# WORLDWIDE wwPDB
## PROTEIN DATA BANK

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

Feb 6, 2024 – 12:50 AM EST

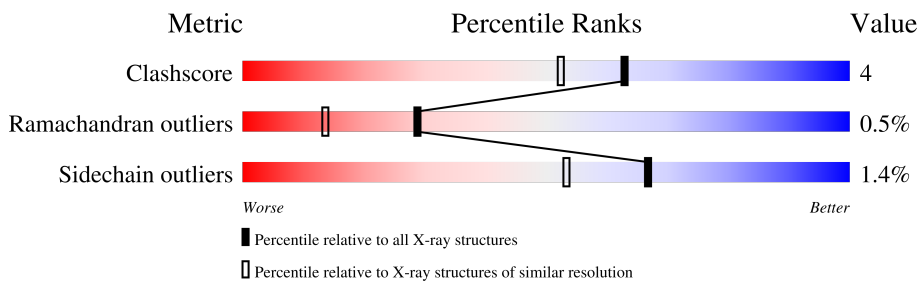|  |  |  |
|---|---|---|
| PDB ID | : | 1ZXI |
| Title | : | Reconstituted CO dehydrogenase from Oligotropha carboxidovorans |
| Authors | : | Resch, M.; Dobbek, H.; Meyer, O. |
| Deposited on | : | 2005-06-08 |
| Resolution | : | 1.70 Å(reported) |

# 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 1.70 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 | Percentile Ranks | Value |
|--------|------------------|-------|
| Clashscore | | 4 |
| Ramachandran outliers | | 0.5% |
| Sidechain outliers | | 1.4% |

*Worse*                                                                 *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|--------|--------------------------|----------------------------------------------------|
| Clashscore | 141614 | 4695 (1.70-1.70) |
| Ramachandran outliers | 138981 | 4610 (1.70-1.70) |
| Sidechain outliers | 138945 | 4610 (1.70-1.70) |

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 <=5%

Note EDS was not executed.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | A | 166 | 90%    7%   • |
| 1 | D | 166 | 89%    7%   5% |
| 2 | B | 809 | 89%    10%   •• |
| 2 | E | 809 | 87%    11%   • |
| 3 | C | 288 | 94%    5% |
| 3 | F | 288 | 93%    6% • |

W O R L D W I D E
wwPDB
PROTEIN DATA BANK

# 2 Entry composition ⓘ

There are 10 unique types of molecules in this entry. The entry contains 21735 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 Carbon monoxide dehydrogenase small chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 161 | Total 1204 | C 746 | N 215 | O 228 | S 15 | 2 | 0 | 0 |
| 1 | D | 158 | Total 1175 | C 727 | N 212 | O 221 | S 15 | 5 | 0 | 0 |

- Molecule 2 is a protein called Carbon monoxide dehydrogenase large chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | B | 804 | Total 6198 | C 3934 | N 1061 | O 1162 | S 41 | 73 | 0 | 0 |
| 2 | E | 795 | Total 6130 | C 3894 | N 1049 | O 1146 | S 41 | 61 | 0 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| B | 670 | ILE | VAL | conflict | UNP P19919 |
| E | 670 | ILE | VAL | conflict | UNP P19919 |

- Molecule 3 is a protein called Carbon monoxide dehydrogenase medium chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 3 | C | 287 | Total 2112 | C 1333 | N 372 | O 396 | S 11 | 26 | 0 | 0 |
| 3 | F | 286 | Total 2103 | C 1327 | N 370 | O 395 | S 11 | 26 | 0 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| C | 211 | SER | THR | conflict | UNP P19920 |
| F | 211 | SER | THR | conflict | UNP P19920 |

• Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: $O_4P$).



