



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7S50 / pdb_00007s50
Title : Serial Macromolecular Crystallography at ALBA Synchrotron Light Source - Phycocyanin
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Deposited on : 2021-09-09
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

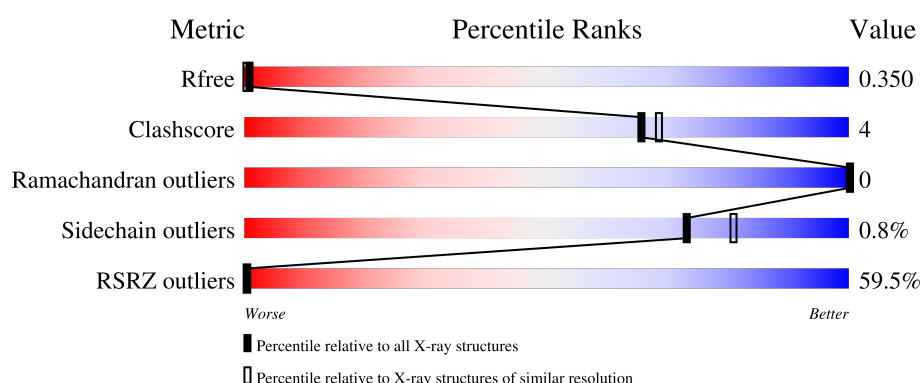
1 Overall quality at a glance

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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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	162	50% 95% 5%
2	B	172	68% 91% 9%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2671 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.

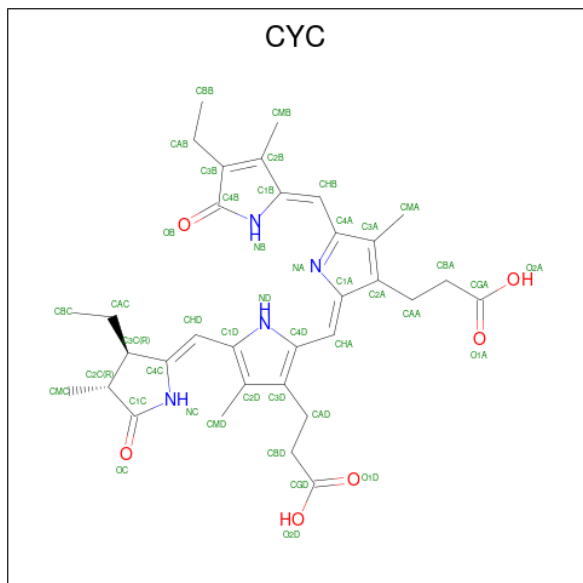
- Molecule 1 is a protein called C-phycocyanin alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	162	Total	C	N	O	S	0	0	0
			1224	771	205	241	7			

- Molecule 2 is a protein called C-phycocyanin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	172	Total	C	N	O	S	0	0	0
			1273	789	228	248	8			

- Molecule 3 is PHYCOCYANOBILIN (CCD ID: CYC) (formula: $C_{33}H_{40}N_4O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			43	33	4	6		
3	B	1	Total	C	N	O	0	0
			43	33	4	6		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			43	33	4	6		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Na	0	0
			1	1		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Cl	0	0
			1	1		

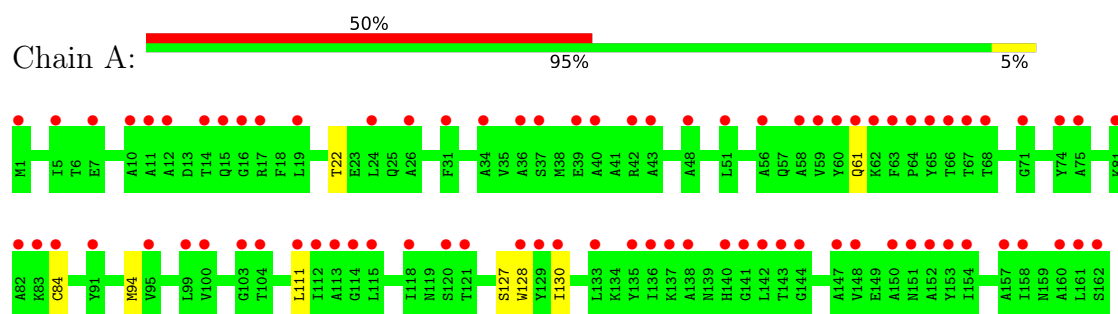
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	17	Total	O	0	0
			17	17		
6	B	26	Total	O	0	0
			26	26		

