1aox
Evolutionary trace report by report_maker
April 9, 2010

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1 INTRODUCTION
From the original Protein Data Bank entry (PDB id 1aox):
Title: I domain from integrin alpha2-beta1
Compound: Mol id: 1; molecule: integrin alpha 2 beta; chain: a, b; fragment: i domain; engineered: yes; mutation: yes
Organism, scientific name: Homo Sapiens:
1aox contains a single unique chain 1aoxA (201 residues long) and its homologue 1aoxB.

2 CHAIN 1AOXA
2.1 P17301 overview
From SwissProt, id P17301, 93% identical to 1aoxA:
Description: Integrin alpha-2 precursor (Platelet membrane glycoprotein Ia) (GPIa) (Collagen receptor) (VLA-2 alpha chain) (CD49b).
Organism, scientific name: Homo sapiens (Human).
Taxonomy: Eukaryota; Metazoa; Chordata; Craniiata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
Function: Integrin alpha-2/beta-1 is a receptor for laminin, collagen, collagen C-propeptides, fibronectin and E-cadherin. It recognizes the proline-hydroxylated sequence G-F-P-G-E-R in collagen. It is responsible for adhesion of platelets and other cells to collagens, modulation of collagen and collagenase gene expression, force generation and organization of newly synthesized extracellular matrix.
Subunit: Heterodimer of an alpha and a beta subunit. Alpha-2 associates with beta-1. Interacts with HP5.
Subcellular location: Type I membrane protein.
Domain: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
Polymorphism: Position 534 is associated with platelet-specific alloantigen HPA-5 (Br). HPA-5A/Br(a) has Lys-534 and HPA-5B/Br(b) has Glu-534. HPA-5B is involved in neonatal alloimmune thrombocytopenia (NAIT or NATP). The Lys-534-Glu polymorphism may play a role in coronary artery disease (CAD).
Similarity: Belongs to the integrin alpha chain family.
Similarity: Contains 7 FG-GAP repeats.
Similarity: Contains 1 VWFA domain.
Fig. 1. Residues 139-238 in 1aoxA colored by their relative importance. (See Appendix, Fig.6, for the coloring scheme.)

Fig. 2. Residues 239-339 in 1aoxA colored by their relative importance. (See Appendix, Fig.6, for the coloring scheme.)

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**2.2 Multiple sequence alignment for 1aoxA**

For the chain 1aoxA, the alignment 1aoxA.msf (attached) with 111 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, under the name of 1aoxA.msf. Its statistics, from the alisstat program are the following:

- **Format:** MSF
- **Number of sequences:** 111
- **Total number of residues:** 19473
- **Smallest:** 93
- **Largest:** 201
- **Average length:** 175.4
- **Alignment length:** 201
- **Average identity:** 33%
- **Most related pair:** 99%
- **Most unrelated pair:** 4%
- **Most distant seq:** 31%

Furthermore, <1% of residues show as conserved in this alignment.

The alignment consists of 58% eukaryotic (.55% vertebrata) sequences. (Descriptions of some sequences were not readily available.) The file containing the sequence descriptions can be found in the attachment, under the name 1aoxA.descr.

**2.3 Residue ranking in 1aoxA**

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

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

In the following we consider residues ranking among top 25% of residues in the protein. Figure 3 shows residues in 1aoxA 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.

**Fig. 3.** Residues in 1aoxA, colored by their relative importance. Clockwise: front, back, top and bottom views.

**2.4.1 Clustering of residues at 25% coverage.** Fig. 4 shows the top 25% of all residues, this time colored according to clusters they belong to. The clusters in Fig.4 are composed of the residues listed in Table 1.

<table>
<thead>
<tr>
<th>cluster color</th>
<th>size</th>
<th>member residues</th>
</tr>
</thead>
<tbody>
<tr>
<td>red</td>
<td>47</td>
<td>145,147,149,151,152,153</td>
</tr>
<tr>
<td></td>
<td></td>
<td>186,187,194,195,197,209</td>
</tr>
<tr>
<td></td>
<td></td>
<td>216,218,221,223,224,226,227</td>
</tr>
<tr>
<td></td>
<td></td>
<td>230,235,240,242,247,248,251</td>
</tr>
<tr>
<td></td>
<td></td>
<td>252,253,254,255,256,257,259</td>
</tr>
<tr>
<td></td>
<td></td>
<td>299,300,303,305,307</td>
</tr>
</tbody>
</table>

**Table 1.** Clusters of top ranking residues in 1aoxA.
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.

Magnesium ion binding site. Table 2 lists the top 25% of residues at the interface with 1aoxMG400 (magnesium ion). The following table (Table 3) suggests possible disruptive replacements for these residues (see Section 3.6).

![Fig. 4](image4.png)

**Fig. 4.** Residues in 1aoxA, 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.

![Table 2](table2.png)

**Table 2.** The top 25% of residues in 1aoxA at the interface with magnesium ion. (Field names: res: residue number in the PDB entry; type: amino acid type; subst: substitutions seen in the alignment; with the percentage of each type 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 3](table3.png)

**Table 3.** List of disruptive mutations for the top 25% of residues in 1aoxA, that are at the interface with magnesium ion.

![Fig. 5](image5.png)

**Fig. 5.** Residues in 1aoxA, at the interface with magnesium ion, colored by their relative importance. The ligand (magnesium ion) is colored green. Atoms further than 30 Å away from the geometric center of the ligand, as well as on the line of sight to the ligand were removed. (See Appendix for the coloring scheme for the protein chain 1aoxA.)

Figure 5 shows residues in 1aoxA colored by their importance, at the interface with 1aoxMG400.
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 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 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), 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 [LPNQDEM1K], large [W FYH R], hydrophobic [LPVAMWFT], polar [GTCY]; positively [KHR], or negatively [DE] charged, aromatic [W FYH], long aliphatic chain [ERKQM], 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)
- **cvg** 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 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, bisque, Light SlateBlue, 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. 6.

4.3 Credits

4.3.1 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).

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

4.7 Attachments

The following files should accompany this report:

- 1aoxA.complex.pdb - coordinates of 1aoxA with all of its interacting partners
- 1aoxA.etvx - ET viewer input file for 1aoxA
- 1aoxA.cluster_report.summary - Cluster report summary for 1aoxA
- 1aoxA.ranks - Ranks file in sequence order for 1aoxA
- 1aoxA.clusters - Cluster descriptions for 1aoxA
- 1aoxA.etvx - ET viewer input file for 1aoxA
- 1aoxA.etvx - ET viewer input file for 1aoxA
- 1aoxA.descr - description of sequences used in 1aoxA msf
- 1aoxA.ranks_sorted - full listing of residues and their ranking for 1aoxA
- 1aoxA.1aoxMG400.if.pml - Pymol script for Figure 5
- 1aoxA.cbcvg - used by other 1aoxA – related pymol scripts