



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 07:05 AM BST

PDB ID : 6BD9  
Title : Saccharomyces cerevisiae acetohydroxyacid synthase  
Authors : Guddat, L.W.; Lonhienne, T.  
Deposited on : 2017-10-22  
Resolution : 1.98 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](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.

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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 : 2.13.1  
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) : 2.13.1

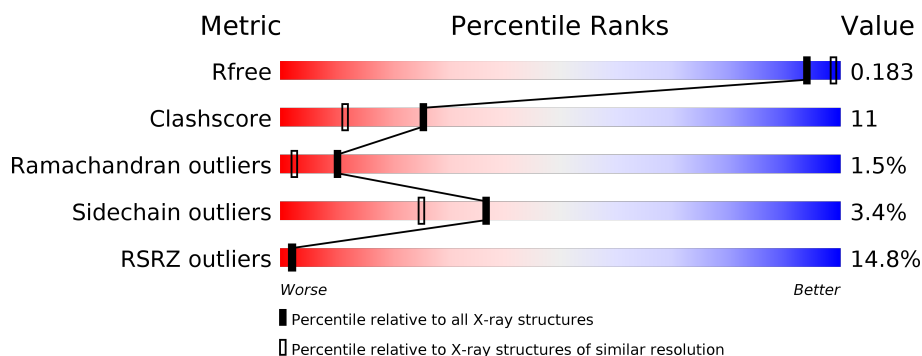
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.98 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	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	677	<div> <div>6%</div> <div> <div></div> <div>76%</div> <div>•</div> <div>20%</div> </div> </div>
1	B	677	<div> <div>18%</div> <div> <div></div> <div>66%</div> <div>13%</div> <div>• •</div> <div>17%</div> </div> </div>

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
6	PYR	A	705	-	-	X	-

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 9258 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 Acetolactate synthase catalytic subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	542	Total	C	N	O	S	0	3	0
			4122	2607	710	786	19			
1	B	564	Total	C	N	O	S	0	0	0
			4294	2718	741	815	20			

There are 94 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	expression tag	UNP P07342
A	12	HIS	-	expression tag	UNP P07342
A	13	HIS	-	expression tag	UNP P07342
A	14	HIS	-	expression tag	UNP P07342
A	15	HIS	-	expression tag	UNP P07342
A	16	HIS	-	expression tag	UNP P07342
A	17	HIS	-	expression tag	UNP P07342
A	18	SER	-	expression tag	UNP P07342
A	19	SER	-	expression tag	UNP P07342
A	20	GLY	-	expression tag	UNP P07342
A	21	LEU	-	expression tag	UNP P07342
A	22	VAL	-	expression tag	UNP P07342
A	23	PRO	-	expression tag	UNP P07342
A	24	ARG	-	expression tag	UNP P07342
A	25	GLY	-	expression tag	UNP P07342
A	26	SER	-	expression tag	UNP P07342
A	27	GLY	-	expression tag	UNP P07342
A	28	MET	-	expression tag	UNP P07342
A	29	LYS	-	expression tag	UNP P07342
A	30	GLU	-	expression tag	UNP P07342
A	31	THR	-	expression tag	UNP P07342
A	32	ALA	-	expression tag	UNP P07342
A	33	ALA	-	expression tag	UNP P07342
A	34	ALA	-	expression tag	UNP P07342
A	35	LYS	-	expression tag	UNP P07342