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

• Molecule 5 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: $Fe_2S_2$).
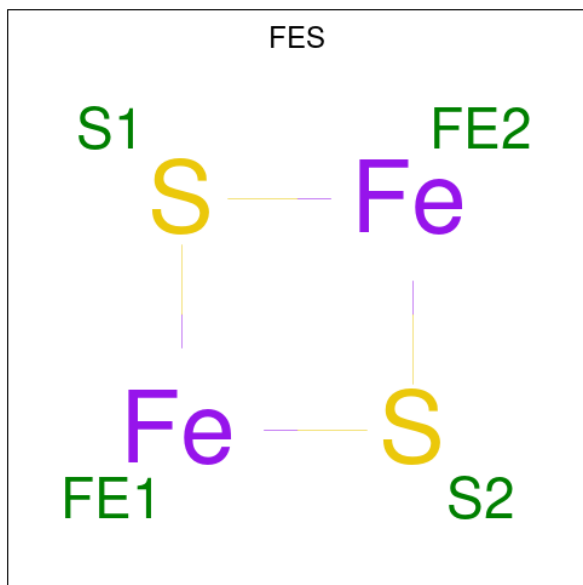


| Mol | Chain | Residues | Atoms | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|
| 5 | A | 1 | Total 4 | Fe 2 | S 2 | 0 | 0 |
| 5 | A | 1 | Total 4 | Fe 2 | S 2 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---------|---------|
| 5 | D | 1 | Total 4 | Fe 2 | S 2 | 0 | 0 |
| 5 | D | 1 | Total 4 | Fe 2 | S 2 | 0 | 0 |

- Molecule 6 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 6 | B | 1 | Total 1 | Cu 1 | 0 | 0 |
| 6 | E | 1 | Total 1 | Cu 1 | 0 | 1 |

- Molecule 7 is CU(I)-S-MO(VI)(=O)OH CLUSTER (three-letter code: CUM) (formula: $CuHMoO_2S$).
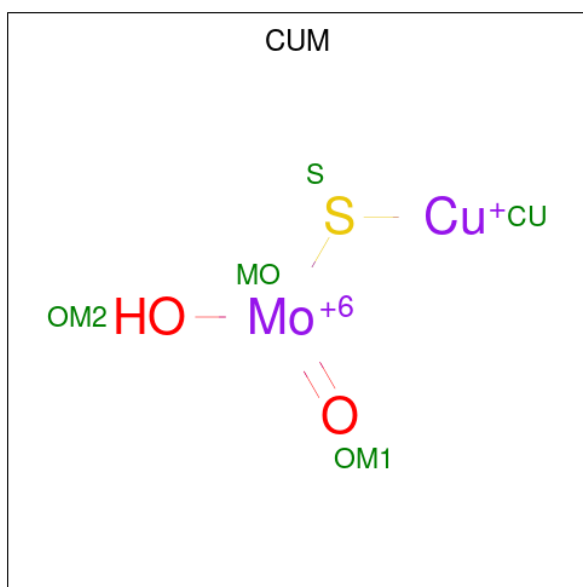


| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---|---|---------|---------|
| 7 | B | 1 | Total 5 | Cu 1 | Mo 1 | O 2 | S 1 | 0 | 0 |
| 7 | E | 1 | Total 5 | Cu 1 | Mo 1 | O 2 | S 1 | 0 | 1 |

- Molecule 8 is PTERIN CYTOSINE DINUCLEOTIDE (three-letter code: MCN) (formula: $C_{19}H_{22}N_8O_{13}P_2S_2$).

MCN

| Mol | Chain | Residues | Atoms | | | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|---|---|
| 8 | B | 1 | Total | C | N | O | P | S | 0 | 0 |
| | | | 44 | 19 | 8 | 13 | 2 | 2 | | |
| 8 | E | 1 | Total | C | N | O | P | S | 0 | 0 |
| | | | 44 | 19 | 8 | 13 | 2 | 2 | | |

• Molecule 9 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



FAD

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|---|
| 9 | C | 1 | Total | C | N | O | P | 0 | 0 |
| | | | 53 | 27 | 9 | 15 | 2 | | |