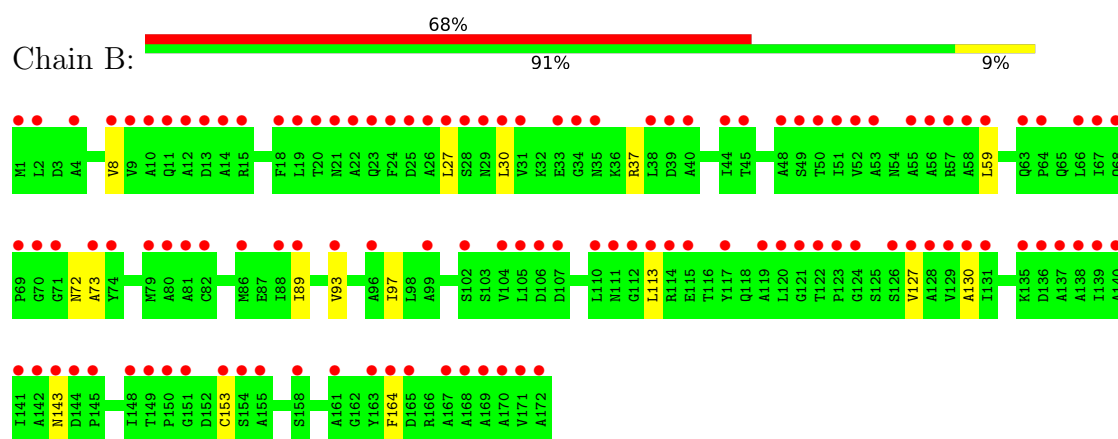
3 Residue-property plots

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 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: C-phycocyanin alpha chain



• Molecule 2: C-phycocyanin beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	188.50Å 188.50Å 61.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.42 – 2.10 43.42 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (43.42-2.10) 99.2 (43.42-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.305 , 0.347 0.310 , 0.350	Depositor DCC
R_{free} test set	1185 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	61.8	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2671	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.12% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MEN, NA, CL, CYC

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	0/1246	1.11	0/1691
2	B	0.52	0/1277	1.11	0/1729
All	All	0.52	0/2523	1.11	0/3420

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1224	0	1203	6	0
2	B	1273	0	1278	13	0
3	A	43	0	38	4	0
3	B	86	0	76	6	0
4	B	1	0	0	0	0
5	B	1	0	0	0	0
6	A	17	0	0	1	0
6	B	26	0	0	0	0
All	All	2671	0	2595	20	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.

All (20) 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:B:113:LEU:HD13	3:B:201:CYC:HMB3	1.72	0.71
2:B:59:LEU:HD22	2:B:130:ALA:HB2	1.75	0.68
1:A:84:CYS:SG	3:A:201:CYC:HAC2	2.41	0.61
2:B:127:VAL:HA	3:B:201:CYC:HBC3	1.92	0.52
2:B:127:VAL:HG22	3:B:201:CYC:H3C	1.92	0.52
2:B:8:VAL:HG21	2:B:27:LEU:HD11	1.91	0.52
1:A:128:TRP:CD2	3:A:201:CYC:HMC3	2.45	0.51
1:A:22:THR:HG22	6:A:308:HOH:O	2.09	0.51
2:B:72:MEN:O	2:B:73:ALA:N	2.44	0.51
1:A:128:TRP:CE3	3:A:201:CYC:HMC3	2.48	0.48
3:A:201:CYC:HMC1	3:A:201:CYC:HBC2	1.97	0.47
2:B:72:MEN:H	2:B:73:ALA:N	2.16	0.44
2:B:113:LEU:CD1	3:B:201:CYC:HMB3	2.44	0.44
1:A:94:MET:HG3	1:A:111:LEU:HD12	1.99	0.43
2:B:37:ARG:NH1	2:B:97:ILE:O	2.46	0.43
2:B:153:CYS:SG	3:B:202:CYC:HAC1	2.59	0.42
2:B:89:ILE:O	2:B:93:VAL:HG23	2.20	0.42
2:B:143:ASN:HA	3:B:202:CYC:HMC1	2.01	0.42
1:A:127:SER:HA	1:A:130:ILE:HD12	2.02	0.42
2:B:93:VAL:HG11	2:B:164:PHE:CZ	2.55	0.41

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	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
2	B	167/172 (97%)	161 (96%)	6 (4%)	0	100	100
All	All	327/334 (98%)	317 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	123/123 (100%)	122 (99%)	1 (1%)	73	81
2	B	127/127 (100%)	126 (99%)	1 (1%)	73	81
All	All	250/250 (100%)	248 (99%)	2 (1%)	73	81

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
2	B	30	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	GLN
2	B	11	GLN
2	B	23	GLN
2	B	35	ASN
2	B	63	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	MEN	B	72	-	7,8,9	0.55	0	4,9,11	0.42	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	MEN	B	72	-	-	3/7/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	72	MEN	C-CA-CB-CG
2	B	72	MEN	N-CA-CB-CG
2	B	72	MEN	CA-CB-CG-OD1

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	72	MEN	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 2 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	CYC	B	202	-	46,46,46	0.81	1 (2%)	63,67,67	0.83	1 (1%)
3	CYC	A	201	-	46,46,46	0.79	1 (2%)	63,67,67	0.91	3 (4%)
3	CYC	B	201	-	46,46,46	0.84	1 (2%)	63,67,67	0.93	3 (4%)