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Chain	Residue	Modelled	Actual	Comment	Reference
A	36	PHE	-	expression tag	UNP P07342
A	37	GLU	-	expression tag	UNP P07342
A	38	ARG	-	expression tag	UNP P07342
A	39	GLN	-	expression tag	UNP P07342
A	40	HIS	-	expression tag	UNP P07342
A	41	MET	-	expression tag	UNP P07342
A	42	ASP	-	expression tag	UNP P07342
A	43	SER	-	expression tag	UNP P07342
A	44	PRO	-	expression tag	UNP P07342
A	45	ASP	-	expression tag	UNP P07342
A	46	LEU	-	expression tag	UNP P07342
A	47	GLY	-	expression tag	UNP P07342
A	48	THR	-	expression tag	UNP P07342
A	49	ASP	-	expression tag	UNP P07342
A	50	ASP	-	expression tag	UNP P07342
A	51	ASP	-	expression tag	UNP P07342
A	52	ASP	-	expression tag	UNP P07342
A	53	LYS	-	expression tag	UNP P07342
A	54	ALA	-	expression tag	UNP P07342
A	55	MET	-	expression tag	UNP P07342
A	56	GLY	-	expression tag	UNP P07342
A	57	SER	-	expression tag	UNP P07342
B	11	MET	-	expression tag	UNP P07342
B	12	HIS	-	expression tag	UNP P07342
B	13	HIS	-	expression tag	UNP P07342
B	14	HIS	-	expression tag	UNP P07342
B	15	HIS	-	expression tag	UNP P07342
B	16	HIS	-	expression tag	UNP P07342
B	17	HIS	-	expression tag	UNP P07342
B	18	SER	-	expression tag	UNP P07342
B	19	SER	-	expression tag	UNP P07342
B	20	GLY	-	expression tag	UNP P07342
B	21	LEU	-	expression tag	UNP P07342
B	22	VAL	-	expression tag	UNP P07342
B	23	PRO	-	expression tag	UNP P07342
B	24	ARG	-	expression tag	UNP P07342
B	25	GLY	-	expression tag	UNP P07342
B	26	SER	-	expression tag	UNP P07342
B	27	GLY	-	expression tag	UNP P07342
B	28	MET	-	expression tag	UNP P07342
B	29	LYS	-	expression tag	UNP P07342
B	30	GLU	-	expression tag	UNP P07342

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Chain	Residue	Modelled	Actual	Comment	Reference
B	31	THR	-	expression tag	UNP P07342
B	32	ALA	-	expression tag	UNP P07342
B	33	ALA	-	expression tag	UNP P07342
B	34	ALA	-	expression tag	UNP P07342
B	35	LYS	-	expression tag	UNP P07342
B	36	PHE	-	expression tag	UNP P07342
B	37	GLU	-	expression tag	UNP P07342
B	38	ARG	-	expression tag	UNP P07342
B	39	GLN	-	expression tag	UNP P07342
B	40	HIS	-	expression tag	UNP P07342
B	41	MET	-	expression tag	UNP P07342
B	42	ASP	-	expression tag	UNP P07342
B	43	SER	-	expression tag	UNP P07342
B	44	PRO	-	expression tag	UNP P07342
B	45	ASP	-	expression tag	UNP P07342
B	46	LEU	-	expression tag	UNP P07342
B	47	GLY	-	expression tag	UNP P07342
B	48	THR	-	expression tag	UNP P07342
B	49	ASP	-	expression tag	UNP P07342
B	50	ASP	-	expression tag	UNP P07342
B	51	ASP	-	expression tag	UNP P07342
B	52	ASP	-	expression tag	UNP P07342
B	53	LYS	-	expression tag	UNP P07342
B	54	ALA	-	expression tag	UNP P07342
B	55	MET	-	expression tag	UNP P07342
B	56	GLY	-	expression tag	UNP P07342
B	57	SER	-	expression tag	UNP P07342

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total K 1 1	0	0
2	A	1	Total K 1 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

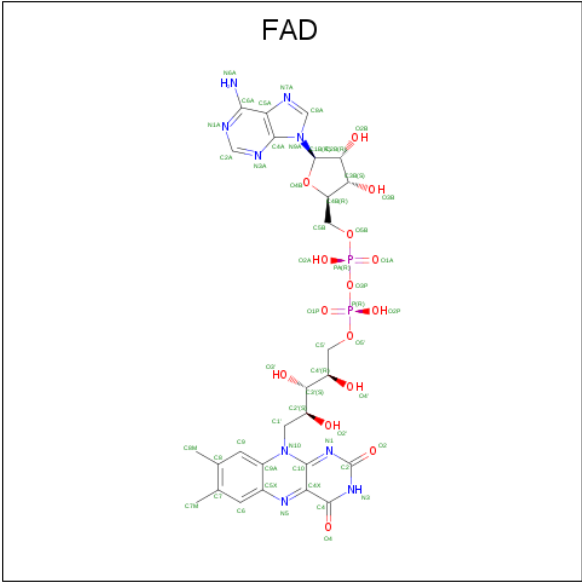
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0