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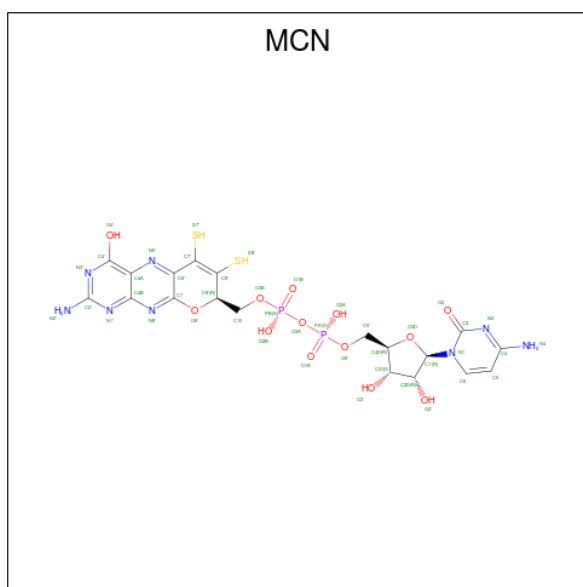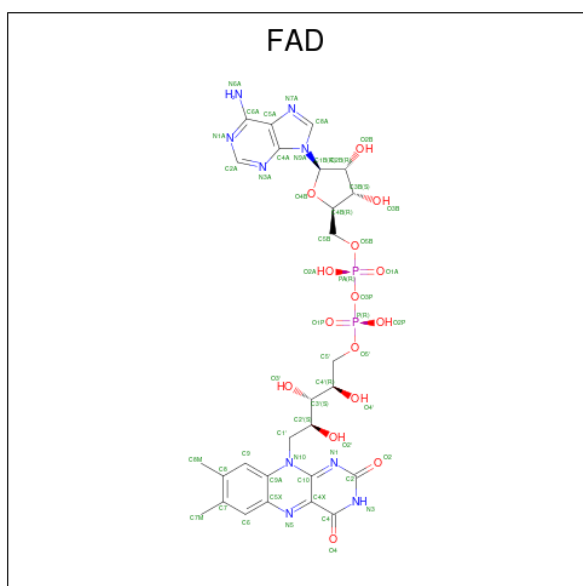
| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---|---|---------|---------|
| | | | Total | C | N | O | P | | |
| 9 | F | 1 | 53 | 27 | 9 | 15 | 2 | 0 | 0 |

- Molecule 10 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 10 | A | 190 | Total | O | 0 | 0 |
| | | | 190 | 190 | | |
| 10 | B | 804 | Total | O | 0 | 0 |
| | | | 804 | 804 | | |
| 10 | C | 342 | Total | O | 0 | 0 |
| | | | 342 | 342 | | |
| 10 | D | 189 | Total | O | 0 | 0 |
| | | | 189 | 189 | | |
| 10 | E | 749 | Total | O | 0 | 0 |
| | | | 749 | 749 | | |
| 10 | F | 312 | Total | O | 0 | 0 |
| | | | 312 | 312 | | |

# 3  Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

Note EDS was not executed.

• Molecule 1: Carbon monoxide dehydrogenase small chain

Chain A:

• Molecule 1: Carbon monoxide dehydrogenase small chain

Chain D:

• Molecule 2: Carbon monoxide dehydrogenase large chain

Chain B:
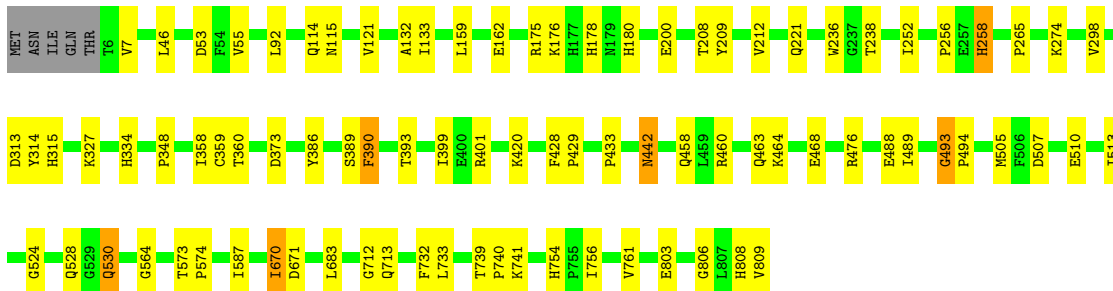
• Molecule 2: Carbon monoxide dehydrogenase large chain

