



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2024 – 08:14 AM EST

PDB ID : 8W0J  
Title : Crystal structure of Acetyl-CoA synthetase 2 from *Candida albicans* in complex with a propyne AMP ester inhibitor  
Authors : Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2024-02-13  
Resolution : 2.85 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), 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

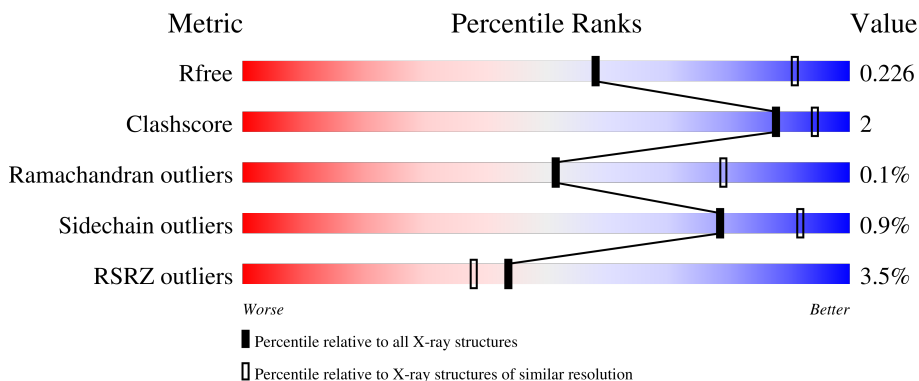
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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  $\geq 3$ , 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	686	
1	B	686	
1	C	686	

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	SO4	A	713	-	-	-	X
5	SO4	C	704	-	-	-	X

## 2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 14241 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 Acetyl-coenzyme A synthetase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	662	5144	3282	873	975	14	0	1	0
1	B	584	4553	2918	770	852	13	0	0	0
1	C	529	4144	2658	695	778	13	0	1	0

There are 51 discrepancies between the modelled and reference sequences:

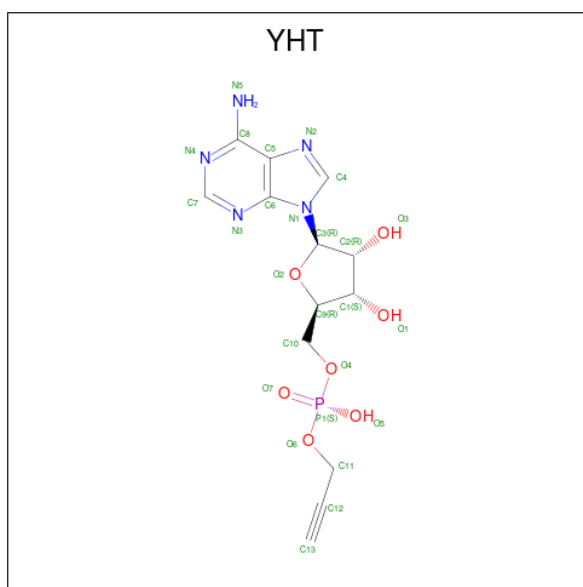
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q8NJN3
A	2	HIS	-	expression tag	UNP Q8NJN3
A	3	HIS	-	expression tag	UNP Q8NJN3
A	4	HIS	-	expression tag	UNP Q8NJN3
A	5	HIS	-	expression tag	UNP Q8NJN3
A	6	HIS	-	expression tag	UNP Q8NJN3
A	7	HIS	-	expression tag	UNP Q8NJN3
A	8	HIS	-	expression tag	UNP Q8NJN3
A	9	HIS	-	expression tag	UNP Q8NJN3
A	10	GLU	-	expression tag	UNP Q8NJN3
A	11	ASN	-	expression tag	UNP Q8NJN3
A	12	LEU	-	expression tag	UNP Q8NJN3
A	13	TYR	-	expression tag	UNP Q8NJN3
A	14	PHE	-	expression tag	UNP Q8NJN3
A	15	GLN	-	expression tag	UNP Q8NJN3
A	16	GLY	-	expression tag	UNP Q8NJN3
A	403	ALA	VAL	engineered mutation	UNP Q8NJN3
B	1	MET	-	initiating methionine	UNP Q8NJN3
B	2	HIS	-	expression tag	UNP Q8NJN3
B	3	HIS	-	expression tag	UNP Q8NJN3
B	4	HIS	-	expression tag	UNP Q8NJN3
B	5	HIS	-	expression tag	UNP Q8NJN3
B	6	HIS	-	expression tag	UNP Q8NJN3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	7	HIS	-	expression tag	UNP Q8N3N3
B	8	HIS	-	expression tag	UNP Q8N3N3
B	9	HIS	-	expression tag	UNP Q8N3N3
B	10	GLU	-	expression tag	UNP Q8N3N3
B	11	ASN	-	expression tag	UNP Q8N3N3
B	12	LEU	-	expression tag	UNP Q8N3N3
B	13	TYR	-	expression tag	UNP Q8N3N3
B	14	PHE	-	expression tag	UNP Q8N3N3
B	15	GLN	-	expression tag	UNP Q8N3N3
B	16	GLY	-	expression tag	UNP Q8N3N3
B	403	ALA	VAL	engineered mutation	UNP Q8N3N3
C	1	MET	-	initiating methionine	UNP Q8N3N3
C	2	HIS	-	expression tag	UNP Q8N3N3
C	3	HIS	-	expression tag	UNP Q8N3N3
C	4	HIS	-	expression tag	UNP Q8N3N3
C	5	HIS	-	expression tag	UNP Q8N3N3
C	6	HIS	-	expression tag	UNP Q8N3N3
C	7	HIS	-	expression tag	UNP Q8N3N3
C	8	HIS	-	expression tag	UNP Q8N3N3
C	9	HIS	-	expression tag	UNP Q8N3N3
C	10	GLU	-	expression tag	UNP Q8N3N3
C	11	ASN	-	expression tag	UNP Q8N3N3
C	12	LEU	-	expression tag	UNP Q8N3N3
C	13	TYR	-	expression tag	UNP Q8N3N3
C	14	PHE	-	expression tag	UNP Q8N3N3
C	15	GLN	-	expression tag	UNP Q8N3N3
C	16	GLY	-	expression tag	UNP Q8N3N3
C	403	ALA	VAL	engineered mutation	UNP Q8N3N3