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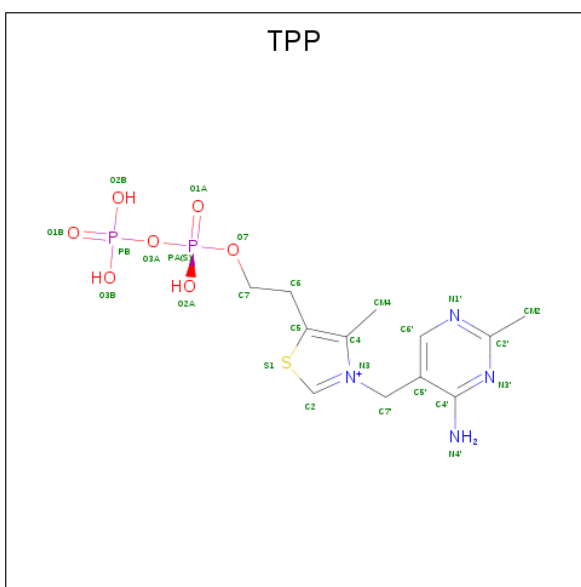
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



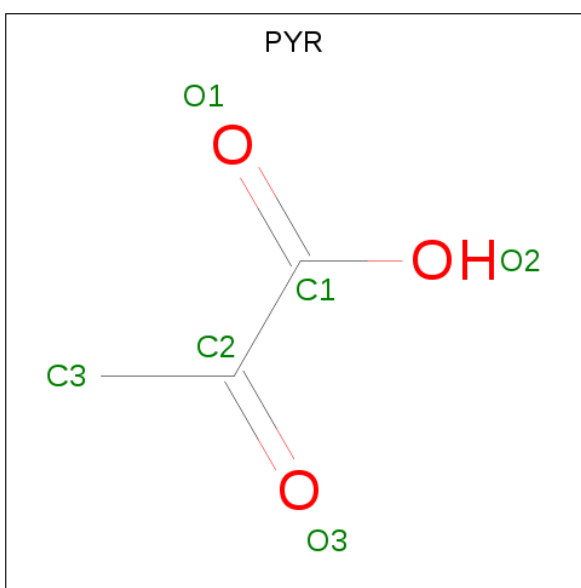
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
4	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 5 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: C<sub>12</sub>H<sub>19</sub>N<sub>4</sub>O<sub>7</sub>P<sub>2</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
5	B	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		

- Molecule 6 is PYRUVIC ACID (three-letter code: PYR) (formula:  $C_3H_4O_3$ ).



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

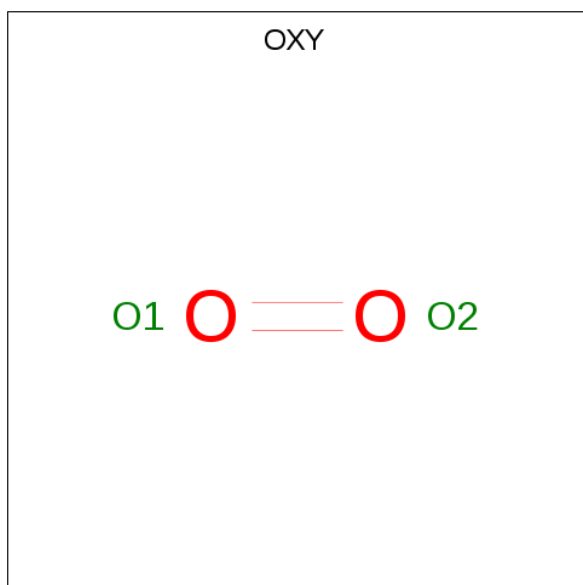
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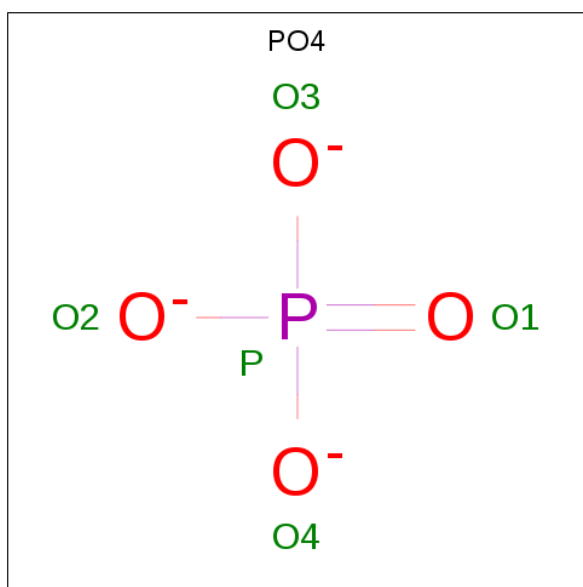
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O<sub>2</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	O	0	0
			2	2		
7	A	1	Total	O	0	0
			2	2		
7	B	1	Total	O	0	0
			2	2		
7	B	1	Total	O	0	0
			2	2		
7	B	1	Total	O	0	0
			2	2		
7	B	1	Total	O	0	0
			2	2		
7	B	1	Total	O	0	0
			2	2		

