



wwPDB X-ray Structure Validation Summary Report i

Feb 26, 2014 – 10:07 PM GMT

PDB ID : 1ANI
Title : ALKALINE PHOSPHATASE (D153H, K328H)
Authors : Murphy, J.E.; Tibbitts, T.T.; Kantrowitz, E.R.
Deposited on : 1995-09-06
Resolution : 2.50 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

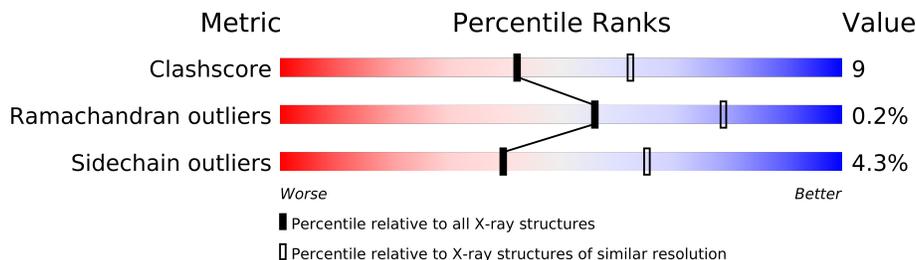
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|---|
| Clashscore | 79885 | 3562 (2.50-2.50) |
| Ramachandran outliers | 78287 | 3480 (2.50-2.50) |
| Sidechain outliers | 78261 | 3482 (2.50-2.50) |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | A | 446 | |
| 1 | B | 446 | |

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6869 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called ALKALINE PHOSPHATASE.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 1 | A | 446 | 3284 | 2030 | 581 | 661 | 12 | 0 | 0 | 0 |
| 1 | B | 446 | 3284 | 2030 | 581 | 661 | 12 | 0 | 0 | 0 |

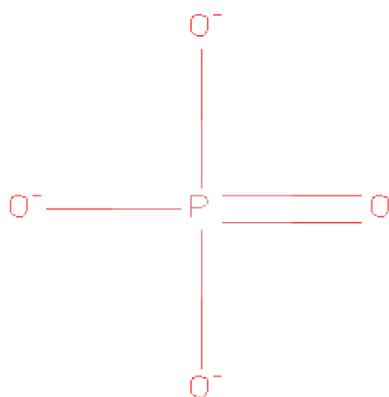
There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|------------|------------|
| A | 153 | HIS | ASP | ENGINEERED | UNP P00634 |
| A | 328 | HIS | LYS | ENGINEERED | UNP P00634 |
| B | 153 | HIS | ASP | ENGINEERED | UNP P00634 |
| B | 328 | HIS | LYS | ENGINEERED | UNP P00634 |

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 2 | B | 3 | Total | Zn | 0 | 0 |
| | | | 3 | 3 | | |
| 2 | A | 3 | Total | Zn | 0 | 0 |
| | | | 3 | 3 | | |

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



| Mol | Chain | Residues | Atoms | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---------|---------|
| 3 | A | 1 | Total | O | P | 0 | 0 |
| | | | 5 | 4 | 1 | | |
| 3 | A | 1 | Total | O | P | 0 | 0 |
| | | | 5 | 4 | 1 | | |
| 3 | A | 1 | Total | O | P | 0 | 0 |
| | | | 5 | 4 | 1 | | |
| 3 | B | 1 | Total | O | P | 0 | 0 |
| | | | 5 | 4 | 1 | | |
| 3 | B | 1 | Total | O | P | 0 | 0 |
| | | | 5 | 4 | 1 | | |

- Molecule 4 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 4 | A | 133 | Total | O | 0 | 0 |
| | | | 133 | 133 | | |
| 4 | B | 137 | Total | O | 0 | 0 |
| | | | 137 | 137 | | |

4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

| Property | Value | Source |
|--|--|-----------|
| Space group | I 2 2 2 | Depositor |
| Cell constants a, b, c, α , β , γ | 194.60Å 167.30Å 76.30Å 90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 8.00 – 2.50 | Depositor |
| % Data completeness (in resolution range) | 91.0 (8.00-2.50) | Depositor |
| R_{merge} | 0.07 | Depositor |
| R_{sym} | (Not available) | Depositor |
| Refinement program | X-PLOR 3.1, IMPLOR, POLYVISION, TIBBITTS | Depositor |
| R, R_{free} | 0.176 , (Not available) | Depositor |
| Estimated twinning fraction | No twinning to report. | Xtrriage |
| Total number of atoms | 6869 | wwPDB-VP |
| Average B, all atoms (Å ²) | 18.0 | wwPDB-VP |

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, PO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|---------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 1 | A | 0.60 | 0/3340 | 0.77 | 3/4534 (0.1%) |
| 1 | B | 0.62 | 0/3340 | 0.77 | 4/4534 (0.1%) |
| All | All | 0.61 | 0/6680 | 0.77 | 7/9068 (0.1%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1 | B | 1 | 0 |

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|------------|-------|-------------|----------|
| 1 | B | 287 | THR | CA-CB-CG2 | 8.62 | 124.47 | 112.40 |
| 1 | A | 128 | ASP | CB-CG-OD1 | 6.10 | 123.79 | 118.30 |
| 1 | B | 248 | GLU | OE1-CD-OE2 | -6.04 | 116.05 | 123.30 |
| 1 | A | 323 | GLY | N-CA-C | -5.33 | 99.78 | 113.10 |
| 1 | B | 287 | THR | OG1-CB-CG2 | 5.15 | 121.85 | 110.00 |

All (1) chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|-----|-------|-----|------|------|
| 1 | B | 287 | THR | CB |

There are no planarity outliers.

