



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 7, 2024 – 07:32 am GMT

PDB ID : 5M85
Title : Three-dimensional structure of the intermediate state of GAF3 from Slr1393 of *Synechocystis* sp. PCC6803
Authors : Xu, X.-L.; Zhao, K.-H.; Gaertner, W.; Hoepfner, A.
Deposited on : 2016-10-28
Resolution : 2.10 Å (reported)

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

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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 : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
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

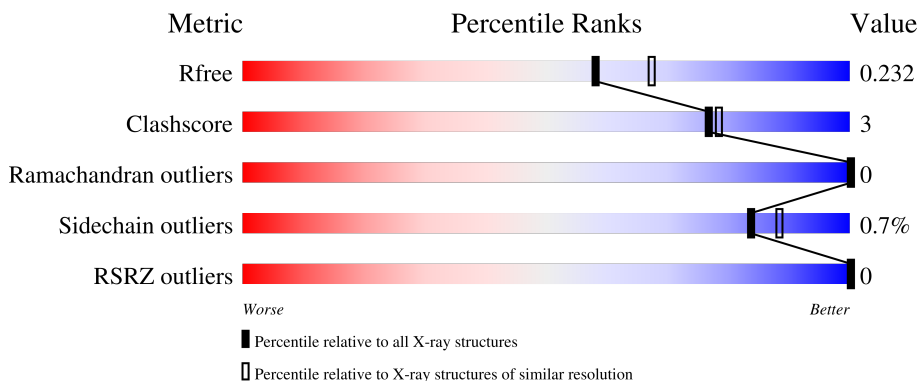
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (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 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	215	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
5	TRS	A	707	-	X	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 1457 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 Sensory transduction histidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	159	1315	837	237	238	3	0	0	0

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	391	MET	-	initiating methionine	UNP P73184
A	392	HIS	-	expression tag	UNP P73184
A	393	HIS	-	expression tag	UNP P73184
A	394	HIS	-	expression tag	UNP P73184
A	395	HIS	-	expression tag	UNP P73184
A	396	HIS	-	expression tag	UNP P73184
A	397	HIS	-	expression tag	UNP P73184
A	398	SER	-	expression tag	UNP P73184
A	399	SER	-	expression tag	UNP P73184
A	400	GLY	-	expression tag	UNP P73184
A	401	LEU	-	expression tag	UNP P73184
A	402	VAL	-	expression tag	UNP P73184
A	403	PRO	-	expression tag	UNP P73184
A	404	ARG	-	expression tag	UNP P73184
A	405	GLY	-	expression tag	UNP P73184
A	406	SER	-	expression tag	UNP P73184
A	407	GLY	-	expression tag	UNP P73184
A	408	MET	-	expression tag	UNP P73184
A	409	LYS	-	expression tag	UNP P73184
A	410	GLU	-	expression tag	UNP P73184
A	411	THR	-	expression tag	UNP P73184
A	412	ALA	-	expression tag	UNP P73184
A	413	ALA	-	expression tag	UNP P73184
A	414	ALA	-	expression tag	UNP P73184
A	415	LYS	-	expression tag	UNP P73184
A	416	PHE	-	expression tag	UNP P73184
A	417	GLU	-	expression tag	UNP P73184

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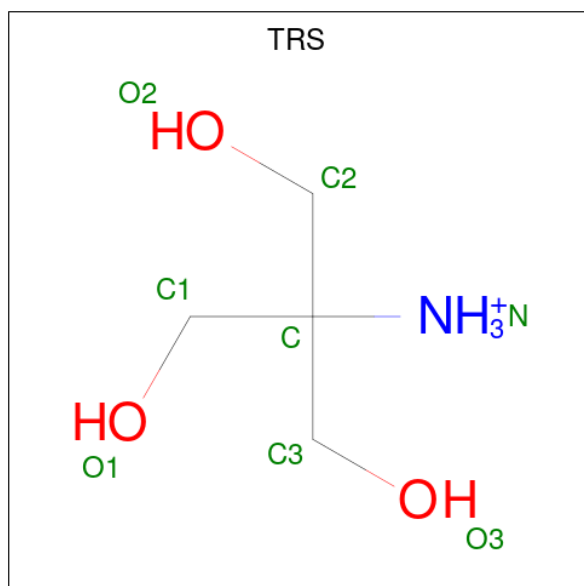
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Chain	Residue	Modelled	Actual	Comment	Reference
A	418	ARG	-	expression tag	UNP P73184
A	419	GLN	-	expression tag	UNP P73184
A	420	HIS	-	expression tag	UNP P73184
A	421	MET	-	expression tag	UNP P73184
A	422	ASP	-	expression tag	UNP P73184
A	423	SER	-	expression tag	UNP P73184
A	424	PRO	-	expression tag	UNP P73184
A	425	ASP	-	expression tag	UNP P73184
A	426	LEU	-	expression tag	UNP P73184
A	427	GLY	-	expression tag	UNP P73184
A	428	THR	-	expression tag	UNP P73184
A	429	ASP	-	expression tag	UNP P73184
A	430	ASP	-	expression tag	UNP P73184
A	431	ASP	-	expression tag	UNP P73184
A	432	ASP	-	expression tag	UNP P73184
A	433	LYS	-	expression tag	UNP P73184
A	434	ALA	-	expression tag	UNP P73184
A	435	MET	-	expression tag	UNP P73184
A	436	ALA	-	expression tag	UNP P73184
A	437	ASP	-	expression tag	UNP P73184
A	438	ILE	-	expression tag	UNP P73184
A	439	GLY	-	expression tag	UNP P73184
A	440	SER	-	expression tag	UNP P73184
A	598	LEU	-	expression tag	UNP P73184
A	599	GLU	-	expression tag	UNP P73184
A	600	HIS	-	expression tag	UNP P73184
A	601	HIS	-	expression tag	UNP P73184
A	602	HIS	-	expression tag	UNP P73184
A	603	HIS	-	expression tag	UNP P73184
A	604	HIS	-	expression tag	UNP P73184
A	605	HIS	-	expression tag	UNP P73184