- Molecule 8 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	O	P	0	0
			5	4	1		

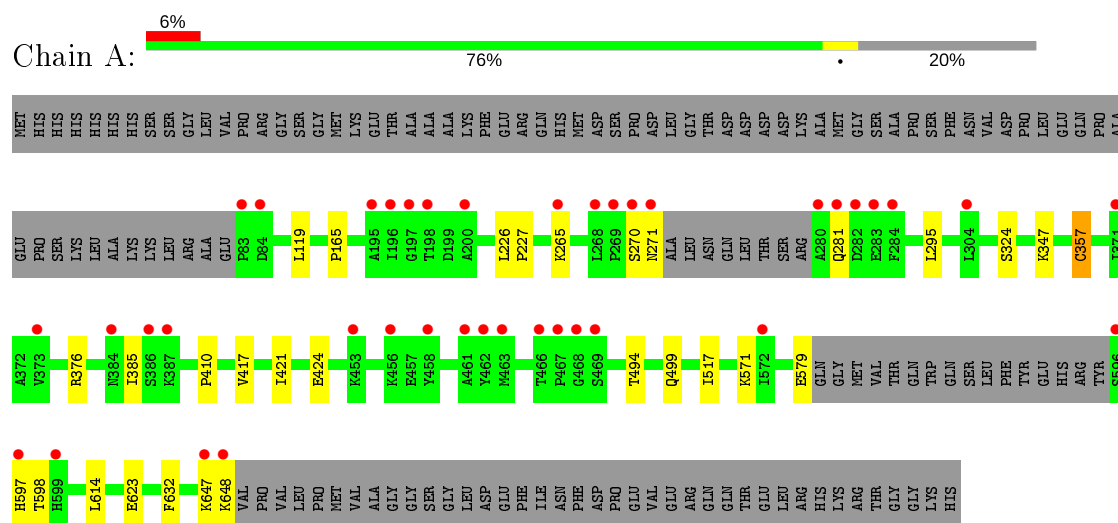
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	385	Total	O	0	0
			385	385		
9	B	250	Total	O	0	0
			250	250		