Chain E:
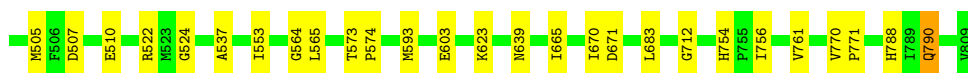
M505 F506 D507 E510 R522 M523 G524 A537 I553 G564 L565 T573 P574 M593 E603 K623 N639 I665 I670 D671 L683 G712 H754 P755 I756 V761 V770 P771 H788 I789 Q790 V809

• Molecule 3: Carbon monoxide dehydrogenase medium chain

Chain C:

94%                                                                 5%

M1 D103 P104 Q105 N115 N118 M125 L138 L167 A197 M204 T217 K240 P241 L275 A286 K287 ASN

• Molecule 3: Carbon monoxide dehydrogenase medium chain

Chain F:

93%                                                                 6%  ·

M1 Y8 H9 R10 H35 T43 R44 L45 E65 F86 I106 P121 L138 L167 A197 I214 T217 N221 D239 K240 P241 L275 A286 LYS ASN

# 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

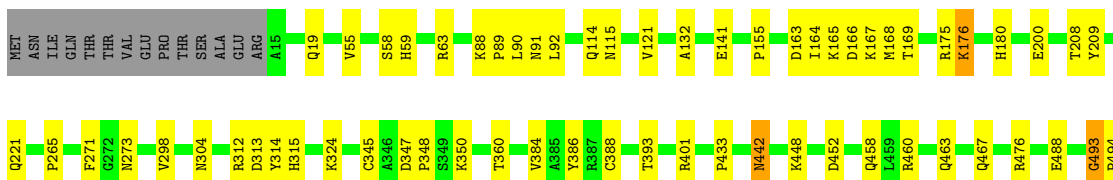| Property | Value | Source |
|---|---|---|
| Space group | P 21 21 21 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 118.84Å    131.32Å    159.99Å<br>90.00°       90.00°       90.00° | Depositor |
| Resolution (Å) | 20.00    –    1.70 | Depositor |
| % Data completeness<br>(in resolution range) | (Not available) (20.00-1.70) | Depositor |
| $R_{merge}$ | (Not available) | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| Refinement program | CNS | Depositor |
| R, $R_{free}$ | 0.166    ,    0.194 | Depositor |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| Total number of atoms | 21735 | 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: FES, FAD, CUM, MCN, PO4, CU

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 | 0.53 | 0/1225 | 0.71 | 0/1656 |
| 1 | D | 0.53 | 0/1195 | 0.74 | 0/1616 |
| 2 | B | 0.51 | 0/6351 | 0.74 | 2/8617 (0.0%) |
| 2 | E | 0.51 | 0/6282 | 0.73 | 2/8522 (0.0%) |
| 3 | C | 0.43 | 0/2149 | 0.70 | 0/2918 |
| 3 | F | 0.45 | 0/2140 | 0.71 | 0/2907 |
| All | All | 0.50 | 0/19342 | 0.73 | 4/26236 (0.0%) |

There are no bond length outliers.

All (4) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|-----|-------|-----|------|-------|-----|-------------|----------|
| 2 | E | 55 | VAL | N-CA-C | -6.30 | 94.00 | 111.00 |
| 2 | B | 55 | VAL | N-CA-C | -6.02 | 94.75 | 111.00 |
| 2 | E | 348 | PRO | N-CA-C | -5.27 | 98.39 | 112.10 |
| 2 | B | 348 | PRO | N-CA-C | -5.16 | 98.69 | 112.10 |