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	CYC	B	202	-	-	10/26/74/74	0/4/4/4
3	CYC	A	201	-	-	10/26/74/74	0/4/4/4
3	CYC	B	201	-	-	14/26/74/74	0/4/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	201	CYC	CHD-C4C	2.48	1.40	1.36
3	A	201	CYC	CHD-C4C	2.26	1.40	1.36
3	B	202	CYC	CHD-C4C	2.14	1.40	1.36

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	201	CYC	CMB-C2B-C1B	3.55	128.48	124.16
3	B	202	CYC	CMB-C2B-C1B	3.22	128.08	124.16
3	A	201	CYC	CMB-C2B-C1B	3.18	128.03	124.16
3	B	201	CYC	C1C-NC-C4C	-3.16	109.44	113.41
3	A	201	CYC	C1C-NC-C4C	-2.82	109.87	113.41
3	A	201	CYC	C1B-NB-C4B	-2.31	107.83	110.66
3	B	201	CYC	C1B-NB-C4B	-2.00	108.21	110.66

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	201	CYC	NA-C4A-CHB-C1B
3	A	201	CYC	C3A-C4A-CHB-C1B
3	A	201	CYC	NC-C4C-CHD-C1D
3	A	201	CYC	C3C-C4C-CHD-C1D
3	B	201	CYC	NA-C4A-CHB-C1B
3	B	201	CYC	C3A-C4A-CHB-C1B
3	B	201	CYC	C2C-C3C-CAC-CBC
3	B	201	CYC	NC-C4C-CHD-C1D
3	B	202	CYC	NA-C4A-CHB-C1B
3	B	202	CYC	C3A-C4A-CHB-C1B
3	B	202	CYC	C4C-C3C-CAC-CBC
3	B	201	CYC	C2B-C3B-CAB-CBB
3	A	201	CYC	ND-C1D-CHD-C4C
3	B	201	CYC	ND-C1D-CHD-C4C
3	B	202	CYC	ND-C1D-CHD-C4C
3	A	201	CYC	C2D-C1D-CHD-C4C
3	B	201	CYC	C2D-C1D-CHD-C4C
3	B	202	CYC	C2D-C1D-CHD-C4C
3	B	201	CYC	C4B-C3B-CAB-CBB
3	B	202	CYC	C2C-C3C-CAC-CBC
3	A	201	CYC	C2B-C3B-CAB-CBB
3	B	201	CYC	C4C-C3C-CAC-CBC
3	B	201	CYC	CAD-CBD-CGD-O2D
3	B	202	CYC	CAD-CBD-CGD-O1D
3	B	201	CYC	CAA-CBA-CGA-O1A
3	B	202	CYC	CAA-CBA-CGA-O2A
3	B	202	CYC	CAD-CBD-CGD-O2D
3	A	201	CYC	C2A-CAA-CBA-CGA
3	B	201	CYC	CAD-CBD-CGD-O1D
3	A	201	CYC	CAA-CBA-CGA-O2A
3	B	201	CYC	CAA-CBA-CGA-O2A
3	A	201	CYC	CAA-CBA-CGA-O1A
3	B	202	CYC	CAA-CBA-CGA-O1A
3	B	201	CYC	C3C-C4C-CHD-C1D

There are no ring outliers.

3 monomers are involved in 10 short contacts:

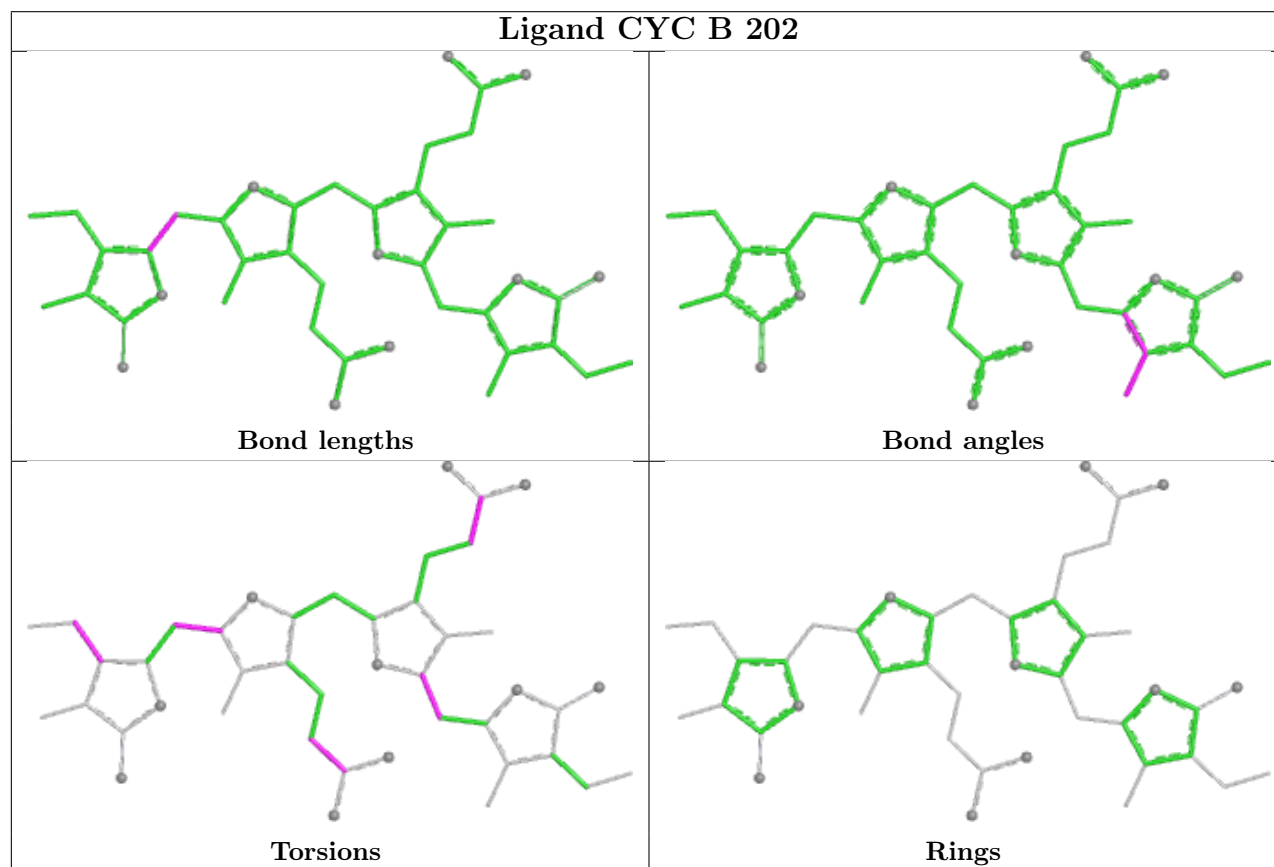
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	202	CYC	2	0
3	A	201	CYC	4	0

