



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2IG7
Title : Crystal structure of Human Choline Kinase B
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Vedadi, M.; Arrowsmith, C.H.; Edwards, A.M.; Sundstrom, M.; Weigelt, J.;
Bochkarev, A.; Park, H.; Structural Genomics Consortium (SGC)
Deposited on : 2006-09-22
Resolution : 1.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

| | | |
|--------------------------------|---|--|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 2022.3.0, CSD as543be (2022) |
| Xtriage (Phenix) | : | 1.20.1 |
| EDS | : | FAILED |
| Percentile statistics | : | 20231227.v01 (using entries in the PDB archive December 27th 2023) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.39 |

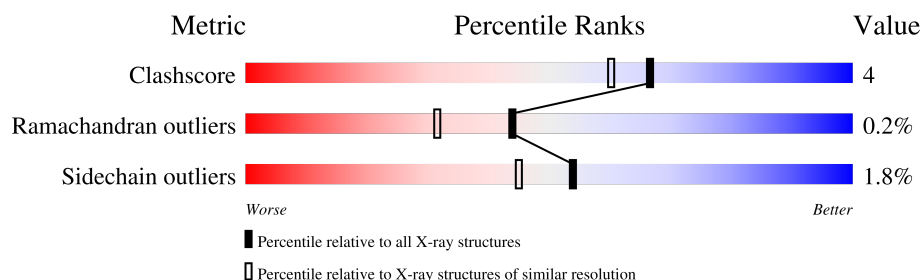
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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 | 180529 | 8162 (1.80-1.80) |
| Ramachandran outliers | 177936 | 8077 (1.80-1.80) |
| Sidechain outliers | 177891 | 8076 (1.80-1.80) |

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS failed to run properly.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | A | 401 | |
| 1 | B | 401 | |

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5895 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Choline/ethanolamine kinase.

| Mol | Chain | Residues | Atoms | | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|----|---------|---------|-------|
| 1 | A | 335 | Total | C | N | O | S | Se | 0 | 9 | 0 |
| | | | 2772 | 1803 | 454 | 501 | 4 | 10 | | | |
| 1 | B | 342 | Total | C | N | O | S | Se | 0 | 13 | 0 |
| | | | 2847 | 1852 | 457 | 524 | 4 | 10 | | | |

There are 38 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|------------------|------------|
| A | -5 | MSE | - | SEE REMARK 999 | UNP Q9Y259 |
| A | -4 | GLY | - | cloning artifact | UNP Q9Y259 |
| A | -3 | SER | - | cloning artifact | UNP Q9Y259 |
| A | -2 | SER | - | cloning artifact | UNP Q9Y259 |
| A | -1 | HIS | - | expression tag | UNP Q9Y259 |
| A | 0 | HIS | - | expression tag | UNP Q9Y259 |
| A | -1 | HIS | - | expression tag | UNP Q9Y259 |
| A | 0 | HIS | - | expression tag | UNP Q9Y259 |
| A | 1 | HIS | - | expression tag | UNP Q9Y259 |
| A | 2 | HIS | - | expression tag | UNP Q9Y259 |
| A | 5 | SER | - | cloning artifact | UNP Q9Y259 |
| A | 6 | SER | - | cloning artifact | UNP Q9Y259 |
| A | 7 | GLY | - | cloning artifact | UNP Q9Y259 |
| A | 8 | LEU | - | cloning artifact | UNP Q9Y259 |
| A | 9 | VAL | - | cloning artifact | UNP Q9Y259 |
| A | 10 | PRO | - | cloning artifact | UNP Q9Y259 |
| A | 11 | ARG | - | cloning artifact | UNP Q9Y259 |
| A | 12 | GLY | - | cloning artifact | UNP Q9Y259 |
| A | 13 | SER | - | cloning artifact | UNP Q9Y259 |
| B | -5 | MSE | - | SEE REMARK 999 | UNP Q9Y259 |
| B | -4 | GLY | - | cloning artifact | UNP Q9Y259 |
| B | -3 | SER | - | cloning artifact | UNP Q9Y259 |
| B | -2 | SER | - | cloning artifact | UNP Q9Y259 |
| B | -1 | HIS | - | expression tag | UNP Q9Y259 |
| B | 0 | HIS | - | expression tag | UNP Q9Y259 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|------------------|------------|
| B | -1 | HIS | - | expression tag | UNP Q9Y259 |
| B | 0 | HIS | - | expression tag | UNP Q9Y259 |
| B | 1 | HIS | - | expression tag | UNP Q9Y259 |
| B | 2 | HIS | - | expression tag | UNP Q9Y259 |
| B | 5 | SER | - | cloning artifact | UNP Q9Y259 |
| B | 6 | SER | - | cloning artifact | UNP Q9Y259 |
| B | 7 | GLY | - | cloning artifact | UNP Q9Y259 |
| B | 8 | LEU | - | cloning artifact | UNP Q9Y259 |
| B | 9 | VAL | - | cloning artifact | UNP Q9Y259 |
| B | 10 | PRO | - | cloning artifact | UNP Q9Y259 |
| B | 11 | ARG | - | cloning artifact | UNP Q9Y259 |
| B | 12 | GLY | - | cloning artifact | UNP Q9Y259 |
| B | 13 | SER | - | cloning artifact | UNP Q9Y259 |

