



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3BXJ
Title : Crystal Structure of the C2-GAP Fragment of synGAP
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Deposited on : 2008-01-14
Resolution : 3.00 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 |
| Xtriage (Phenix) | : | 1.20.1 |
| EDS | : | 2.36.2 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.36.2 |

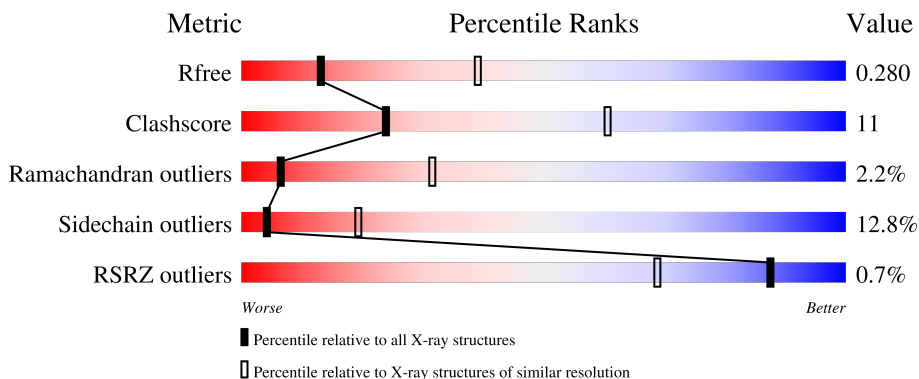
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 3.00 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)) |
|-----------------------|-----------------------------|---|
| R_{free} | 130704 | 2092 (3.00-3.00) |
| Clashscore | 141614 | 2416 (3.00-3.00) |
| Ramachandran outliers | 138981 | 2333 (3.00-3.00) |
| Sidechain outliers | 138945 | 2336 (3.00-3.00) |
| RSRZ outliers | 127900 | 1990 (3.00-3.00) |

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.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 1 | A | 483 |  |
| 1 | B | 483 |  |

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5491 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 Ras GTPase-activating protein SynGAP.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| 1 | A | 348 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2695 | 1711 | 458 | 505 | 21 | | | |
| 1 | B | 358 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2796 | 1774 | 474 | 527 | 21 | | | |



4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | P 61 | Depositor |
| Cell constants a, b, c, α , β , γ | 113.32Å 113.32Å 166.09Å 90.00° 90.00° 120.00° | Depositor |
| Resolution (Å) | 19.97 – 3.00 19.80 – 2.70 | Depositor EDS |
| % Data completeness (in resolution range) | 100.0 (19.97-3.00) 99.5 (19.80-2.70) | Depositor EDS |
| R_{merge} | 0.07 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 1.89 (at 2.71Å) | Xtriage |
| Refinement program | REFMAC | Depositor |
| R, R_{free} | 0.244 , 0.289 0.233 , 0.280 | Depositor DCC |
| R_{free} test set | 1644 reflections (5.00%) | wwPDB-VP |
| Wilson B-factor (Å ²) | 56.4 | Xtriage |
| Anisotropy | 0.023 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.31 , 47.7 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$ | Xtriage |
| Estimated twinning fraction | 0.058 for h,-h-k,-l | Xtriage |
| F_o, F_c correlation | 0.91 | EDS |
| Total number of atoms | 5491 | wwPDB-VP |
| Average B, all atoms (Å ²) | 46.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.14% 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](#)

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 | 0.72 | 1/2738 (0.0%) | 0.74 | 0/3693 |
| 1 | B | 0.76 | 1/2842 (0.0%) | 0.80 | 2/3832 (0.1%) |
| All | All | 0.74 | 2/5580 (0.0%) | 0.77 | 2/7525 (0.0%) |

All (2) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 1 | B | 404 | GLU | CB-CG | 5.81 | 1.63 | 1.52 |
| 1 | A | 537 | CYS | CB-SG | -5.81 | 1.72 | 1.81 |

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|---------|------|-------------|----------|
| 1 | B | 719 | PRO | N-CA-CB | 6.42 | 111.01 | 103.30 |
| 1 | B | 237 | PRO | N-CA-CB | 5.92 | 110.41 | 103.30 |

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 | 2695 | 0 | 2604 | 67 | 0 |
| 1 | B | 2796 | 0 | 2714 | 56 | 0 |
| All | All | 5491 | 0 | 5318 | 120 | 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 11.

The worst 5 of 120 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:470:ARG:O | 1:B:476:THR:HG21 | 1.62 | 1.00 |
| 1:A:470:ARG:O | 1:A:476:THR:HG21 | 1.65 | 0.95 |
| 1:A:462:MET:HA | 1:A:462:MET:HE2 | 1.57 | 0.85 |
| 1:A:462:MET:HA | 1:A:462:MET:CE | 2.10 | 0.82 |
| 1:B:563:GLU:O | 1:B:564:ARG:HB2 | 1.81 | 0.80 |

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 | 338/483 (70%) | 308 (91%) | 22 (6%) | 8 (2%) | 6 | 29 |
| 1 | B | 348/483 (72%) | 318 (91%) | 23 (7%) | 7 (2%) | 7 | 34 |
| All | All | 686/966 (71%) | 626 (91%) | 45 (7%) | 15 (2%) | 6 | 31 |

5 of 15 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 409 | VAL |
| 1 | A | 447 | LYS |
| 1 | A | 494 | ALA |
| 1 | B | 295 | GLU |
| 1 | B | 450 | LEU |

5.3.2 Protein sidechains ⓘ

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 | 278/413 (67%) | 241 (87%) | 37 (13%) | 4 | 17 |
| 1 | B | 294/413 (71%) | 258 (88%) | 36 (12%) | 5 | 21 |
| All | All | 572/826 (69%) | 499 (87%) | 73 (13%) | 4 | 19 |

5 of 73 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | B | 626 | SER |
| 1 | B | 699 | LEU |
| 1 | B | 630 | PHE |
| 1 | B | 670 | LEU |
| 1 | A | 622 | SER |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | B | 541 | ASN |
| 1 | B | 616 | GLN |
| 1 | B | 646 | GLN |
| 1 | B | 425 | ASN |
| 1 | B | 438 | HIS |

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ > 2 | | OWAB(Å ²) | Q < 0.9 |
|-----|-------|---------------|--------|-----------|-----------|-----------------------|---------|
| 1 | A | 348/483 (72%) | -0.57 | 0 | 100 100 | 35, 46, 60, 66 | 0 |
| 1 | B | 358/483 (74%) | -0.51 | 5 (1%) | 75 49 | 36, 46, 55, 65 | 0 |
| All | All | 706/966 (73%) | -0.54 | 5 (0%) | 87 69 | 35, 46, 58, 66 | 0 |

All (5) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | B | 718 | GLN | 3.5 |
| 1 | B | 342 | HIS | 2.7 |
| 1 | B | 627 | LYS | 2.1 |
| 1 | B | 719 | PRO | 2.1 |
| 1 | B | 393 | THR | 2.1 |

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.