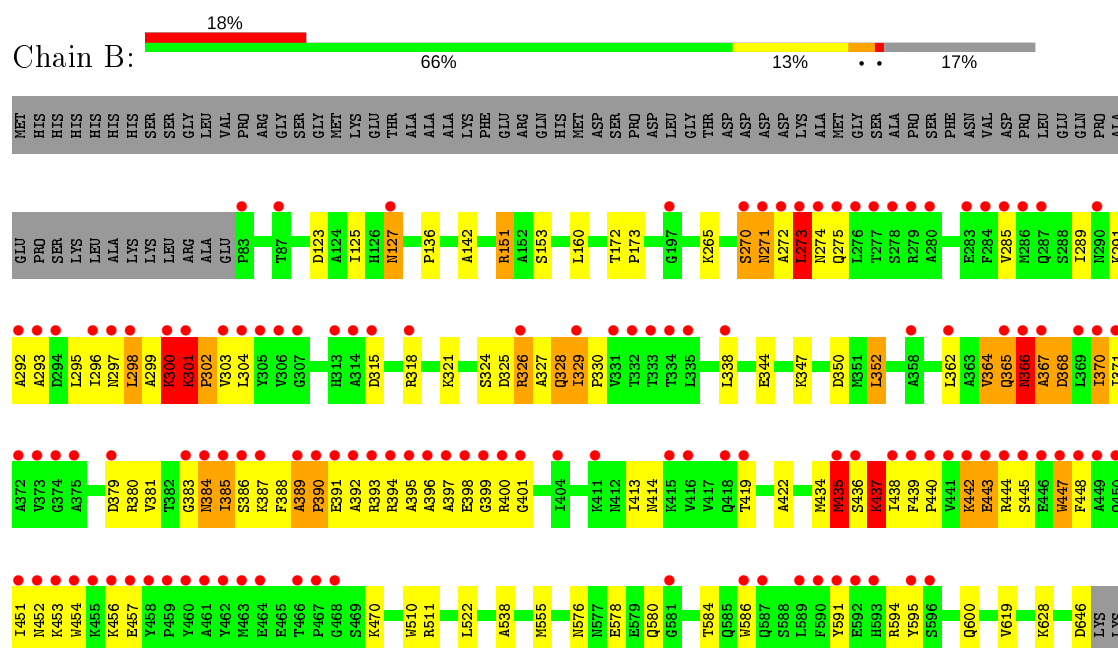
### 3 Residue-property plots

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: Acetolactate synthase catalytic subunit, mitochondrial



- Molecule 1: Acetolactate synthase catalytic subunit, mitochondrial



VAL	PRO	VAL	LEU	PRO	MET	VAL	ALA	GLY	GLY	SER	GLY	LEU	ASP	GLU	PHE	ILE	ASN	PHE	ASP	PRO	GLU	VAL	GLU	ARG	GLN	GLN	THR	GLU	LEU	ARG	HIS	LYS	ARG	THR	GLY	GLY	LYS	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.02Å 110.97Å 180.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.93 – 1.98 29.93 – 1.98	Depositor EDS
% Data completeness (in resolution range)	95.2 (29.93-1.98) 95.2 (29.93-1.98)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.59 (at 1.98Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.159 , 0.181 0.164 , 0.183	Depositor DCC
$R_{free}$ test set	2000 reflections (1.57%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.0	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 64.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9258	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: MG, PYR, PO4, TPP, K, FAD, OXY

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	0.87	0/4203	0.78	0/5700
1	B	0.83	0/4383	0.81	1/5950 (0.0%)
All	All	0.85	0/8586	0.80	1/11650 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	301	LYS	C-N-CD	5.19	139.29	128.40