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 | 1204 | 0 | 1178 | 10 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | D | 1175 | 0 | 1157 | 5 | 0 |
| 2 | B | 6198 | 0 | 6072 | 61 | 0 |
| 2 | E | 6130 | 0 | 6007 | 60 | 0 |
| 3 | C | 2112 | 0 | 2170 | 11 | 0 |
| 3 | F | 2103 | 0 | 2157 | 15 | 0 |
| 4 | A | 5 | 0 | 0 | 0 | 0 |
| 5 | A | 8 | 0 | 0 | 0 | 0 |
| 5 | D | 8 | 0 | 0 | 0 | 0 |
| 6 | B | 1 | 0 | 0 | 0 | 0 |
| 6 | E | 1 | 0 | 0 | 0 | 0 |
| 7 | B | 5 | 0 | 0 | 1 | 0 |
| 7 | E | 5 | 0 | 0 | 0 | 0 |
| 8 | B | 44 | 0 | 17 | 0 | 0 |
| 8 | E | 44 | 0 | 17 | 1 | 0 |
| 9 | C | 53 | 0 | 31 | 1 | 0 |
| 9 | F | 53 | 0 | 31 | 0 | 0 |
| 10 | A | 190 | 0 | 0 | 2 | 0 |
| 10 | B | 804 | 0 | 0 | 6 | 0 |
| 10 | C | 342 | 0 | 0 | 0 | 0 |
| 10 | D | 189 | 0 | 0 | 1 | 0 |
| 10 | E | 749 | 0 | 0 | 5 | 0 |
| 10 | F | 312 | 0 | 0 | 2 | 0 |
| All | All | 21735 | 0 | 18837 | 159 | 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 159 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) |
|--------|--------|--------------------------|-------------------|
| 2:E:537:ALA:HB2 | 2:E:553:ILE:HD11 | 1.49 | 0.92 |
| 2:B:528:GLN:H | 2:B:530:GLN:HE22 | 1.20 | 0.86 |
| 1:D:11:ASN:HD21 | 1:D:76:THR:H | 1.23 | 0.86 |
| 2:E:460:ARG:HH11 | 2:E:463:GLN:HE22 | 1.25 | 0.84 |
| 2:E:670:ILE:HD12 | 2:E:671:ASP:N | 1.94 | 0.83 |

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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 | 159/166 (96%) | 156 (98%) | 3 (2%) | 0 | 100 | 100 |
| 1 | D | 156/166 (94%) | 153 (98%) | 3 (2%) | 0 | 100 | 100 |
| 2 | B | 802/809 (99%) | 775 (97%) | 22 (3%) | 5 (1%) | 25 | 11 |
| 2 | E | 793/809 (98%) | 761 (96%) | 25 (3%) | 7 (1%) | 17 | 5 |
| 3 | C | 285/288 (99%) | 280 (98%) | 5 (2%) | 0 | 100 | 100 |
| 3 | F | 284/288 (99%) | 280 (99%) | 4 (1%) | 0 | 100 | 100 |
| All | All | 2479/2526 (98%) | 2405 (97%) | 62 (2%) | 12 (0%) | 29 | 13 |

5 of 12 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | E | 176 | LYS |
| 2 | E | 167 | LYS |
| 2 | B | 493 | GLY |
| 2 | B | 712 | GLY |
| 2 | E | 493 | GLY |

### 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 | 129/131 (98%) | 129 (100%) | 0 | 100 | 100 |
| 1 | D | 126/131 (96%) | 124 (98%) | 2 (2%) | 62 | 48 |
| 2 | B | 648/653 (99%) | 635 (98%) | 13 (2%) | 55 | 38 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------|-----------|----------|-------------|---|
| 2 | E | 640/653 (98%) | 628 (98%) | 12 (2%) | 57 | 41 |
| 3 | C | 211/212 (100%) | 211 (100%) | 0 | 100 | 100 |
| 3 | F | 210/212 (99%) | 209 (100%) | 1 (0%) | 88 | 83 |
| All | All | 1964/1992 (99%) | 1936 (99%) | 28 (1%) | 67 | 53 |

5 of 28 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | D | 100 | LEU |
| 3 | F | 221 | ASN |
| 2 | E | 313 | ASP |
| 2 | E | 507 | ASP |
| 2 | E | 209 | TYR |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | E | 442 | ASN |
| 2 | E | 790 | GLN |
| 2 | E | 463 | GLN |
| 2 | E | 698 | GLN |
| 3 | F | 78 | GLN |