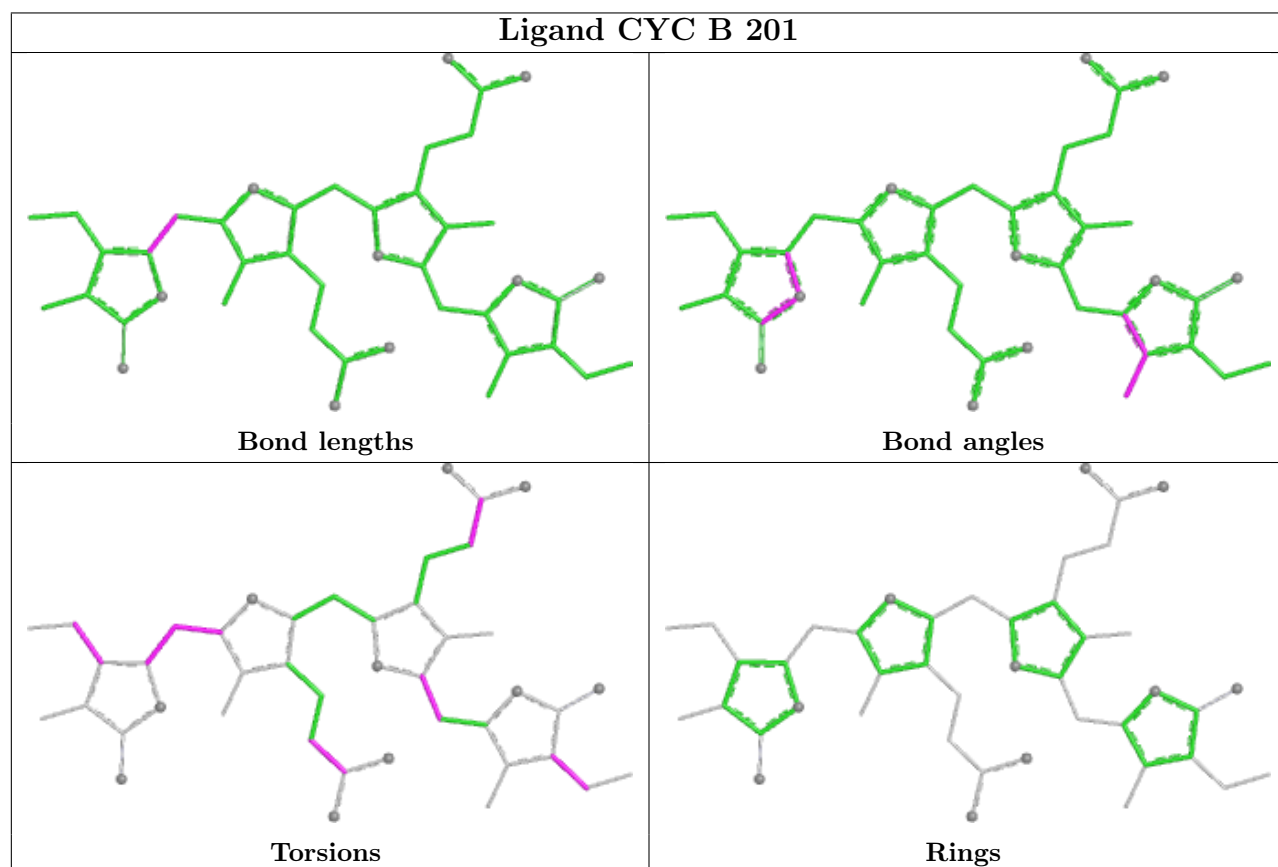
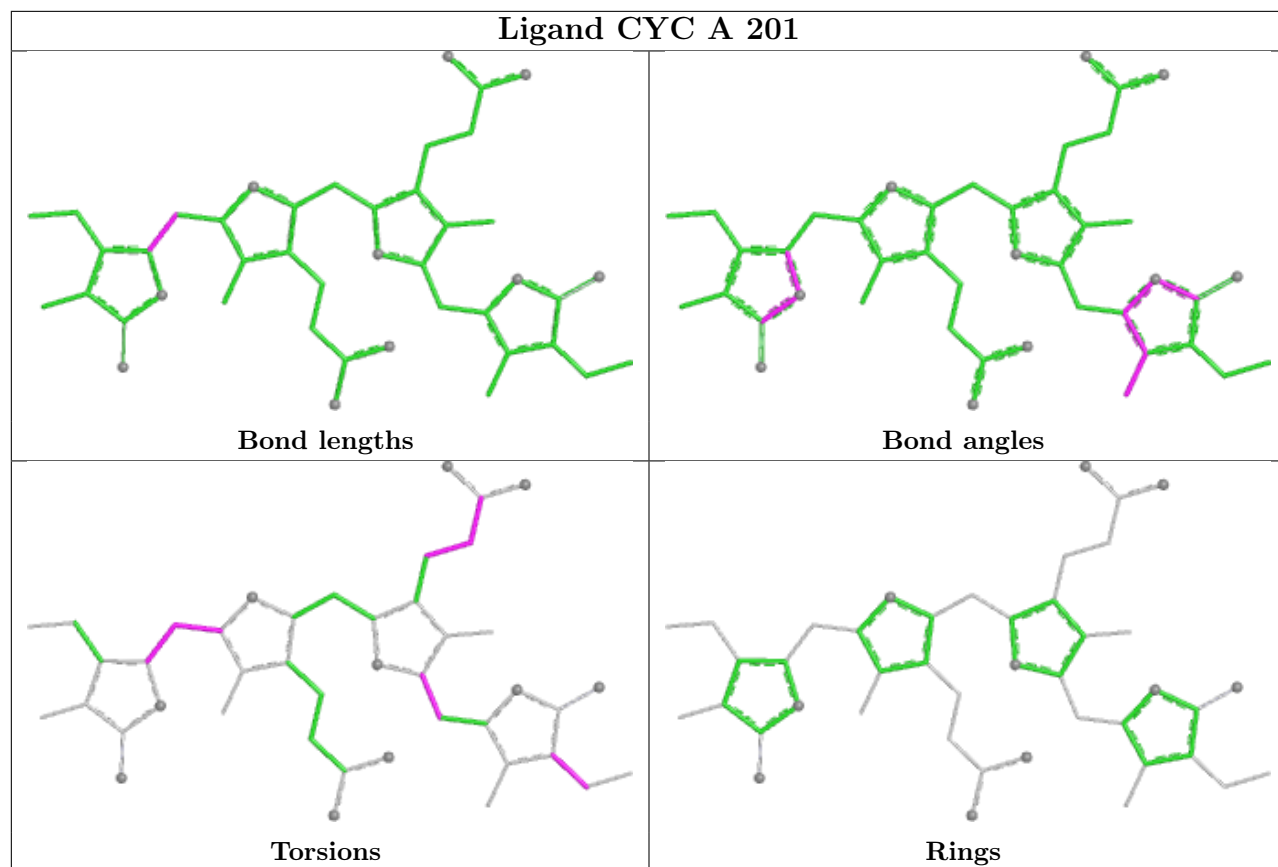
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	201	CYC	4	0

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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	71:GLY	C	72:MEN	N	3.43
1	B	72:MEN	C	73:ALA	N	3.23

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	162/162 (100%)	2.08	81 (50%) 0 0	45, 51, 59, 61	0
2	B	171/172 (99%)	2.60	117 (68%) 0 0	48, 56, 66, 72	0
All	All	333/334 (99%)	2.35	198 (59%) 0 0	45, 54, 64, 72	0