- Molecule 2 is 5'-O-{(S)-hydroxy[(prop-2-yn-1-yl)oxy]phosphoryl}adenosine (three-letter code: YHT) (formula: C<sub>13</sub>H<sub>16</sub>N<sub>5</sub>O<sub>7</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			26	13	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			26	13	5	7	1		
2	C	1	Total	C	N	O	P	0	0
			26	13	5	7	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



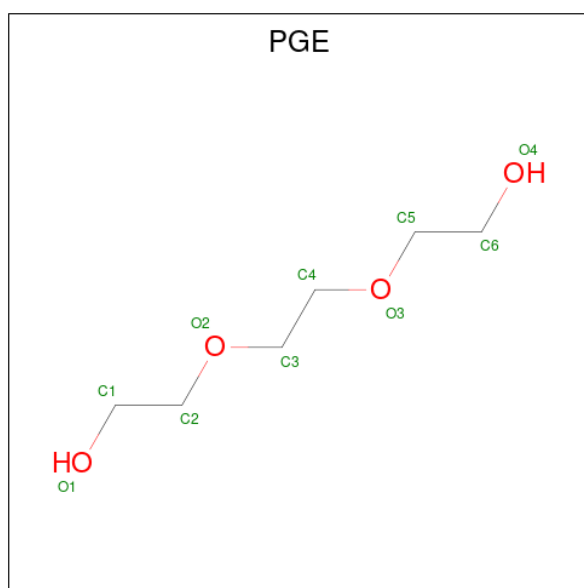
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	2	Total Cl 2 2	0	0

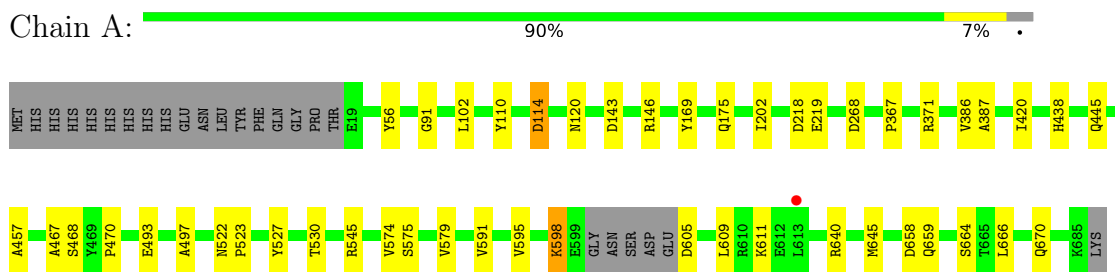
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	94	Total O 94 94	0	0
7	B	73	Total O 73 73	0	0
7	C	10	Total O 10 10	0	0

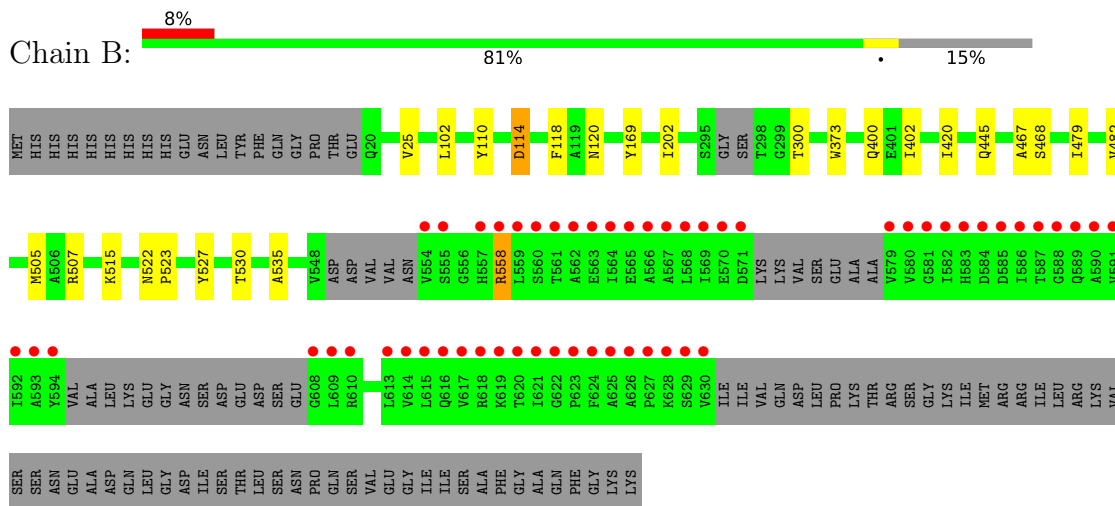
### 3 Residue-property plots

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.