### 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 ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 13 ligands modelled in this entry, 2 are monoatomic - leaving 11 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 | #$|Z| > 2$ |
| 5 | FES | A | 3908 | 1 | 0,4,4 | - | - | - | | |
| 5 | FES | D | 3908 | 1 | 0,4,4 | - | - | - | | |
| 9 | FAD | C | 4932 | - | 53,58,58 | 1.86 | 19 (35%) | 68,89,89 | 1.17 | 9 (13%) |
| 4 | PO4 | A | 3001 | - | 4,4,4 | 1.21 | 0 | 6,6,6 | 0.45 | 0 |
| 5 | FES | A | 3907 | 1 | 0,4,4 | - | - | - | | |
| 7 | CUM | B | 3920 | 2,8,6 | 0,4,4 | - | - | - | | |
| 5 | FES | D | 3907 | 1 | 0,4,4 | - | - | - | | |
| 8 | MCN | E | 3923 | 7 | 41,48,48 | 3.23 | 15 (36%) | 49,74,74 | 2.12 | 14 (28%) |
| 9 | FAD | F | 4931 | - | 53,58,58 | 1.79 | 14 (26%) | 68,89,89 | 1.10 | 5 (7%) |
| 8 | MCN | B | 3921 | 7 | 41,48,48 | 3.33 | 17 (41%) | 49,74,74 | 2.08 | 13 (26%) |

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 |
|-----|------|-------|-----|------|---------|----------|-------|
| 5 | FES | A | 3908 | 1 | - | - | 0/1/1/1 |
| 9 | FAD | C | 4932 | - | - | 5/30/50/50 | 0/6/6/6 |
| 5 | FES | D | 3908 | 1 | - | - | 0/1/1/1 |
| 5 | FES | A | 3907 | 1 | - | - | 0/1/1/1 |
| 5 | FES | D | 3907 | 1 | - | - | 0/1/1/1 |
| 8 | MCN | E | 3923 | 7 | - | 2/22/54/54 | 0/5/5/5 |
| 9 | FAD | F | 4931 | - | - | 1/30/50/50 | 0/6/6/6 |
| 8 | MCN | B | 3921 | 7 | - | 2/22/54/54 | 0/5/5/5 |

The worst 5 of 65 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|------|-------------|----------|
| 8 | B | 3921 | MCN | C6'-N5' | 15.81 | 1.55 | 1.32 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|---------|-------|-------------|----------|
| 8 | E | 3923 | MCN | C6'-N5' | 15.42 | 1.54 | 1.32 |
| 8 | E | 3923 | MCN | C7-N8' | 7.64 | 1.49 | 1.30 |
| 8 | B | 3921 | MCN | C7-N8' | 7.38 | 1.48 | 1.30 |
| 8 | B | 3921 | MCN | O9'-C7 | 5.99 | 1.42 | 1.35 |

The worst 5 of 41 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|-----|-------|------|------|-------------|-------|-------------|----------|
| 8 | E | 3923 | MCN | O9'-C7-N8' | -5.85 | 108.05 | 115.30 |
| 8 | B | 3921 | MCN | O9'-C7-N8' | -5.37 | 108.64 | 115.30 |
| 8 | B | 3921 | MCN | C6'-N5'-C4A | -5.12 | 106.63 | 117.26 |
| 8 | E | 3923 | MCN | C6'-N5'-C4A | -5.04 | 106.79 | 117.26 |
| 8 | E | 3923 | MCN | O4'-C4'-C4A | 4.35 | 127.81 | 119.67 |

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|------|------|-------------------|
| 8 | B | 3921 | MCN | C10-O3B-PB-O1B |
| 8 | E | 3923 | MCN | C10-O3B-PB-O1B |
| 8 | B | 3921 | MCN | C10-O3B-PB-O3A |
| 8 | E | 3923 | MCN | C10-O3B-PB-O3A |
| 9 | F | 4931 | FAD | PA-O3P-P-O2P |

There are no ring outliers.