5.2 Close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 3284 | 0 | 3222 | 58 | 0 |
| 1 | B | 3284 | 0 | 3223 | 65 | 0 |
| 2 | A | 3 | 0 | 0 | 0 | 0 |
| 2 | B | 3 | 0 | 0 | 0 | 0 |
| 3 | A | 15 | 0 | 0 | 1 | 0 |
| 3 | B | 10 | 0 | 0 | 3 | 0 |
| 4 | A | 133 | 0 | 0 | 4 | 0 |
| 4 | B | 137 | 0 | 0 | 6 | 0 |
| All | All | 6869 | 0 | 6445 | 117 | 0 |

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

The worst 5 of 117 close contacts within the same asymmetric unit are listed below.

| Atom-1 | Atom-2 | Distance(Å) | Clash(Å) |
|-----------------|----------------|-------------|----------|
| 1:A:172:SER:HB2 | 4:A:502:HOH:O | 1.67 | 0.94 |
| 1:B:244:ASN:HA | 1:B:305:LYS:NZ | 1.93 | 0.84 |
| 1:A:244:ASN:HA | 1:A:305:LYS:NZ | 1.94 | 0.81 |
| 1:B:47:LEU:HD23 | 1:B:442:MET:SD | 2.25 | 0.76 |
| 1:A:101:ASP:HB2 | 3:A:453:PO4:O3 | 1.87 | 0.75 |

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------------|-----------|---------|----------|-------------|----|
| 1 | A | 444/446 (100%) | 431 (97%) | 12 (3%) | 1 (0%) | 56 | 79 |
| 1 | B | 444/446 (100%) | 431 (97%) | 12 (3%) | 1 (0%) | 56 | 79 |
| All | All | 888/892 (100%) | 862 (97%) | 24 (3%) | 2 (0%) | 56 | 79 |

All (2) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 293 | ASN |
| 1 | B | 293 | ASN |

5.3.2 Protein sidechains i

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 1 | A | 337/337 (100%) | 323 (96%) | 14 (4%) | 40 | 66 |
| 1 | B | 337/337 (100%) | 322 (96%) | 15 (4%) | 38 | 63 |
| All | All | 674/674 (100%) | 645 (96%) | 29 (4%) | 40 | 65 |

5 of 29 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 446 | LEU |
| 1 | B | 73 | LYS |
| 1 | B | 407 | GLU |
| 1 | B | 40 | LYS |
| 1 | B | 84 | TYR |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 329 | GLN |
| 1 | A | 338 | GLN |
| 1 | B | 276 | HIS |
| 1 | A | 328 | HIS |
| 1 | B | 252 | GLN |

5.3.3 RNA

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 11 ligands modelled in this entry, 6 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|-------------|-------------|------|-------------|
| | | | | | Counts | RMSZ | $\# Z > 2$ | Counts | RMSZ | $\# Z > 2$ |
| 3 | PO4 | A | 453 | - | 4,4,4 | 1.55 | 1 (25%) | 6,6,6 | 0.34 | 0 |
| 3 | PO4 | A | 457 | - | 4,4,4 | 0.89 | 0 | 6,6,6 | 0.33 | 0 |
| 3 | PO4 | A | 458 | - | 4,4,4 | 0.82 | 0 | 6,6,6 | 0.33 | 0 |
| 3 | PO4 | B | 453 | 2 | 4,4,4 | 1.05 | 0 | 6,6,6 | 0.35 | 0 |
| 3 | PO4 | B | 457 | - | 4,4,4 | 1.19 | 0 | 6,6,6 | 0.31 | 0 |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|----------|---------|
| 3 | PO4 | A | 453 | - | - | 0/0/0/0 | 0/0/0/0 |
| 3 | PO4 | A | 457 | - | - | 0/0/0/0 | 0/0/0/0 |
| 3 | PO4 | A | 458 | - | - | 0/0/0/0 | 0/0/0/0 |
| 3 | PO4 | B | 453 | 2 | - | 0/0/0/0 | 0/0/0/0 |
| 3 | PO4 | B | 457 | - | - | 0/0/0/0 | 0/0/0/0 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 3 | A | 453 | PO4 | P-O3 | -2.25 | 1.43 | 1.52 |

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.