# wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 02:45 PM GMT

| | | |
|---|---|---|
| PDB ID | : | 4ACS |
| Title | : | Crystal structure of mutant GST A2-2 with enhanced catalytic efficiency with azathioprine |
| Authors | : | Zhang, W.; Moden, O.; Tars, K.; Mannervik, B. |
| Deposited on | : | 2011-12-19 |
| Resolution | : | 2.10 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

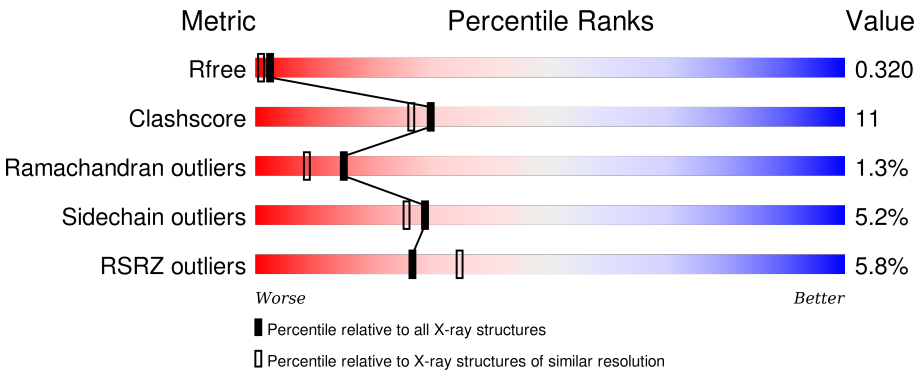
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.7 (RC4), CSD as536be (2015) |
| Xtriage (Phenix) | : | 1.9-1692 |
| EDS | : | rb-20026688 |
| Percentile statistics | : | 20151230.v01 (using entries in the PDB archive December 30th 2015) |
| Refmac | : | 5.8.0135 |
| CCP4 | : | 6.5.0 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | trunk26865 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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)) |
|---|---|---|
| $R_{free}$ | 91344 | 3939 (2.10-2.10) |
| Clashscore | 102246 | 4460 (2.10-2.10) |
| Ramachandran outliers | 100387 | 4413 (2.10-2.10) |
| Sidechain outliers | 100360 | 4414 (2.10-2.10) |
| RSRZ outliers | 91569 | 3948 (2.10-2.10) |

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. 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 <=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 | 222 | 2%, 75%, 22% |
| 1 | B | 222 | 4%, 69%, 27% |
| 1 | C | 222 | 6%, 64%, 31% |
| 1 | D | 222 | 10%, 70%, 26% |

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|---|---|---|---|---|---|---|---|
| 2 | GSH | A | 230 | X | - | - | - |
| 2 | GSH | B | 230 | X | - | - | - |
| 2 | GSH | C | 230 | X | - | - | - |
| 2 | GSH | D | 230 | X | - | - | - |

# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7665 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.

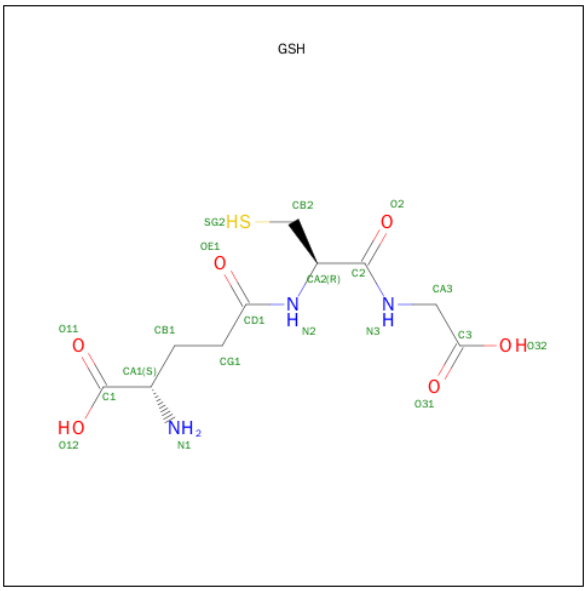
- Molecule 1 is a protein called GLUTATHIONE S-TRANSFERASE A2.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 1 | A | 219 | 1778 | 1144 | 299 | 328 | 7 | 0 | 0 | 0 |
| 1 | B | 217 | 1757 | 1132 | 292 | 326 | 7 | 0 | 0 | 0 |
| 1 | C | 219 | 1778 | 1144 | 299 | 328 | 7 | 0 | 0 | 0 |
| 1 | D | 217 | 1757 | 1132 | 292 | 326 | 7 | 0 | 0 | 0 |