3 monomers are involved in 3 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|------|------|---------|--------------|
| 9 | C | 4932 | FAD | 1 | 0 |
| 7 | B | 3920 | CUM | 1 | 0 |
| 8 | E | 3923 | MCN | 1 | 0 |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



Ligand FAD C 4932

Bond lengths

Bond angles

Torsions

Rings



Ligand MCN E 3923

Bond lengths

Bond angles

Torsions

Rings

## Ligand FAD F 4931


Bond lengths


Bond angles


Torsions


Rings

## Ligand MCN B 3921


Bond lengths


Bond angles


Torsions


Rings
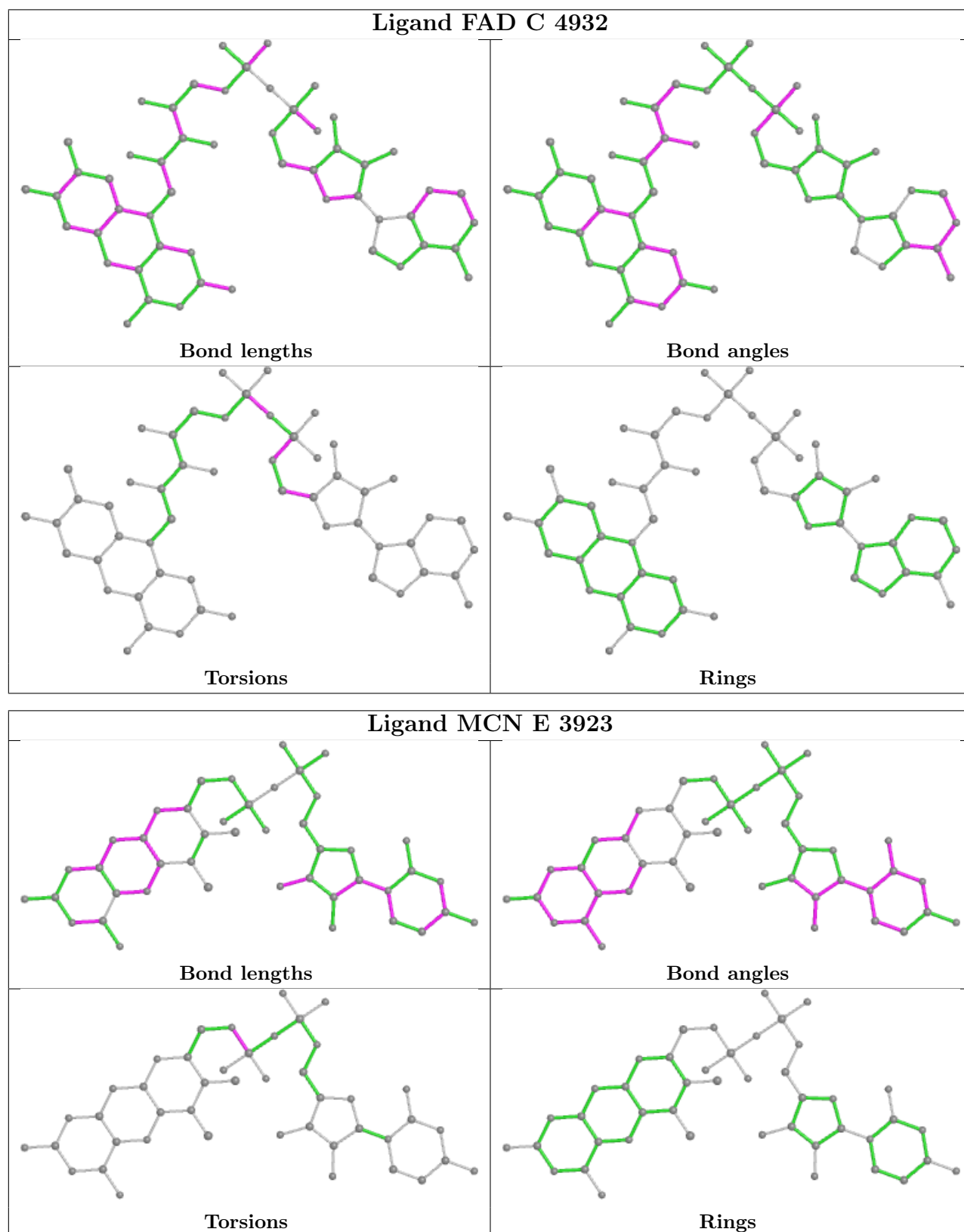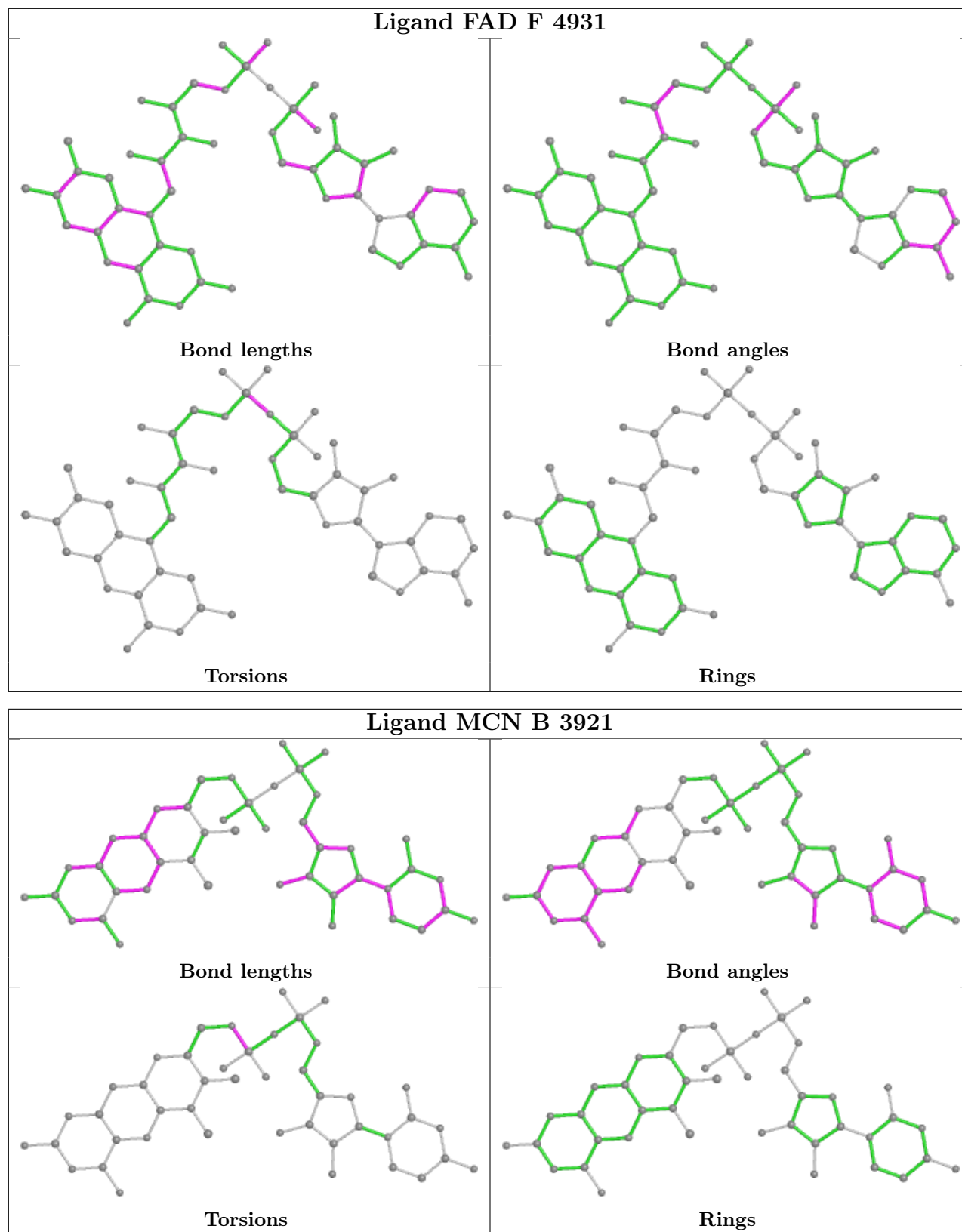
## 5.7 Other polymers ⓘ

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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

## 6.3   Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

## 6.4   Ligands ⓘ

EDS was not executed - this section is therefore empty.

## 6.5   Other polymers ⓘ

EDS was not executed - this section is therefore empty.