- Molecule 2 is PHYCOCYANOBILIN (three-letter code: CYC) (formula: $C_{33}H_{40}N_4O_6$).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	4	Total Na 4 4	0	0

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O 8 4 1 3	0	0

- Molecule 6 is water.

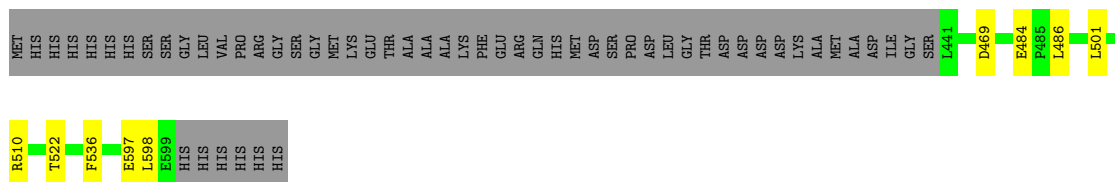
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	72	Total O 72 72	0	0

3 Residue-property plots [i](#)

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 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: Sensory transduction histidine kinase

Chain A:  70% 26%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	75.10Å 75.10Å 71.21Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	65.04 – 2.10 65.04 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (65.04-2.10) 99.8 (65.04-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.29 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.170 , 0.222 0.177 , 0.232	Depositor DCC
R_{free} test set	640 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	37.8	Xtrriage
Anisotropy	0.062	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.053 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	1457	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.64% 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: 3CX, CYC, NA, TRS

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	0.95	1/1350 (0.1%)	0.98	3/1835 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	484	GLU	CG-CD	5.67	1.60	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	510	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	469	ASP	CB-CG-OD2	-5.53	113.32	118.30
1	A	469	ASP	CB-CG-OD1	5.11	122.90	118.30

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	1315	0	1248	3	0
2	A	43	0	36	5	0
3	A	15	0	19	0	0
4	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	8	0	12	5	0
6	A	72	0	0	0	0
All	All	1457	0	1315	8	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 3.

The worst 5 of 8 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:A:701:CYC:CHB	5:A:707:TRS:H32	2.06	0.85
5:A:707:TRS:O3	5:A:707:TRS:O1	2.06	0.69
2:A:701:CYC:CHB	5:A:707:TRS:C3	2.82	0.57
2:A:701:CYC:HHB	5:A:707:TRS:C3	2.41	0.50
1:A:486:LEU:HD12	1:A:536:PHE:CE2	2.49	0.47

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	157/215 (73%)	152 (97%)	5 (3%)	0	100 100

There are no Ramachandran outliers to report.

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	137/183 (75%)	136 (99%)	1 (1%)	84 88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	522	THR

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 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	3CX	A	702	-	15,15,15	0.80	0	16,20,20	2.02	3 (18%)
5	TRS	A	707	-	7,7,7	0.92	0	9,9,9	3.15	5 (55%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CYC	A	701	1,4	42,46,46	2.84	13 (30%)	50,67,67	3.29	26 (52%)

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	3CX	A	702	-	-	6/10/18/18	0/1/1/1
5	TRS	A	707	-	-	6/9/9/9	-
2	CYC	A	701	1,4	-	9/25/74/74	0/4/4/4