There are 16 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 107 | GLY | LEU | ENGINEERED MUTATION | UNP P09210 |
| A | 108 | ASP | LEU | ENGINEERED MUTATION | UNP P09210 |
| A | 110 | SER | PRO | CONFLICT | UNP P09210 |
| A | 222 | HIS | PHE | ENGINEERED MUTATION | UNP P09210 |
| B | 107 | GLY | LEU | ENGINEERED MUTATION | UNP P09210 |
| B | 108 | ASP | LEU | ENGINEERED MUTATION | UNP P09210 |
| B | 110 | SER | PRO | CONFLICT | UNP P09210 |
| B | 222 | HIS | PHE | ENGINEERED MUTATION | UNP P09210 |
| C | 107 | GLY | LEU | ENGINEERED MUTATION | UNP P09210 |
| C | 108 | ASP | LEU | ENGINEERED MUTATION | UNP P09210 |
| C | 110 | SER | PRO | CONFLICT | UNP P09210 |
| C | 222 | HIS | PHE | ENGINEERED MUTATION | UNP P09210 |
| D | 107 | GLY | LEU | ENGINEERED MUTATION | UNP P09210 |
| D | 108 | ASP | LEU | ENGINEERED MUTATION | UNP P09210 |
| D | 110 | SER | PRO | CONFLICT | UNP P09210 |
| D | 222 | HIS | PHE | ENGINEERED MUTATION | UNP P09210 |

- Molecule 2 is GLUTATHIONE (three-letter code: GSH) (formula: $C_{10}H_{17}N_3O_6S$).




| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 2 | A | 1 | 20 | 10 | 3 | 6 | 1 | 0 | 0 |
| | | | Total | C | N | O | S | | |
| 2 | B | 1 | 20 | 10 | 3 | 6 | 1 | 0 | 0 |
| | | | Total | C | N | O | S | | |
| 2 | C | 1 | 20 | 10 | 3 | 6 | 1 | 0 | 0 |
| | | | Total | C | N | O | S | | |
| 2 | D | 1 | 20 | 10 | 3 | 6 | 1 | 0 | 0 |

- Molecule 3 is water.

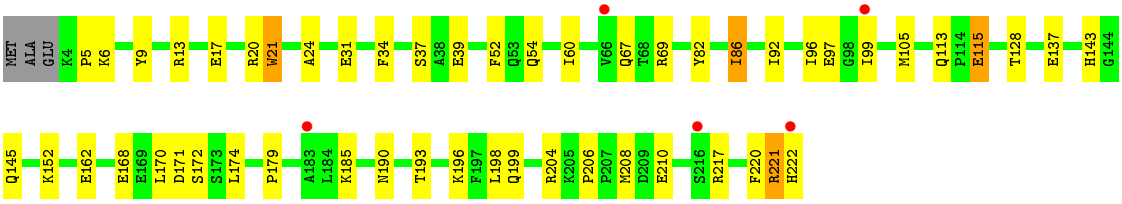
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | O | | |
| 3 | A | 180 | 180 | 180 | 0 | 0 |
| | | | Total | O | | |
| 3 | B | 110 | 110 | 110 | 0 | 0 |
| | | | Total | O | | |
| 3 | C | 118 | 118 | 118 | 0 | 0 |
| | | | Total | O | | |
| 3 | D | 107 | 107 | 107 | 0 | 0 |

# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: GLUTATHIONE S-TRANSFERASE A2

Chain A:

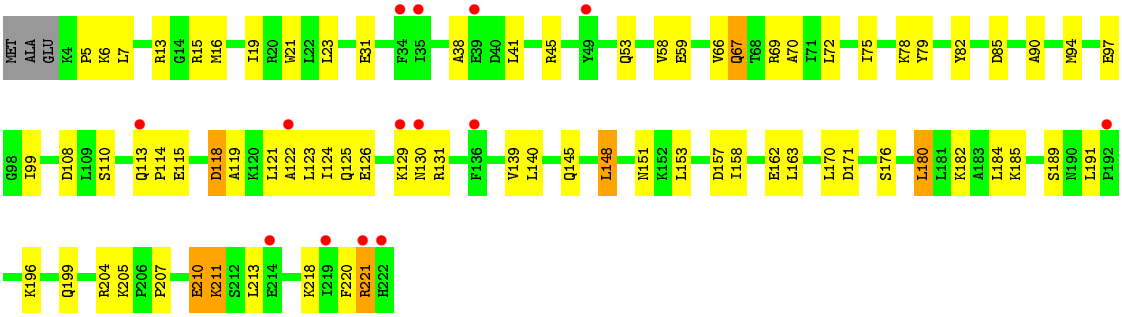



- Molecule 1: GLUTATHIONE S-TRANSFERASE A2

Chain B:

- Molecule 1: GLUTATHIONE S-TRANSFERASE A2

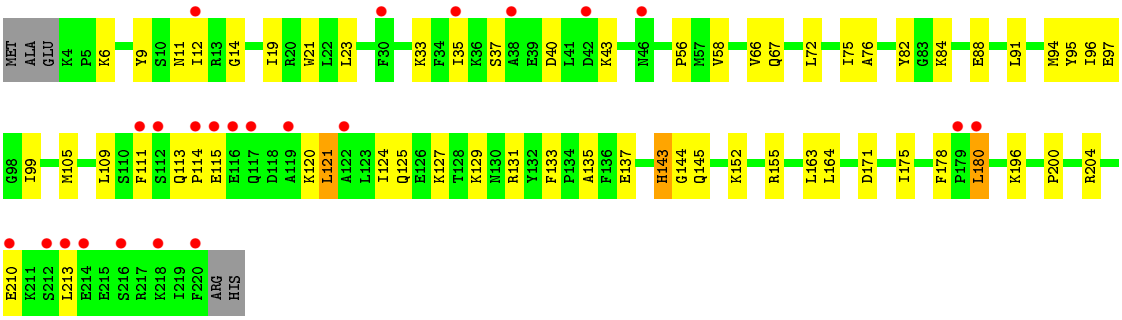
Chain C:




- Molecule 1: GLUTATHIONE S-TRANSFERASE A2

Chain D:

10%
70%
26%


MET ALA GLU K4 P5 K6 Y9 S10 N11 I12 R13 G14 I19 R20 W21 L22 L23 F30 K33 F34 I35 K36 S37 A38 E39 D40 L41 D42 K43 N46 P56 M57 V58 V66 Q67 L72 I75 A76 Y82 G83 K84 E88 L91 M94 Y95 I96 E97
G98 I99 M105 L109 S110 F111 S112 Q113 P114 E115 E116 Q117 D118 A119 K120 L121 A122 L123 I124 Q125 E126 K127 T128 K129 N130 R131 Y132 F133 P134 A135 F136 E137 H143 G144 Q145 K152 R155 L163 L164 D171 I175 F178 P179 L180 K196 P200 R204
E210 K211 S212 L213 E214 E215 S216 R217 K218 I219 F220 ARG HIS

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 1 21 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 48.66Å 94.80Å 113.72Å<br>90.00° 92.77° 90.00° | Depositor |
| Resolution (Å) | 40.00 – 2.10<br>37.84 – 2.10 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 92.4 (40.00-2.10)<br>92.5 (37.84-2.10) | Depositor<br>EDS |
| $R_{merge}$ | 0.12 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 3.26 (at 2.10Å) | Xtriage |
| Refinement program | REFMAC 5.6.0117 | Depositor |
| R, $R_{free}$ | 0.261 , 0.321<br>0.261 , 0.320 | Depositor<br>DCC |
| $R_{free}$ test set | 2821 reflections (5.34%) | DCC |
| Wilson B-factor (Å$^2$) | 13.3 | Xtriage |
| Anisotropy | 0.477 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.28 , 40.2 | EDS |
| Estimated twinning fraction | 0.229 for h,-k,-l | Xtriage |
| L-test for twinning[2] | $< \|L\| > = 0.37$, $< L^2 > = 0.20$ | Xtriage |
| Outliers | 0 of 55688 reflections | Xtriage |
| $F_o$,$F_c$ correlation | 0.83 | EDS |
| Total number of atoms | 7665 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 16.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.68% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: GSH