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	4122	0	4146	20	0
1	B	4294	0	4307	151	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	53	0	31	1	0
4	B	53	0	30	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	26	0	16	2	0
5	B	26	0	16	6	0
6	A	12	0	6	7	0
6	B	12	0	6	3	0
7	A	4	0	0	1	0
7	B	12	0	0	0	0
8	B	5	0	0	0	0
9	A	385	0	0	3	0
9	B	250	0	0	5	0
All	All	9258	0	8558	182	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (182) 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:383:GLY:HA3	1:B:384:ASN:CB	1.69	1.19
1:B:383:GLY:CA	1:B:384:ASN:HB2	1.74	1.17
1:B:386:SER:HA	1:B:393:ARG:NH1	1.68	1.06
1:B:385:ILE:HD12	1:B:386:SER:H	1.24	0.99
1:B:297:ASN:OD1	1:B:439:PHE:N	1.95	0.99
1:B:300:LYS:NZ	1:B:400:ARG:HH22	1.60	0.98
6:B:705:PYR:H33	6:B:706:PYR:O1	1.64	0.97
1:B:386:SER:HA	1:B:393:ARG:HH12	1.31	0.94
1:B:442:LYS:HG2	1:B:443:GLU:H	1.32	0.93
1:B:326:ARG:HH21	1:B:326:ARG:HG3	1.34	0.92
1:B:368:ASP:H	1:B:392:ALA:HB2	1.33	0.91
1:B:385:ILE:CD1	1:B:386:SER:H	1.87	0.88
1:B:300:LYS:NZ	1:B:400:ARG:NH2	2.22	0.88
1:B:125:ILE:HD11	1:B:160:LEU:HD22	1.56	0.87
1:B:300:LYS:HZ1	1:B:400:ARG:HH22	1.17	0.86
1:A:357:CYS:SG	9:A:1116:HOH:O	2.35	0.85
1:B:302:PRO:O	1:B:447:TRP:HZ3	1.62	0.83
1:B:442:LYS:HG2	1:B:443:GLU:N	1.95	0.81
1:B:445:SER:HA	1:B:448:PHE:HB2	1.62	0.80
1:B:298:LEU:O	1:B:298:LEU:HD12	1.83	0.78
1:B:442:LYS:H	1:B:442:LYS:HD3	1.48	0.77
6:A:705:PYR:C3	5:B:704:TPP:H2	2.14	0.77
6:A:705:PYR:H32	5:B:704:TPP:H2	1.67	0.76
1:B:300:LYS:HZ1	1:B:400:ARG:NH2	1.80	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:SER:OG	1:B:271:ASN:N	2.18	0.76
1:A:385:ILE:HD11	1:A:417:VAL:HG12	1.70	0.73
1:B:385:ILE:HD12	1:B:386:SER:N	2.02	0.73
1:B:367:ALA:HB3	1:B:392:ALA:HB2	1.71	0.72
1:B:291:LYS:O	1:B:293:ALA:N	2.21	0.72
1:B:388:PHE:C	1:B:390:PRO:HD3	2.10	0.72
6:A:705:PYR:H32	5:B:704:TPP:HN42	1.55	0.72
1:B:299:ALA:O	1:B:300:LYS:HB2	1.89	0.71
1:B:302:PRO:O	1:B:447:TRP:CZ3	2.43	0.71
1:B:325:ASP:OD1	1:B:347:LYS:NZ	2.22	0.71
1:B:344:GLU:HG3	1:B:511:ARG:HH21	1.55	0.71
1:B:365:GLN:O	1:B:366:ASN:HB3	1.91	0.70
1:B:347:LYS:HG2	1:B:448:PHE:HZ	1.54	0.70
1:B:296:ILE:O	1:B:299:ALA:N	2.22	0.69
1:B:385:ILE:CG1	1:B:386:SER:H	2.02	0.69
1:B:347:LYS:HG2	1:B:448:PHE:CZ	2.28	0.68
1:B:352:LEU:HD13	1:B:381:VAL:HG13	1.74	0.68
1:B:326:ARG:HG3	1:B:326:ARG:NH2	2.00	0.67
1:B:584:THR:OG1	1:B:594:ARG:NE	2.22	0.67
1:B:298:LEU:HD12	1:B:298:LEU:C	2.15	0.66
1:B:327:ALA:O	1:B:444:ARG:NH2	2.21	0.66
1:B:366:ASN:HA	1:B:391:GLU:HB2	1.78	0.66
1:B:398:GLU:HB2	1:B:400:ARG:HE	1.60	0.65