All (198) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	172	ALA	6.3
2	B	169	ALA	5.6
2	B	120	LEU	5.5
1	A	61	GLN	5.4
2	B	119	ALA	5.3
1	A	26	ALA	5.0
2	B	117	TYR	4.7
2	B	168	ALA	4.6
1	A	133	LEU	4.6
2	B	89	ILE	4.5
2	B	148	ILE	4.4
2	B	107	ASP	4.3
2	B	18	PHE	4.3
2	B	171	VAL	4.3
2	B	126	SER	4.3
1	A	138	ALA	4.2
2	B	29	ASN	4.2
2	B	69	PRO	4.2
1	A	12	ALA	4.2
2	B	20	THR	4.1
1	A	64	PRO	4.1
2	B	15	ARG	4.0
2	B	10	ALA	4.0
2	B	8	VAL	4.0

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Mol	Chain	Res	Type	RSRZ
2	B	30	LEU	3.9
2	B	170	ALA	3.9
2	B	141	ILE	3.8
2	B	113	LEU	3.7
1	A	71	GLY	3.7
1	A	58	ALA	3.7
1	A	160	ALA	3.7
2	B	136	ASP	3.7
2	B	50	THR	3.7
2	B	96	ALA	3.6
2	B	138	ALA	3.6
2	B	22	ALA	3.6
2	B	123	PRO	3.6
2	B	70	GLY	3.6
2	B	110	LEU	3.5
2	B	31	VAL	3.5
1	A	81	LYS	3.5
2	B	38	LEU	3.5
2	B	106	ASP	3.5
2	B	104	VAL	3.5
1	A	128	TRP	3.4
1	A	118	ILE	3.4
2	B	167	ALA	3.4
2	B	105	LEU	3.4
2	B	67	ILE	3.4
2	B	73	ALA	3.4
2	B	57	ARG	3.4
2	B	149	THR	3.4
2	B	79	MET	3.4
2	B	150	PRO	3.4
1	A	17	ARG	3.3
2	B	71	GLY	3.3
1	A	36	ALA	3.3
2	B	19	LEU	3.3
2	B	27	LEU	3.3
2	B	112	GLY	3.2
2	B	128	ALA	3.2
1	A	91	TYR	3.2
2	B	25	ASP	3.2
2	B	11	GLN	3.2
2	B	40	ALA	3.1
2	B	21	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	139	ILE	3.1
1	A	151	ASN	3.1
1	A	152	ALA	3.1
2	B	58	ALA	3.1
2	B	66	LEU	3.1
2	B	111	ASN	3.1
2	B	4	ALA	3.1
2	B	140	ALA	3.1
2	B	131	ILE	3.1
1	A	66	THR	3.0
2	B	142	ALA	3.0
2	B	9	VAL	3.0
1	A	82	ALA	3.0
1	A	147	ALA	3.0
2	B	52	VAL	3.0
2	B	74	TYR	3.0
2	B	14	ALA	3.0
2	B	48	ALA	3.0
1	A	63	PHE	3.0
2	B	63	GLN	2.9
1	A	10	ALA	2.9
2	B	164	PHE	2.9
1	A	24	LEU	2.9
1	A	84	CYS	2.9
2	B	88	ILE	2.9
1	A	95	VAL	2.8
2	B	51	ILE	2.8
1	A	150	ALA	2.8
2	B	161	ALA	2.8
2	B	129	VAL	2.8
1	A	42	ARG	2.8
2	B	13	ASP	2.8
1	A	34	ALA	2.8
1	A	153	TYR	2.8
2	B	23	GLN	2.7
1	A	162	SER	2.7
2	B	135	LYS	2.7
1	A	65	TYR	2.7
2	B	115	GLU	2.7
1	A	31	PHE	2.7
2	B	26	ALA	2.7
1	A	143	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	112	ILE	2.7
1	A	115	LEU	2.7
2	B	24	PHE	2.6
1	A	137	LYS	2.6
2	B	153	CYS	2.6
1	A	16	GLY	2.6
1	A	56	ALA	2.6
2	B	130	ALA	2.6
1	A	39	GLU	2.6
2	B	122	THR	2.6
1	A	142	LEU	2.6
1	A	104	THR	2.6
2	B	93	VAL	2.5
1	A	74	TYR	2.5
1	A	135	TYR	2.5
2	B	124	GLY	2.5
2	B	151	GLY	2.5
1	A	157	ALA	2.5
2	B	64	PRO	2.5
1	A	148	VAL	2.5
1	A	83	LYS	2.5
1	A	120	SER	2.5
1	A	60	TYR	2.5
1	A	48	ALA	2.5
2	B	80	ALA	2.5
1	A	59	VAL	2.4
1	A	154	ILE	2.5
1	A	158	ILE	2.5
2	B	56	ALA	2.4
1	A	136	ILE	2.4
2	B	12	ALA	2.4
2	B	55	ALA	2.4
1	A	62	LYS	2.4
1	A	68	THR	2.4
2	B	137	ALA	2.4
1	A	141	GLY	2.4
2	B	145	PRO	2.4
1	A	51	LEU	2.3
2	B	59	LEU	2.3
2	B	121	GLY	2.3
2	B	45	THR	2.3
2	B	82	CYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	113	ALA	2.3
1	A	99	LEU	2.3
1	A	140	HIS	2.3
2	B	33	GLU	2.3
1	A	43	ALA	2.3
2	B	155	ALA	2.3
2	B	34	GLY	2.3
1	A	130	ILE	2.3
2	B	127	VAL	2.3
2	B	35	ASN	2.3
2	B	81	ALA	2.3
2	B	144	ASP	2.3
2	B	165	ASP	2.3
2	B	2	LEU	2.3
1	A	100	VAL	2.2
2	B	143	ASN	2.2
1	A	11	ALA	2.2
1	A	40	ALA	2.2
1	A	37	SER	2.2
2	B	86	MET	2.2
1	A	114	GLY	2.2
1	A	111	LEU	2.2
1	A	161	LEU	2.2
1	A	15	GLN	2.2
2	B	28	SER	2.2
1	A	103	GLY	2.2
2	B	49	SER	2.2
1	A	1	MET	2.2
1	A	14	THR	2.2
1	A	129	TYR	2.1
1	A	121	THR	2.1
1	A	5	ILE	2.1
1	A	75	ALA	2.1
2	B	53	ALA	2.1
2	B	99	ALA	2.1
2	B	102	SER	2.1
2	B	158	SER	2.1
1	A	7	GLU	2.1
2	B	39	ASP	2.1
2	B	163	TYR	2.1
1	A	19	LEU	2.1
2	B	114	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	144	GLY	2.1
2	B	154	SER	2.1
2	B	1	MET	2.0
2	B	68	GLN	2.0
2	B	44	ILE	2.0
1	A	67	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	MEN	B	72	9/10	0.77	0.28	65,65,66,66	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