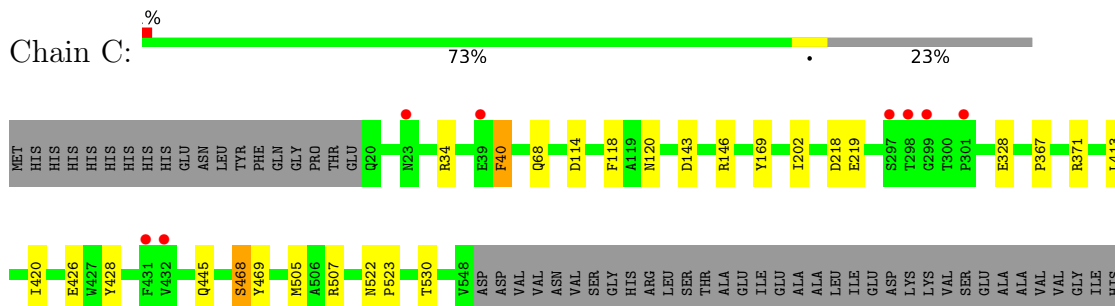
- Molecule 1: Acetyl-coenzyme A synthetase 2



- Molecule 1: Acetyl-coenzyme A synthetase 2



- Molecule 1: Acetyl-coenzyme A synthetase 2



ASP ASP  
ILE ILE  
THR THR  
GLY GLY  
GLN GLN  
ALA ALA  
VAL VAL  
ILE ILE  
ALA ALA  
TYR TYR  
SER SER  
VAL VAL  
ALA ALA  
LEU LEU  
LYS LYS  
GLN GLN  
GLY GLY  
ASN ASN  
SER SER  
ASP ASP  
GLU GLU  
ASP ASP  
SER SER  
LEU LEU  
SER SER  
GLY GLY  
LEU LEU  
ARG ARG  
LYS LYS  
GLU GLU  
VAL VAL  
LEU LEU  
LEU LEU  
GLN GLN  
VAL VAL  
ARG ARG  
LYS LYS  
THR THR  
ILE ILE  
GLY GLY  
PRO PRO  
PHE PHE  
ALA ALA  
ALA ALA  
PRO PRO  
LYS LYS  
SER SER  
VAL VAL  
ILE ILE  
ILE ILE  
VAL VAL  
GLN GLN  
ASP ASP  
LEU LEU  
PRO PRO  
LYS LYS  
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ALA  
PHE  
GLY  
ALA  
GLN  
PHE  
GLY  
LYS  
LYS

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	139.07Å 139.07Å 544.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.62 – 2.85 49.62 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.62-2.85) 100.0 (49.62-2.85)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.97 (at 2.86Å)	Xtrriage
Refinement program	PHENIX (dev_5233: ???)	Depositor
R, $R_{free}$	0.196 , 0.226 0.199 , 0.226	Depositor DCC
$R_{free}$ test set	3675 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	58.1	Xtrriage
Anisotropy	0.581	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 38.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	14241	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.21% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: YHT, PGE, GOL, CL, SO4

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	0.28	0/5276	0.50	0/7173
1	B	0.27	0/4675	0.49	0/6360
1	C	0.26	0/4267	0.47	0/5812
All	All	0.27	0/14218	0.49	0/19345

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 [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	5144	0	5034	25	0
1	B	4553	0	4426	16	0
1	C	4144	0	4002	16	0
2	A	26	0	0	0	0
2	B	26	0	0	0	0
2	C	26	0	0	0	0
3	A	24	0	32	2	0
3	B	12	0	16	0	0
3	C	12	0	16	0	0
4	A	20	0	28	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	10	0	14	0	0
5	A	30	0	0	0	0
5	B	20	0	0	0	0
5	C	15	0	0	1	0
6	B	2	0	0	1	0
7	A	94	0	0	0	0
7	B	73	0	0	2	0
7	C	10	0	0	0	0
All	All	14241	0	13568	55	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 2.