6:A:705:PYR:H32	5:B:704:TPP:H7'2	1.79	0.65
1:B:301:LYS:HG3	1:B:368:ASP:HB2	1.77	0.64
1:B:383:GLY:HA3	1:B:384:ASN:HB2	0.81	0.64
1:B:395:ALA:HA	1:B:400:ARG:HG2	1.80	0.63
1:B:302:PRO:HG2	1:B:329:ILE:HG23	1.80	0.63
1:B:395:ALA:O	1:B:400:ARG:N	2.28	0.62
1:B:470:LYS:HE2	1:B:646:ASP:HA	1.82	0.62
1:A:499:GLN:OE1	1:A:648:LYS:HD3	1.99	0.61
1:B:299:ALA:HB1	1:B:444:ARG:HH12	1.65	0.60
1:B:456:LYS:N	1:B:456:LYS:HD2	2.16	0.60
1:B:324:SER:O	1:B:328:GLN:HA	2.01	0.60
1:B:365:GLN:HA	1:B:389:ALA:HA	1.84	0.59
1:B:368:ASP:HA	1:B:391:GLU:O	2.03	0.59
1:B:365:GLN:HE21	1:B:387:LYS:HE2	1.66	0.59
1:B:297:ASN:OD1	1:B:439:PHE:HB2	2.03	0.58
1:B:392:ALA:C	1:B:394:ARG:H	2.07	0.58
1:B:300:LYS:HZ3	1:B:400:ARG:HH22	1.44	0.58
1:B:368:ASP:H	1:B:392:ALA:CB	2.13	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:300:LYS:HZ3	1:B:400:ARG:NH2	2.00	0.57
1:B:295:LEU:HD12	1:B:295:LEU:O	2.04	0.57
1:B:291:LYS:O	1:B:292:ALA:HB3	2.06	0.56
1:B:367:ALA:O	1:B:368:ASP:HB2	2.06	0.56
1:B:367:ALA:O	1:B:368:ASP:CB	2.53	0.56
1:B:389:ALA:O	1:B:392:ALA:N	2.30	0.55
1:B:385:ILE:O	1:B:388:PHE:N	2.24	0.55
1:B:301:LYS:HB2	1:B:447:TRP:CZ2	2.42	0.55
1:B:123:ASP:O	1:B:127:ASN:ND2	2.41	0.54
6:A:705:PYR:H33	5:B:704:TPP:H2	1.87	0.54
1:B:297:ASN:OD1	1:B:439:PHE:CB	2.56	0.54
1:A:410:PRO:HG3	1:A:424:GLU:OE2	2.09	0.53
1:B:413:ILE:HD13	1:B:422:ALA:HB1	1.91	0.53
1:B:391:GLU:HA	1:B:391:GLU:OE1	2.09	0.53
1:B:395:ALA:O	1:B:401:GLY:N	2.40	0.53
1:B:368:ASP:O	1:B:392:ALA:HA	2.09	0.53
1:A:270:SER:HA	1:A:271:ASN:HB2	1.92	0.52
1:B:436:SER:C	1:B:438:ILE:H	2.12	0.52
1:B:303:VAL:HG23	1:B:447:TRP:HH2	1.74	0.52
1:B:397:ALA:C	1:B:399:GLY:H	2.13	0.52
1:B:151:ARG:CD	9:B:1030:HOH:O	2.57	0.52
1:B:451:ILE:C	1:B:453:LYS:H	2.13	0.52
1:A:165:PRO:HD3	1:B:522:LEU:HG	1.92	0.52
1:B:385:ILE:HD12	1:B:386:SER:CB	2.40	0.52
1:B:299:ALA:HB1	1:B:444:ARG:NH1	2.25	0.51
1:B:393:ARG:HG2	1:B:393:ARG:O	2.09	0.51
1:B:385:ILE:CG1	1:B:386:SER:N	2.72	0.51
1:A:385:ILE:HD11	1:A:417:VAL:CG1	2.40	0.51
1:A:295:LEU:HD22	1:A:421:ILE:HD12	1.93	0.51
1:B:315:ASP:OD1	1:B:318:ARG:NH1	2.44	0.51
1:B:326:ARG:NE	1:B:438:ILE:O	2.39	0.51
5:A:704:TPP:H2	9:A:895:HOH:O	2.10	0.50
1:B:395:ALA:CA	1:B:400:ARG:HG2	2.41	0.50
6:A:705:PYR:C3	5:B:704:TPP:HN42	2.23	0.49
1:B:151:ARG:HD2	9:B:1030:HOH:O	2.12	0.49
1:B:125:ILE:HD11	1:B:160:LEU:CD2	2.37	0.49
1:B:293:ALA:O	1:B:297:ASN:ND2	2.46	0.49
1:B:435:MET:O	1:B:438:ILE:N	2.46	0.48
1:B:398:GLU:HB2	1:B:400:ARG:NE	2.28	0.48
1:B:285:VAL:O	1:B:289:ILE:HG13	2.14	0.48