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	CYC	CHA-C1A	12.84	1.45	1.35
2	A	701	CYC	C3B-C2B	5.54	1.48	1.36
2	A	701	CYC	C1B-C2B	4.03	1.52	1.45
2	A	701	CYC	C2A-C3A	3.89	1.45	1.36
2	A	701	CYC	OB-C4B	3.69	1.30	1.23

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	CYC	C3B-C4B-NB	10.63	115.37	106.78
5	A	707	TRS	C1-C-N	6.37	127.00	107.98
2	A	701	CYC	CMA-C3A-C4A	6.23	134.66	125.06
2	A	701	CYC	OB-C4B-C3B	-6.09	121.43	128.04
2	A	701	CYC	CBD-CAD-C3D	-5.71	102.88	112.62

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

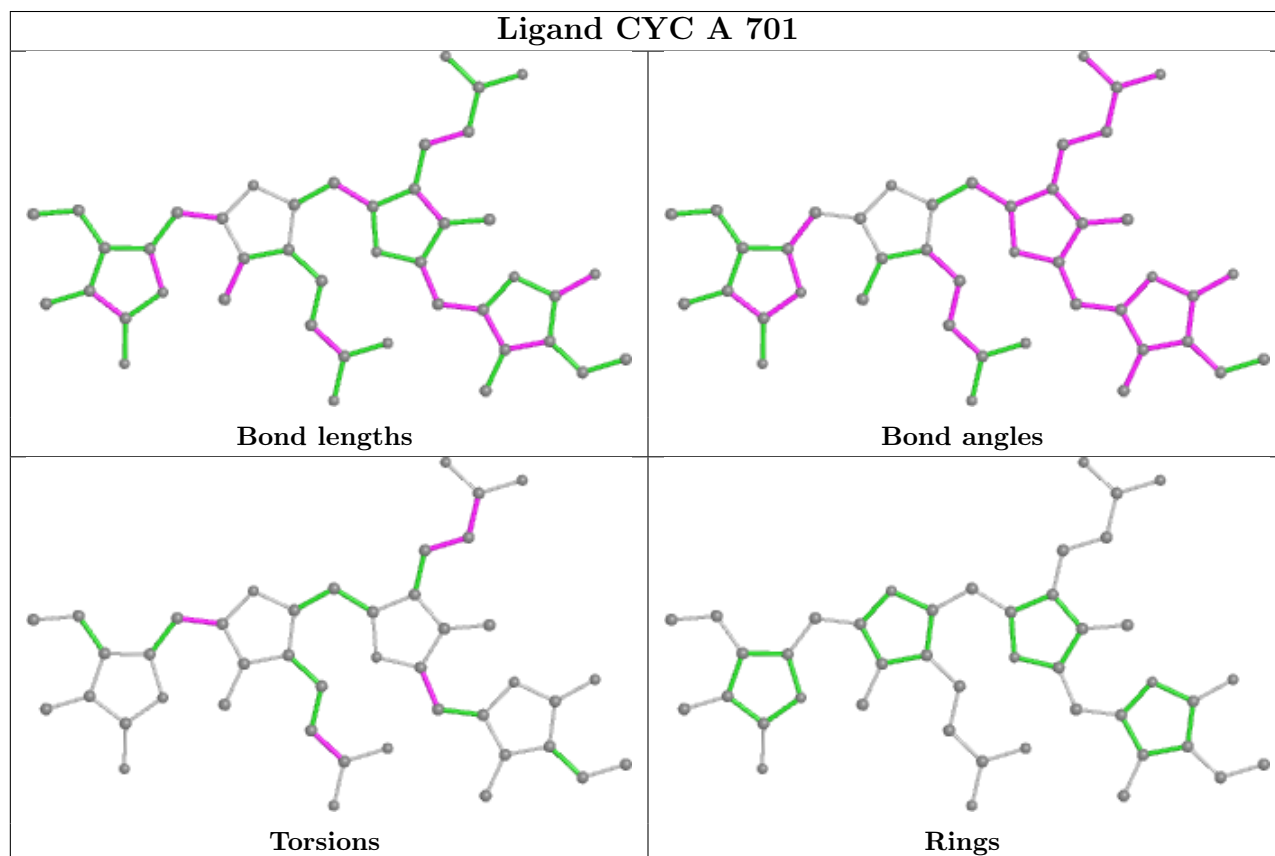
Mol	Chain	Res	Type	Atoms
2	A	701	CYC	NA-C4A-CHB-C1B
2	A	701	CYC	C3A-C4A-CHB-C1B
2	A	701	CYC	ND-C1D-CHD-C4C
2	A	701	CYC	C2D-C1D-CHD-C4C
3	A	702	3CX	NAL-CAJ-CAM-OAC

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	707	TRS	5	0
2	A	701	CYC	5	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 than 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.