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 | 1/1812 (0.1%) | 0.77 | 0/2433 |
| 1 | B | 0.56 | 1/1790 (0.1%) | 0.75 | 0/2404 |
| 1 | C | 0.56 | 0/1812 | 0.75 | 0/2433 |
| 1 | D | 0.53 | 1/1790 (0.1%) | 0.71 | 0/2404 |
| All | All | 0.56 | 3/7204 (0.0%) | 0.75 | 0/9674 |

All (3) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | D | 21 | TRP | CD2-CE2 | 5.44 | 1.47 | 1.41 |
| 1 | B | 21 | TRP | CD2-CE2 | 5.22 | 1.47 | 1.41 |
| 1 | A | 21 | TRP | CD2-CE2 | 5.09 | 1.47 | 1.41 |

There are no bond angle outliers.

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 | 1778 | 0 | 1826 | 34 | 0 |
| 1 | B | 1757 | 0 | 1806 | 40 | 0 |
| 1 | C | 1778 | 0 | 1826 | 53 | 0 |
| 1 | D | 1757 | 0 | 1806 | 46 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 2 | A | 20 | 0 | 15 | 2 | 0 |
| 2 | B | 20 | 0 | 15 | 0 | 0 |
| 2 | C | 20 | 0 | 15 | 0 | 0 |
| 2 | D | 20 | 0 | 15 | 1 | 0 |
| 3 | A | 180 | 0 | 0 | 7 | 0 |
| 3 | B | 110 | 0 | 0 | 6 | 0 |
| 3 | C | 118 | 0 | 0 | 9 | 0 |
| 3 | D | 107 | 0 | 0 | 8 | 0 |
| All | All | 7665 | 0 | 7324 | 162 | 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 162 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:D:105:MET:HG3 | 3:D:2056:HOH:O | 1.65 | 0.96 |
| 1:C:15:ARG:HG2 | 1:C:15:ARG:HH11 | 1.42 | 0.84 |
| 1:D:121:LEU:O | 1:D:125:GLN:HG3 | 1.78 | 0.83 |
| 1:A:217:ARG:HA | 1:A:222:HIS:CE1 | 2.15 | 0.82 |
| 1:B:36:LYS:HD3 | 3:B:2032:HOH:O | 1.80 | 0.81 |

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 | 217/222 (98%) | 204 (94%) | 10 (5%) | 3 (1%) | 14 7 |
| 1 | B | 215/222 (97%) | 200 (93%) | 13 (6%) | 2 (1%) | 21 15 |
| 1 | C | 217/222 (98%) | 205 (94%) | 9 (4%) | 3 (1%) | 14 7 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | D | 215/222 (97%) | 193 (90%) | 19 (9%) | 3 (1%) | 14 | 7 |
| All | All | 864/888 (97%) | 802 (93%) | 51 (6%) | 11 (1%) | 15 | 9 |

5 of 11 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 221 | ARG |
| 1 | C | 221 | ARG |
| 1 | D | 144 | GLY |
| 1 | D | 171 | ASP |
| 1 | B | 13 | ARG |

### 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 | 195/197 (99%) | 188 (96%) | 7 (4%) | 42 | 43 |
| 1 | B | 193/197 (98%) | 181 (94%) | 12 (6%) | 23 | 19 |
| 1 | C | 195/197 (99%) | 184 (94%) | 11 (6%) | 26 | 22 |
| 1 | D | 193/197 (98%) | 183 (95%) | 10 (5%) | 29 | 25 |
| All | All | 776/788 (98%) | 736 (95%) | 40 (5%) | 29 | 25 |