The worst 5 of 55 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:515:LYS:NZ	6:B:706:CL:CL	2.68	0.63
1:C:505:MET:O	1:C:507:ARG:NH1	2.34	0.60
1:B:400:GLN:NE2	7:B:802:HOH:O	2.36	0.58
1:C:68[A]:GLN:NE2	5:C:706:SO4:O3	2.38	0.56
1:B:467:ALA:O	1:B:468:SER:OG	2.23	0.55

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	659/686 (96%)	641 (97%)	18 (3%)	0	100	100
1	B	574/686 (84%)	560 (98%)	14 (2%)	0	100	100
1	C	528/686 (77%)	512 (97%)	15 (3%)	1 (0%)	47	75

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1761/2058 (86%)	1713 (97%)	47 (3%)	1 (0%)	51 79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	468	SER

### 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	544/568 (96%)	538 (99%)	6 (1%)	73 90
1	B	477/568 (84%)	473 (99%)	4 (1%)	81 93
1	C	435/568 (77%)	432 (99%)	3 (1%)	84 94
All	All	1456/1704 (85%)	1443 (99%)	13 (1%)	78 92

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	120	ASN
1	B	300	THR
1	C	120	ASN
1	C	40	PHE
1	C	114	ASP

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 29 ligands modelled in this entry, 2 are monoatomic - leaving 27 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	$\# Z  > 2$
4	PGE	A	707	-	9,9,9	0.33	0	8,8,8	0.58	0
5	SO4	B	709	-	4,4,4	0.66	0	6,6,6	0.19	0
5	SO4	B	708	-	4,4,4	0.65	0	6,6,6	0.07	0
5	SO4	A	709	-	4,4,4	0.66	0	6,6,6	0.16	0
5	SO4	B	710	-	4,4,4	0.63	0	6,6,6	0.12	0
4	PGE	A	706	-	9,9,9	0.32	0	8,8,8	0.55	0
3	GOL	A	702	-	5,5,5	0.29	0	5,5,5	0.41	0
3	GOL	A	703	-	5,5,5	0.31	0	5,5,5	0.36	0
5	SO4	A	710	-	4,4,4	0.61	0	6,6,6	0.32	0
3	GOL	B	702	-	5,5,5	0.35	0	5,5,5	0.18	0
3	GOL	B	703	-	5,5,5	0.30	0	5,5,5	0.38	0
3	GOL	C	702	-	5,5,5	0.35	0	5,5,5	0.36	0
2	YHT	A	701	-	25,28,28	0.65	0	26,41,41	0.78	1 (3%)
3	GOL	A	705	-	5,5,5	0.31	0	5,5,5	0.40	0
5	SO4	C	706	-	4,4,4	0.65	0	6,6,6	0.11	0
5	SO4	B	707	-	4,4,4	0.64	0	6,6,6	0.18	0
5	SO4	A	713	-	4,4,4	0.70	0	6,6,6	0.16	0
5	SO4	C	704	-	4,4,4	0.63	0	6,6,6	0.09	0
5	SO4	C	705	-	4,4,4	0.62	0	6,6,6	0.08	0
5	SO4	A	711	-	4,4,4	0.63	0	6,6,6	0.26	0
3	GOL	A	704	-	5,5,5	0.32	0	5,5,5	0.30	0
5	SO4	A	708	-	4,4,4	0.58	0	6,6,6	0.24	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GOL	C	703	-	5,5,5	0.33	0	5,5,5	0.46	0
2	YHT	B	701	-	25,28,28	0.65	0	26,41,41	0.79	1 (3%)
5	SO4	A	712	-	4,4,4	0.67	0	6,6,6	0.11	0
2	YHT	C	701	-	25,28,28	0.65	0	26,41,41	0.82	1 (3%)
4	PGE	B	704	-	9,9,9	0.31	0	8,8,8	0.48	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
4	PGE	A	707	-	-	2/7/7/7	-
2	YHT	A	701	-	-	0/11/31/31	0/3/3/3
3	GOL	A	705	-	-	4/4/4/4	-
3	GOL	C	703	-	-	1/4/4/4	-
2	YHT	B	701	-	-	1/11/31/31	0/3/3/3
3	GOL	B	702	-	-	4/4/4/4	-
3	GOL	B	703	-	-	0/4/4/4	-
2	YHT	C	701	-	-	1/11/31/31	0/3/3/3
3	GOL	C	702	-	-	2/4/4/4	-
4	PGE	A	706	-	-	6/7/7/7	-
3	GOL	A	702	-	-	2/4/4/4	-
3	GOL	A	704	-	-	3/4/4/4	-
3	GOL	A	703	-	-	0/4/4/4	-
4	PGE	B	704	-	-	3/7/7/7	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	701	YHT	C5-C8-N5	2.28	123.82	120.35
2	B	701	YHT	C5-C8-N5	2.25	123.77	120.35
2	A	701	YHT	C5-C8-N5	2.13	123.59	120.35