- Molecule 2 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|------------------|---------|---------|
| 2 | A | 8 | Total X 8 8 | 0 | 0 |
| 2 | B | 16 | Total X 16 16 | 0 | 0 |

- Molecule 3 is water.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|--------------------|---------|---------|
| 3 | A | 109 | Total O 109 109 | 0 | 0 |
| 3 | B | 143 | Total O 143 143 | 0 | 0 |

4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

| Property | Value | Source |
|--|---|-----------|
| Space group | P 21 21 21 | Depositor |
| Cell constants a, b, c, α , β , γ | 52.66Å 109.21Å 157.95Å 90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 30.00 – 1.80 | Depositor |
| % Data completeness (in resolution range) | 97.4 (30.00-1.80) | Depositor |
| R_{merge} | 0.07 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 2.90 (at 1.80Å) | Xtriage |
| Refinement program | REFMAC refmac_5.2.0019 | Depositor |
| R, R_{free} | 0.192 , 0.227 | Depositor |
| Wilson B-factor (Å ²) | 25.5 | Xtriage |
| Anisotropy | 0.077 | Xtriage |
| L-test for twinning ² | $\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| Total number of atoms | 5895 | wwPDB-VP |
| Average B, all atoms (Å ²) | 28.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: UNX

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 | 0.79 | 0/2867 | 0.72 | 1/3874 (0.0%) |
| 1 | B | 0.89 | 0/2958 | 0.77 | 2/4002 (0.0%) |
| All | All | 0.84 | 0/5825 | 0.75 | 3/7876 (0.0%) |

There are no bond length outliers.

All (3) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 1 | B | 159 | ARG | NE-CZ-NH2 | 7.76 | 124.18 | 120.30 |
| 1 | B | 159 | ARG | NE-CZ-NH1 | -6.39 | 117.11 | 120.30 |
| 1 | A | 159 | ARG | NE-CZ-NH2 | 5.11 | 122.85 | 120.30 |

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 2772 | 0 | 2662 | 22 | 0 |
| 1 | B | 2847 | 0 | 2737 | 21 | 0 |
| 2 | A | 8 | 0 | 0 | 0 | 0 |
| 2 | B | 16 | 0 | 0 | 0 | 0 |
| 3 | A | 109 | 0 | 0 | 0 | 0 |
| 3 | B | 143 | 0 | 0 | 3 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| All | All | 5895 | 0 | 5399 | 40 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 40 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---------------------|------------------|--------------------------|-------------------|
| 1:B:310[B]:LEU:HD21 | 1:B:339:LEU:HD11 | 1.52 | 0.90 |
| 1:B:310[B]:LEU:CD2 | 1:B:339:LEU:HD11 | 2.13 | 0.78 |
| 1:B:182[B]:THR:HG23 | 3:B:1063:HOH:O | 1.85 | 0.77 |
| 1:B:184[A]:GLU:OE2 | 1:B:186:HIS:NE2 | 2.21 | 0.73 |
| 1:B:156:GLN:O | 1:B:159:ARG:HG2 | 1.90 | 0.71 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

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 | 338/401 (84%) | 327 (97%) | 10 (3%) | 1 (0%) | 37 | 25 |
| 1 | B | 349/401 (87%) | 341 (98%) | 8 (2%) | 0 | 100 | 100 |
| All | All | 687/802 (86%) | 668 (97%) | 18 (3%) | 1 (0%) | 44 | 34 |

All (1) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 89 | ASP |

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 | 289/343 (84%) | 285 (99%) | 4 (1%) | 62 | 56 |
| 1 | B | 302/343 (88%) | 295 (98%) | 7 (2%) | 45 | 34 |
| All | All | 591/686 (86%) | 580 (98%) | 11 (2%) | 54 | 43 |

5 of 11 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|--------|------|
| 1 | B | 244[A] | GLN |
| 1 | B | 244[B] | GLN |
| 1 | B | 380 | PHE |
| 1 | B | 276 | ASP |
| 1 | B | 52 | TRP |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 24 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.