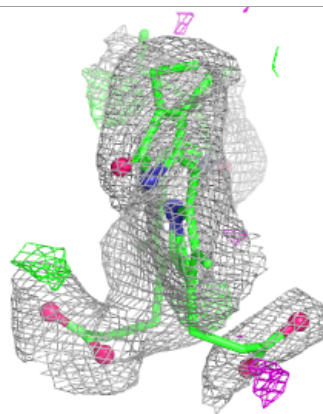
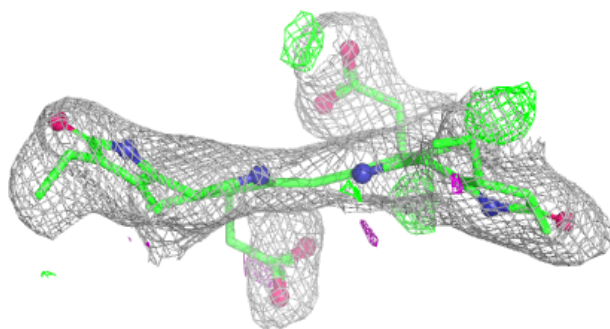
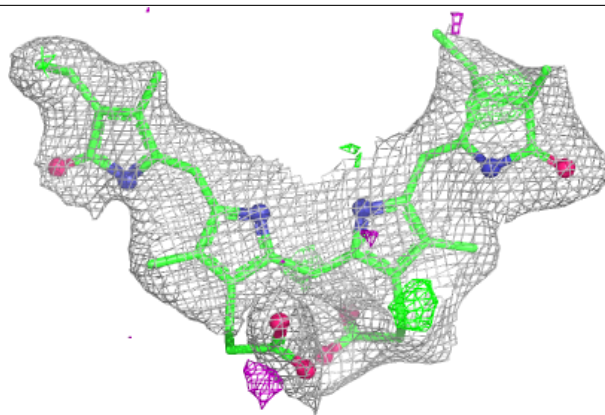
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NA	B	203	1/1	0.61	0.28	83,83,83,83	0
5	CL	B	204	1/1	0.67	0.26	91,91,91,91	0
3	CYC	B	202	43/43	0.75	0.20	59,60,61,61	0
3	CYC	A	201	43/43	0.77	0.17	45,48,49,49	0
3	CYC	B	201	43/43	0.78	0.21	63,66,67,68	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.