5 of 40 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | B | 215 | GLU |
| 1 | C | 123 | LEU |
| 1 | D | 152 | LYS |
| 1 | C | 108 | ASP |
| 1 | C | 126 | GLU |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | B | 143 | HIS |
| 1 | C | 46 | ASN |
| 1 | C | 190 | ASN |
| 1 | B | 130 | ASN |
| 1 | C | 113 | GLN |

#### 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 carbohydrates in this entry.

### 5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

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 | $\#\|Z\| > 2$ |
| 2 | GSH | A | 230 | - | 13,19,19 | 0.43 | 0 | 15,24,24 | 0.76 | 1 (6%) |
| 2 | GSH | B | 230 | - | 13,19,19 | 0.48 | 0 | 15,24,24 | 2.04 | 4 (26%) |
| 2 | GSH | C | 230 | - | 13,19,19 | 0.61 | 0 | 15,24,24 | 1.63 | 2 (13%) |
| 2 | GSH | D | 230 | - | 13,19,19 | 0.58 | 0 | 15,24,24 | 0.55 | 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 |
|---|---|---|---|---|---|---|---|
| 2 | GSH | A | 230 | - | 1/1/6/8 | 0/18/24/24 | 0/0/0/0 |
| 2 | GSH | B | 230 | - | 1/1/6/8 | 0/18/24/24 | 0/0/0/0 |
| 2 | GSH | C | 230 | - | 1/1/6/8 | 0/18/24/24 | 0/0/0/0 |
| 2 | GSH | D | 230 | - | 1/1/6/8 | 0/18/24/24 | 0/0/0/0 |

There are no bond length outliers.

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

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | B | 230 | GSH | CB2-CA2-N2 | -4.90 | 104.52 | 111.40 |
| 2 | B | 230 | GSH | CA2-CB2-SG2 | -3.20 | 110.22 | 114.16 |
| 2 | B | 230 | GSH | CG1-CD1-N2 | -3.09 | 110.79 | 115.83 |
| 2 | C | 230 | GSH | O2-C2-N3 | -2.67 | 117.72 | 123.08 |
| 2 | A | 230 | GSH | CA2-CB2-SG2 | 2.02 | 116.64 | 114.16 |

All (4) chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|---|---|---|---|---|
| 2 | A | 230 | GSH | CA1 |
| 2 | B | 230 | GSH | CA1 |
| 2 | C | 230 | GSH | CA1 |
| 2 | D | 230 | GSH | CA1 |

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 2 | A | 230 | GSH | 2 | 0 |
| 2 | D | 230 | GSH | 1 | 0 |

## 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, $95^{th}$ 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 | 219/222 (98%) | 0.40 | 5 (2%) | 64 | 70 | 4, 10, 22, 38 | 0 |
| 1 | B | 217/222 (97%) | 0.67 | 9 (4%) | 41 | 50 | 7, 14, 28, 37 | 0 |
| 1 | C | 219/222 (98%) | 0.80 | 14 (6%) | 23 | 30 | 8, 17, 29, 55 | 0 |
| 1 | D | 217/222 (97%) | 0.84 | 23 (10%) | 8 | 11 | 8, 18, 39, 45 | 0 |
| All | All | 872/888 (98%) | 0.67 | 51 (5%) | 26 | 34 | 4, 14, 30, 55 | 0 |

The worst 5 of 51 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | C | 222 | HIS | 5.8 |
| 1 | A | 222 | HIS | 3.8 |
| 1 | D | 46 | ASN | 3.4 |
| 1 | B | 210 | GLU | 3.2 |
| 1 | D | 210 | GLU | 3.1 |

## 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 carbohydrates in this entry.

## 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, $95^{th}$ percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | LLDF | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|---|
| 2 | GSH | D | 230 | 20/20 | 0.78 | 0.20 | 0.93 | 16,21,23,23 | 0 |
| 2 | GSH | C | 230 | 20/20 | 0.90 | 0.16 | -0.40 | 13,15,16,16 | 0 |
| 2 | GSH | A | 230 | 20/20 | 0.91 | 0.14 | -0.46 | 8,10,13,15 | 0 |
| 2 | GSH | B | 230 | 20/20 | 0.90 | 0.14 | -0.77 | 11,14,15,16 | 0 |

## 6.5 Other polymers (i)

There are no such residues in this entry.