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

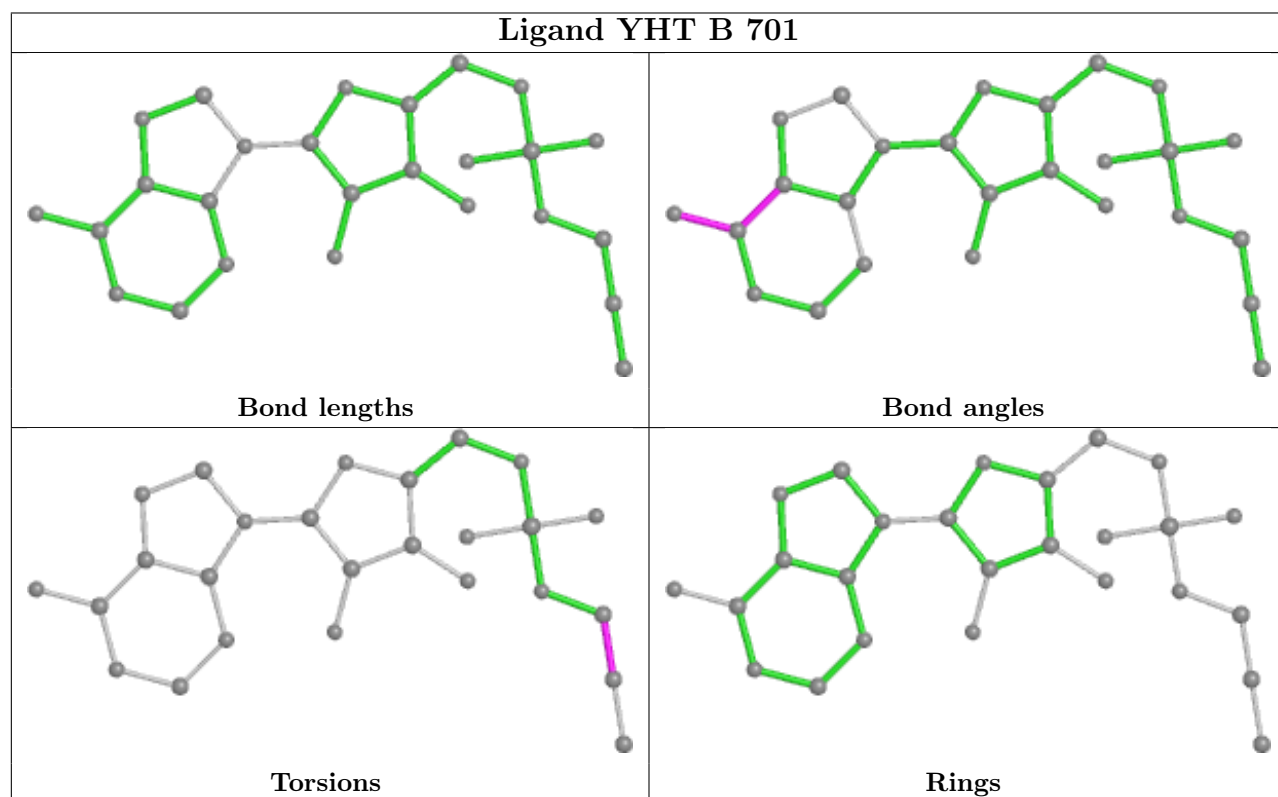
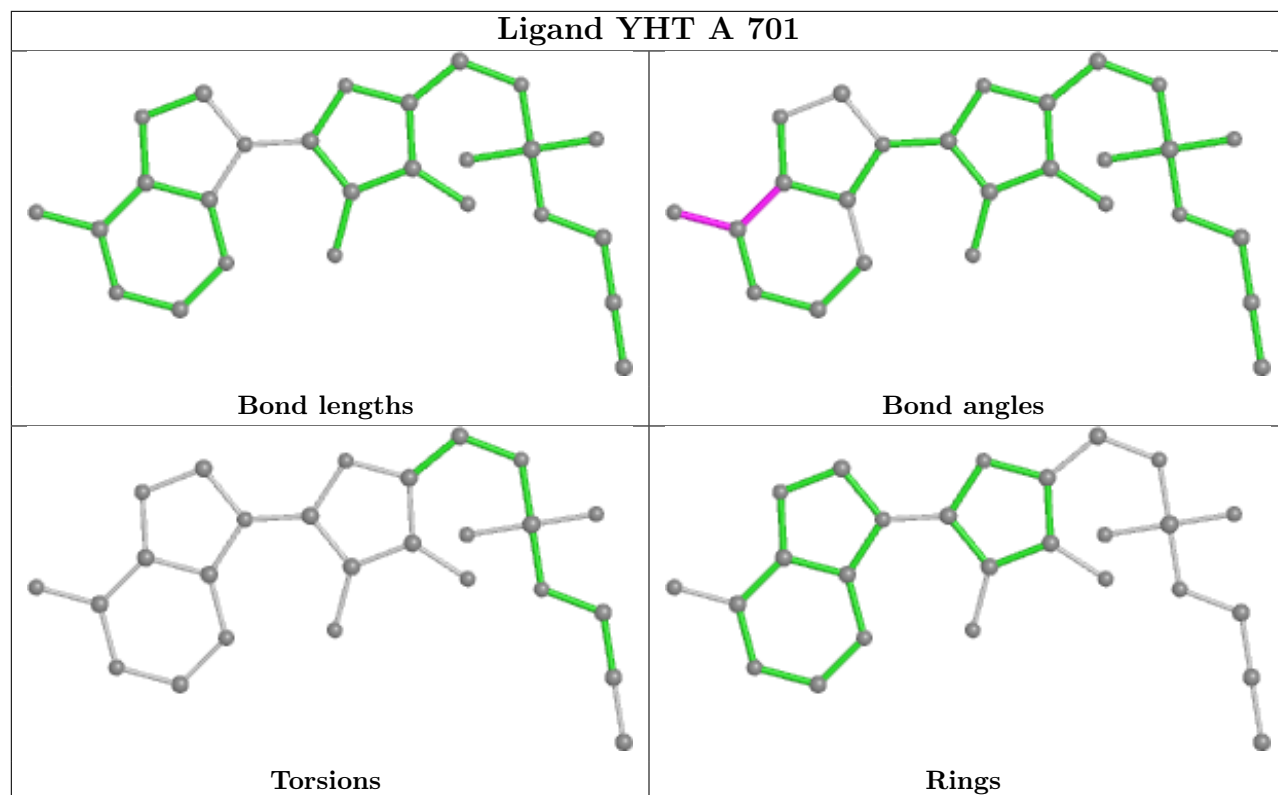
Mol	Chain	Res	Type	Atoms
2	B	701	YHT	O6-C11-C12-C13
2	C	701	YHT	O6-C11-C12-C13
3	A	705	GOL	O1-C1-C2-C3
3	B	702	GOL	C1-C2-C3-O3
3	B	702	GOL	O2-C2-C3-O3