5.7 Other polymers [i](#)

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 [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	159/215 (73%)	-0.56	0 100 100	29, 39, 68, 89	0

There are no RSRZ outliers to report.

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.

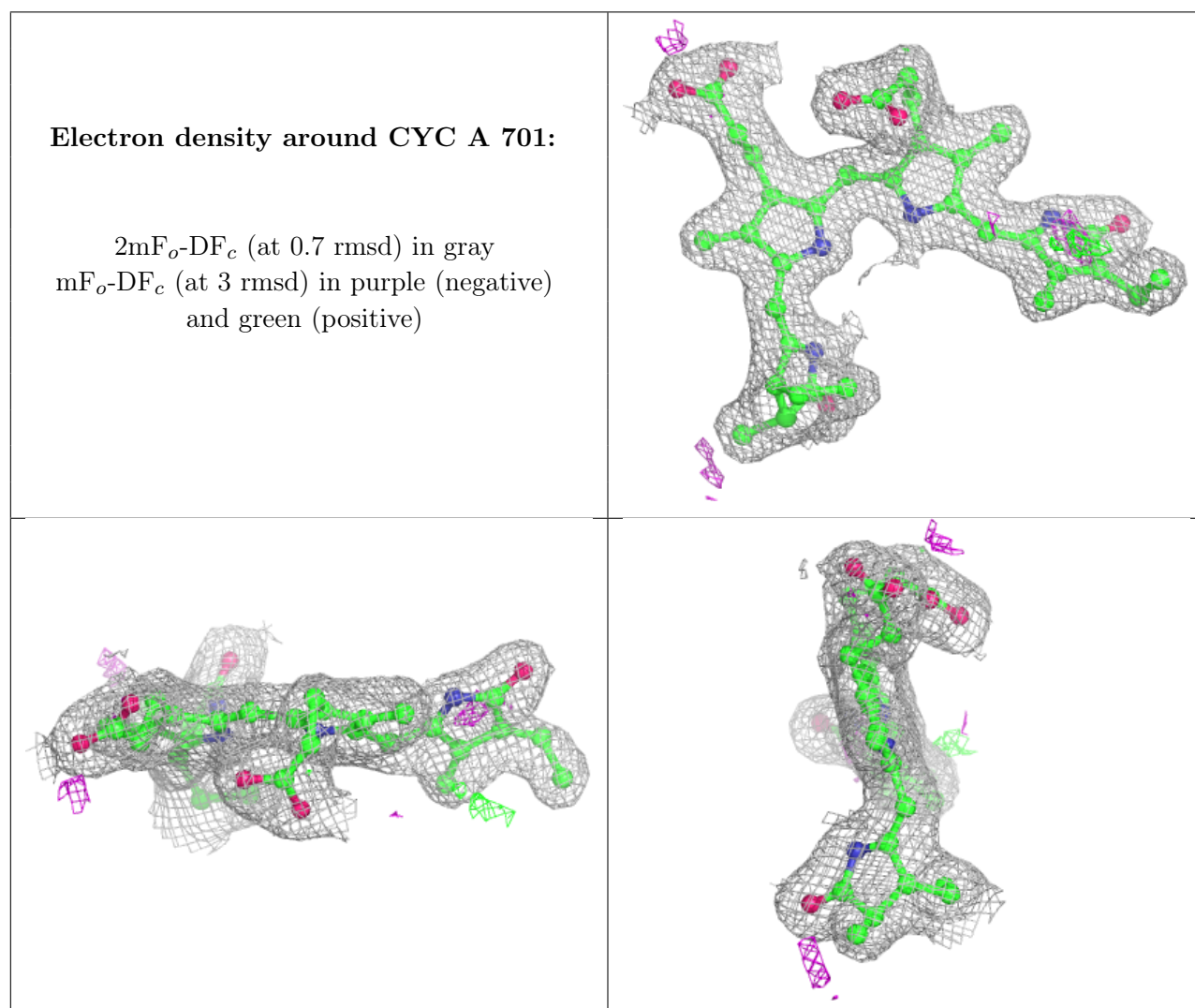
6.4 Ligands [i](#)

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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å ²)	Q<0.9
5	TRS	A	707	8/8	0.91	0.12	33,51,55,56	0
4	NA	A	706	1/1	0.95	0.08	41,41,41,41	0
2	CYC	A	701	43/43	0.95	0.10	25,29,41,42	0
3	3CX	A	702	15/15	0.98	0.10	31,37,46,51	0
4	NA	A	705	1/1	0.99	0.10	30,30,30,30	0
4	NA	A	703	1/1	0.99	0.05	44,44,44,44	0
4	NA	A	704	1/1	0.99	0.24	52,52,52,52	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.