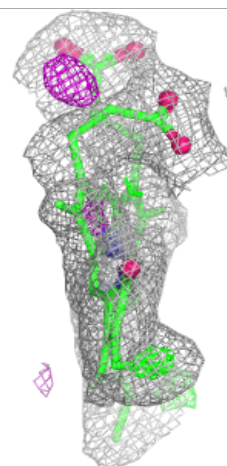
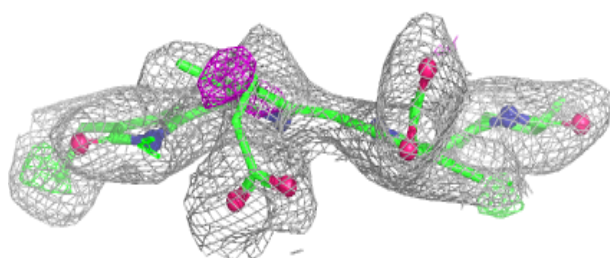
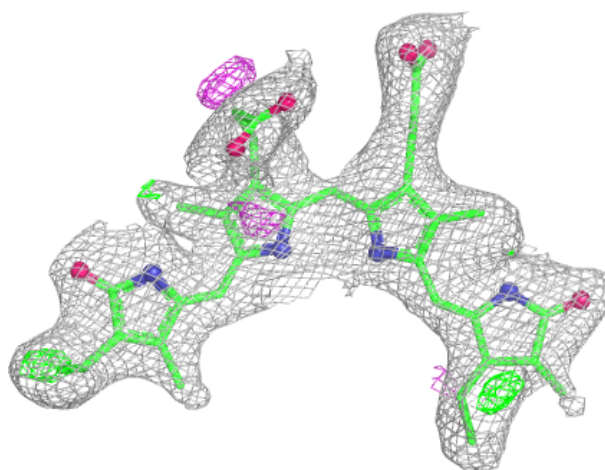
Electron density around CYC B 202:

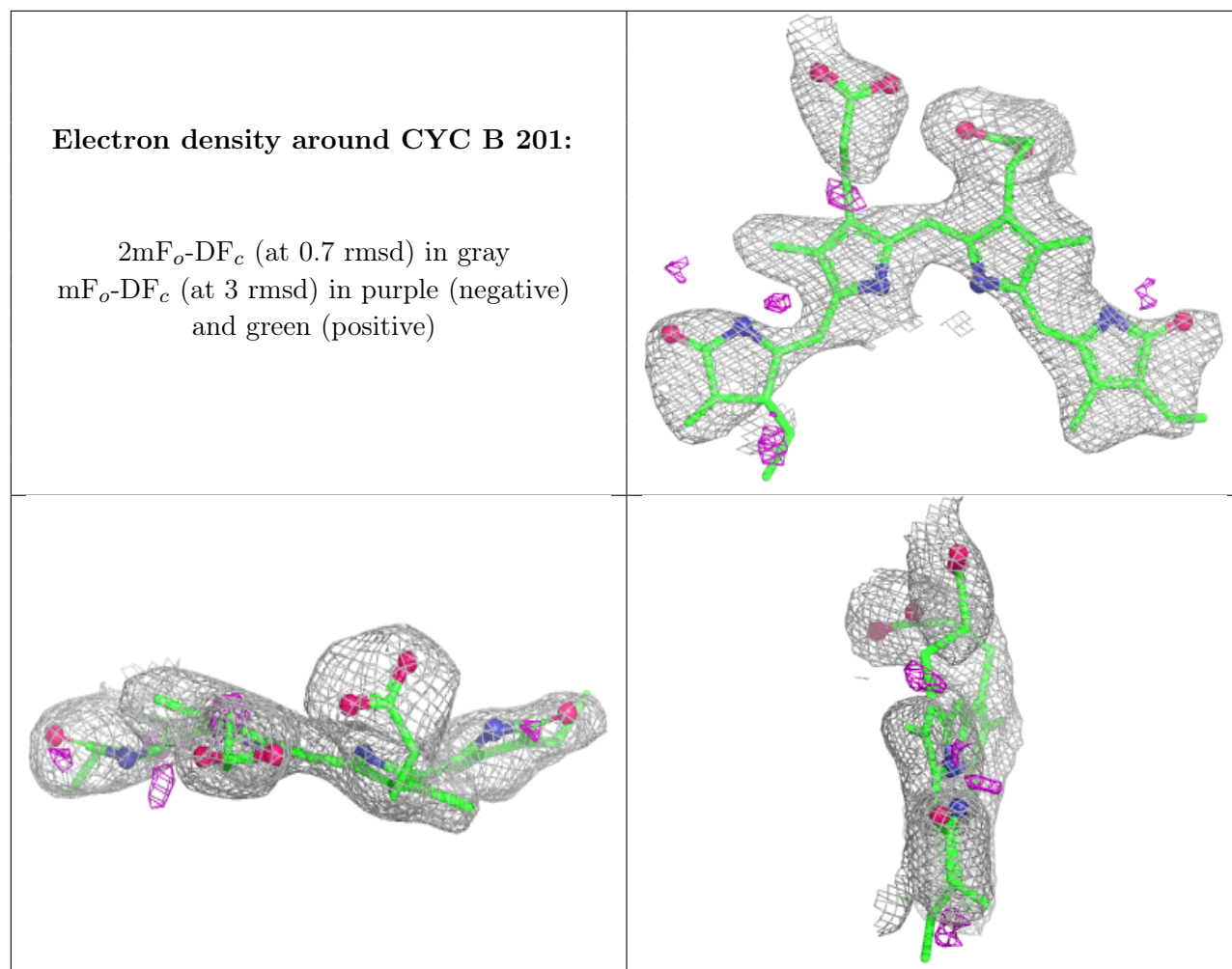
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CYC A 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers ⓘ

There are no such residues in this entry.