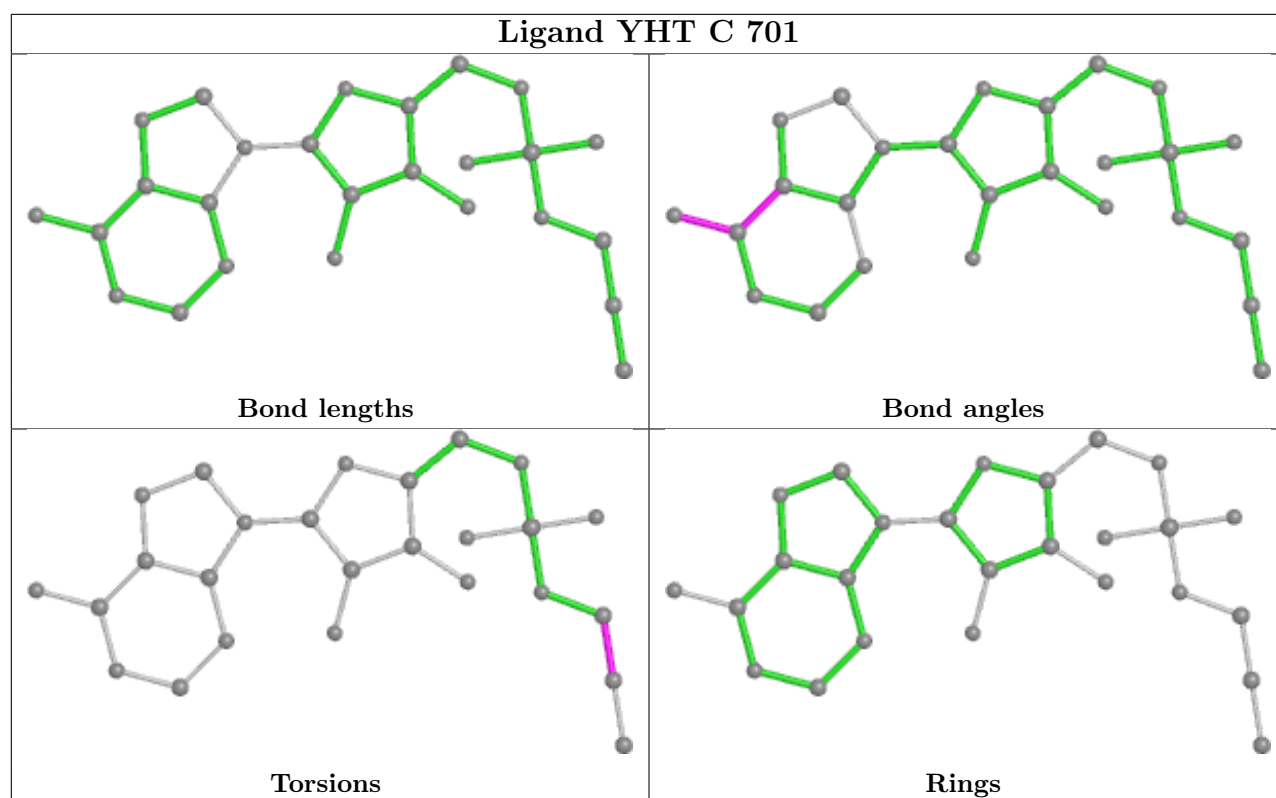
There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	705	GOL	1	0
5	C	706	SO4	1	0
3	A	704	GOL	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 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](#)

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	662/686 (96%)	-0.33	1 (0%) 95 95	41, 56, 91, 201	0
1	B	584/686 (85%)	0.06	54 (9%) 9 6	41, 59, 149, 170	0
1	C	529/686 (77%)	-0.15	8 (1%) 73 72	51, 84, 122, 164	0
All	All	1775/2058 (86%)	-0.15	63 (3%) 44 38	41, 63, 123, 201	0

