</tr>
<tr>
<td>------</td>
</tr>
<tr>
<td>12</td>
</tr>
<tr>
<td>36</td>
</tr>
<tr>
<td>38</td>
</tr>
<tr>
<td>115</td>
</tr>
<tr>
<td>91</td>
</tr>
<tr>
<td>14</td>
</tr>
<tr>
<td>45</td>
</tr>
<tr>
<td>118</td>
</tr>
<tr>
<td>73</td>
</tr>
<tr>
<td>116</td>
</tr>
<tr>
<td>68</td>
</tr>
</tbody>
</table>

**Table 8.** Residues forming surface "patch" in 1ag0A.

![Fig. 7](image3.png)

**Fig. 7.** Another possible active surface on the chain 1ag0A. The larger cluster it belongs to is shown in blue.
### Table 9.

**Disruptive mutations for the surface patch in 1ag0A.**

<table>
<thead>
<tr>
<th>res</th>
<th>type</th>
<th>disruptive mutations</th>
</tr>
</thead>
<tbody>
<tr>
<td>12</td>
<td>D</td>
<td>(R) (FWH) (KVVCAG) (TQM)</td>
</tr>
<tr>
<td>36</td>
<td>H</td>
<td>(E) (TQMD) (SNKVCAP) (YR)</td>
</tr>
<tr>
<td>38</td>
<td>G</td>
<td>(KER) (FQMWH) (NYLPI) (SVA)</td>
</tr>
<tr>
<td>115</td>
<td>F</td>
<td>(K) (E) (Q) (D)</td>
</tr>
<tr>
<td>91</td>
<td>G</td>
<td>(R) (KE) (H) (FYQWD)</td>
</tr>
<tr>
<td>14</td>
<td>M</td>
<td>(TY) (SCHR) (D) (KE)</td>
</tr>
<tr>
<td>45</td>
<td>M</td>
<td>(Y) (TH) (R) (SCG)</td>
</tr>
<tr>
<td>118</td>
<td>H</td>
<td>(E) (QM) (KD) (NLPI)</td>
</tr>
<tr>
<td>73</td>
<td>Y</td>
<td>(K) (Q) (EM) (NR)</td>
</tr>
<tr>
<td>116</td>
<td>P</td>
<td>(YR) (H) (TKE) (SQC) (DG)</td>
</tr>
<tr>
<td>68</td>
<td>G</td>
<td>(KR) (E) (QH) (FMW)</td>
</tr>
</tbody>
</table>

### 3 NOTES ON USING TRACE RESULTS

#### 3.1 Coverage

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 10 Å², 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 5 Å 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 won’t 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), and sb (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 [LPNQDEMHIK], large [WFYHR], hydrophobic [LPVAMWF], polar [GTCY]; positively [KHR], or negatively [DE] charged, aromatic [WFYH], long aliphatic chain [EKQRM], OH-group possession [SDETY], and NH2 group possession [NQKR]. 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)
- cvg coverage - percentage of the residues on the structure which have this rho or smaller

4.2 Color schemes used

The following color scheme is used in figures with residues colored by cluster size: black is a single-residue cluster; clusters composed of more than one residue colored according to this hierarchy (ordered by descending size): red, blue, yellow, green, purple, azure, turquoise, brown, coral, magenta, LightSalmon, SkyBlue, violet, gold, turquoise, LightSlateBlue, orchid, RosyBrown, MediumAquamarine, DarkOliveGreen, CornflowerBlue, grey55, burlywood, LimeGreen, tan, DarkOrange, DeepPink, maroon, BlanchedAlmond.

The colors used to distinguish the residues by the estimated evolutionary pressure they experience can be seen in Fig. 8.

4.3 Credits

4.3.1 Alistat listat 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). listat is copyrighted by HHMI/Washington University School of Medicine, 1992-2001, and freely distributed under the GNU General Public License.

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.
by Elmar.Krieger@cmbi.kun.nl November 18,2002,

4.3.4 HSSP Whenever available, report_maker uses HSSP ali-
gnment as a starting point for the analysis (sequences shorter than
75% of the query are taken out, however); R. Schneider, A. de
Daruvar, and C. Sander. “The HSSP database of protein structure-
http://swift.cmbi.kun.nl/hssp/

4.3.5 LaTeX The text for this report was processed using LATEX;
Leslie Lamport, “LATEX: A Document Preparation System Addison-

4.3.6 Muscle When making alignments “from scratch”, report
maker uses Muscle alignment program: Edgar, Robert C. (2004),
“MUSCLE: multiple sequence alignment with high accuracy and
http://www.drive5.com/muscle/

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
The method used to rank residues and make predictions in this report
can be found in Mihalek, I., I. Res, O. Lichtarge. (2004). “A Family of
Evolution-Entropy Hybrid Methods for Ranking of Protein Residues
by Importance” J. Mol. Bio. 336: 1265-82. For the original version
of ET see O. Lichtarge, H.Bourne and F. Cohen (1996). “An Evolution-
ary Trace Method Defines Binding Surfaces Common to Protein
report_maker itself is described in Mihalek I., I. Res and O.
of service for comparative analysis of proteins.” Bioinformatics

4.6 About report_maker
report_maker was written in 2006 by Ivana Mihalek. The 1D ran-
kng 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:

- 1ag0A.complex.pdb - coordinates of 1ag0A with all of its
interacting partners
- 1ag0A.etvx - ET viewer input file for 1ag0A
- 1ag0A.cluster_report.summary - Cluster report summary for
  1ag0A
- 1ag0A.ranks - Ranks file in sequence order for 1ag0A
- 1ag0A.clusters - Cluster descriptions for 1ag0A
- 1ag0A.msf - the multiple sequence alignment used for the chain
  1ag0A
- 1ag0A.descr - description of sequences used in 1ag0A msf
- 1ag0A.ranks_sorted - full listing of residues and their ranking
  for 1ag0A
- 1ag0A.1ag0ACU129.if.pml - Pymol script for Figure 4
- 1ag0A.cbcvg - used by other 1ag0A – related pymol scripts
- 1ag0A.1ag0B.if.pml - Pymol script for Figure 5