The worst 5 of 63 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	564	ILE	7.5
1	B	591	VAL	6.8
1	B	630	VAL	6.7
1	B	613	LEU	6.6
1	B	568	LEU	6.5

### 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](#)

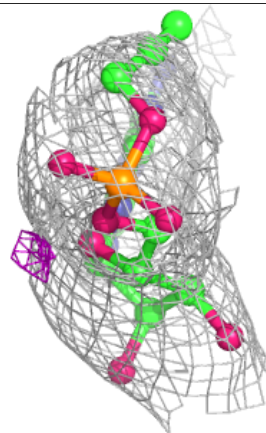
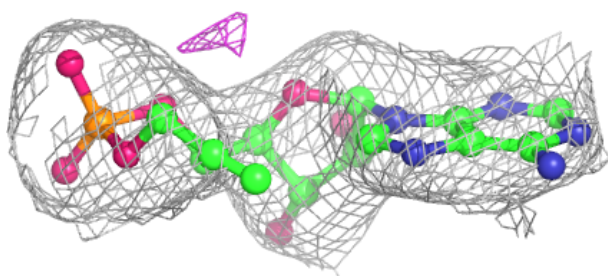
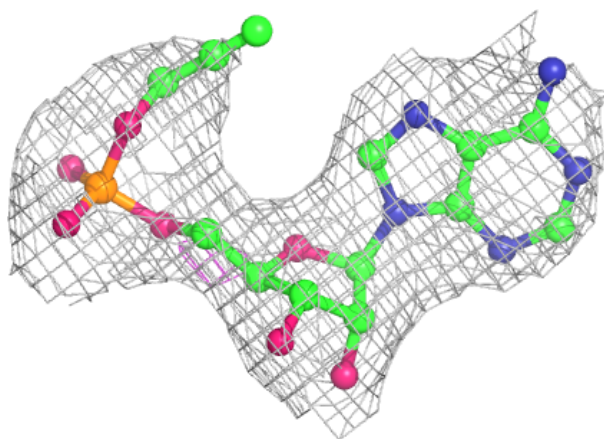
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	SO4	A	713	5/5	0.71	0.42	81,89,95,109	0
4	PGE	A	707	10/10	0.73	0.30	72,81,93,96	0
5	SO4	B	708	5/5	0.73	0.39	100,102,120,129	0
5	SO4	C	704	5/5	0.75	0.69	114,120,124,136	0
4	PGE	A	706	10/10	0.80	0.27	64,69,74,78	0
5	SO4	C	706	5/5	0.80	0.35	94,102,107,122	0
6	CL	B	705	1/1	0.80	0.14	95,95,95,95	0
6	CL	B	706	1/1	0.83	0.07	87,87,87,87	0
3	GOL	A	704	6/6	0.84	0.31	64,68,71,77	0
3	GOL	A	705	6/6	0.86	0.21	62,73,76,83	0
5	SO4	B	707	5/5	0.86	0.23	88,99,116,122	0
5	SO4	C	705	5/5	0.86	0.23	131,131,132,143	0
3	GOL	C	702	6/6	0.87	0.24	98,99,102,103	0
5	SO4	A	711	5/5	0.87	0.18	70,78,102,104	0
4	PGE	B	704	10/10	0.88	0.37	72,81,84,84	0
5	SO4	A	712	5/5	0.89	0.35	69,92,94,117	0
3	GOL	C	703	6/6	0.90	0.16	50,68,72,74	0
3	GOL	B	702	6/6	0.90	0.21	43,51,63,66	0
3	GOL	B	703	6/6	0.91	0.51	73,73,80,87	0
5	SO4	B	710	5/5	0.92	0.27	94,100,124,125	0
3	GOL	A	703	6/6	0.92	0.46	64,69,75,79	0
5	SO4	A	710	5/5	0.93	0.16	61,72,87,91	0
3	GOL	A	702	6/6	0.95	0.11	66,72,73,75	0
5	SO4	A	708	5/5	0.95	0.18	61,64,68,69	0
5	SO4	A	709	5/5	0.95	0.14	58,66,77,78	0
2	YHT	C	701	26/26	0.96	0.15	71,88,90,98	0
5	SO4	B	709	5/5	0.96	0.09	36,47,62,70	0
2	YHT	B	701	26/26	0.97	0.15	43,56,59,65	0
2	YHT	A	701	26/26	0.97	0.18	43,47,50,56	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.

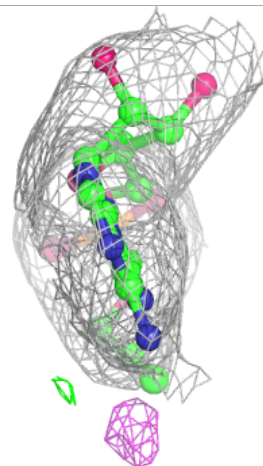
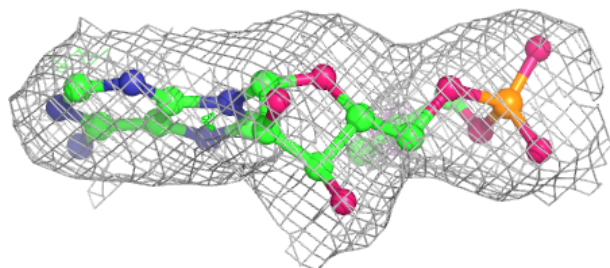
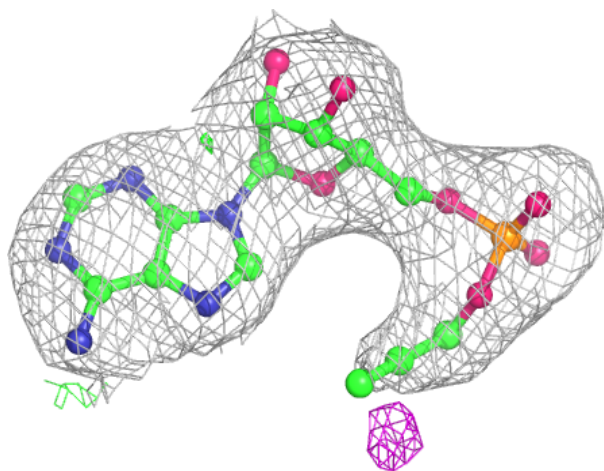
**Electron density around YHT C 701:**

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

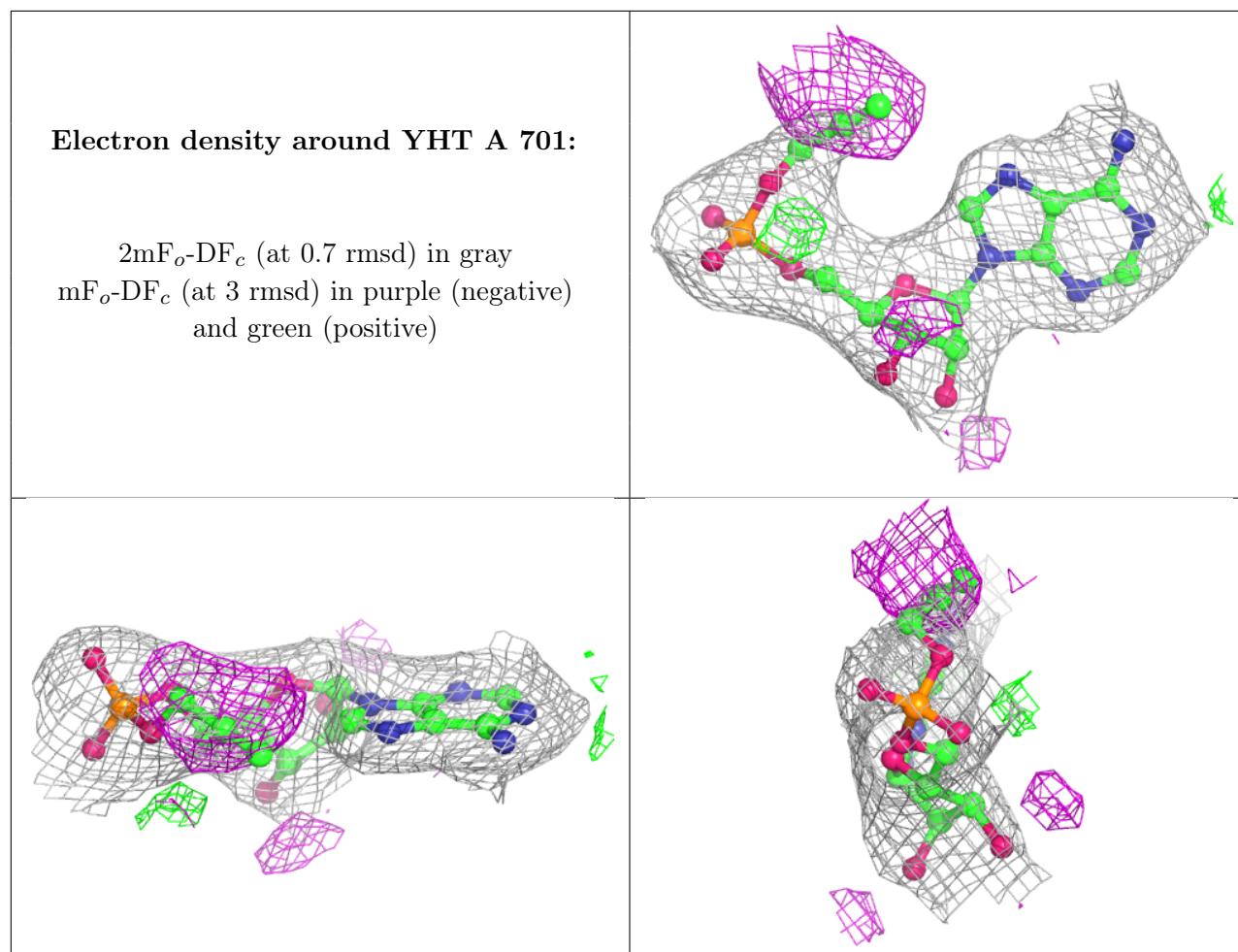


**Electron density around YHT B 701:**

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







## 6.5 Other polymers [i](#)

There are no such residues in this entry.