1:B:300:LYS:HB3	1:B:368:ASP:OD1	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:350:ASP:HB3	9:B:863:HOH:O	2.14	0.48
1:B:435:MET:CE	1:B:435:MET:HA	2.44	0.48
1:B:414:ASN:OD1	1:B:419:THR:HG22	2.14	0.47
1:B:586:TRP:CZ3	1:B:595:TYR:CE1	3.02	0.47
1:B:619:VAL:HG22	1:B:628:LYS:HG3	1.96	0.47
1:A:324:SER:OG	1:A:347:LYS:HE2	2.14	0.47
1:A:494:THR:HG22	1:A:517:ILE:HB	1.97	0.47
1:B:367:ALA:HB1	1:B:370:ILE:HG23	1.96	0.47
1:B:394:ARG:HE	1:B:400:ARG:HH11	1.62	0.47
1:B:434:MET:O	1:B:438:ILE:HG12	2.15	0.47
1:B:367:ALA:CB	1:B:392:ALA:HB2	2.44	0.47
1:B:366:ASN:C	1:B:391:GLU:HB3	2.35	0.47
5:A:704:TPP:H7'2	6:B:705:PYR:O3	2.15	0.46
1:B:364:VAL:HG12	1:B:365:GLN:N	2.30	0.46
1:B:364:VAL:O	1:B:365:GLN:C	2.54	0.46
1:B:291:LYS:C	1:B:293:ALA:N	2.66	0.46
1:A:119:LEU:HA	1:A:119:LEU:HD12	1.79	0.46
1:B:436:SER:O	1:B:438:ILE:N	2.49	0.45
1:B:451:ILE:HA	1:B:454:TRP:CD1	2.51	0.45
1:B:456:LYS:N	1:B:456:LYS:CD	2.79	0.45
1:B:297:ASN:HD21	1:B:438:ILE:HA	1.81	0.45
1:B:364:VAL:HG12	1:B:365:GLN:H	1.81	0.45
1:B:151:ARG:HG3	9:B:968:HOH:O	2.17	0.45
1:B:395:ALA:HB1	1:B:401:GLY:N	2.33	0.44
1:B:296:ILE:C	1:B:298:LEU:N	2.68	0.44
1:B:435:MET:O	1:B:438:ILE:HB	2.18	0.44
1:B:394:ARG:HE	1:B:400:ARG:NH1	2.15	0.44
1:A:623:GLU:CD	1:A:623:GLU:H	2.20	0.44
1:B:394:ARG:C	1:B:396:ALA:N	2.71	0.44
1:B:136:PRO:HG3	1:B:142:ALA:HB2	2.00	0.44
1:A:597:HIS:CG	1:A:598:THR:H	2.36	0.44
1:B:324:SER:O	1:B:328:GLN:CA	2.65	0.44
1:A:579:GLU:HG3	1:A:579:GLU:O	2.18	0.43
1:A:295:LEU:CD2	1:A:421:ILE:HD12	2.48	0.43
6:A:705:PYR:C2	7:A:708:OXY:O2	2.66	0.43
1:B:273:LEU:HD12	1:B:275:GLN:HB2	1.99	0.43
1:B:435:MET:HE2	1:B:435:MET:HA	1.99	0.43
1:B:390:PRO:HA	1:B:393:ARG:HB3	2.00	0.43
1:B:298:LEU:O	1:B:299:ALA:HB3	2.18	0.43
1:B:580:GLN:HG3	9:B:966:HOH:O	2.18	0.43
1:B:297:ASN:OD1	1:B:439:PHE:CA	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:436:SER:C	1:B:438:ILE:N	2.72	0.43
1:B:395:ALA:CB	1:B:401:GLY:HA3	2.49	0.43
1:B:437:LYS:H	1:B:437:LYS:HG2	1.45	0.43
1:A:270:SER:HB2	1:A:271:ASN:O	2.19	0.43
1:B:388:PHE:C	1:B:390:PRO:CD	2.85	0.43
1:B:292:ALA:HA	1:B:295:LEU:HB3	2.02	0.42
1:B:380:ARG:HD3	4:B:702:FAD:N5	2.34	0.42
9:A:895:HOH:O	6:B:705:PYR:C2	2.67	0.42
1:B:304:LEU:HD23	1:B:371:ILE:HB	2.01	0.42
1:B:365:GLN:NE2	1:B:387:LYS:HE2	2.32	0.42
4:B:702:FAD:H8A	4:B:702:FAD:H2B	1.88	0.42
1:B:321:LYS:HE2	1:B:325:ASP:OD2	2.18	0.42
1:B:397:ALA:C	1:B:399:GLY:N	2.72	0.42
1:B:398:GLU:CB	1:B:400:ARG:HE	2.27	0.42
1:B:580:GLN:NE2	1:B:646:ASP:O	2.52	0.42
1:B:413:ILE:HG22	1:B:414:ASN:ND2	2.35	0.42
1:B:153:SER:HB3	1:B:538:ALA:HB1	2.02	0.41
1:A:647:LYS:HG2	1:A:647:LYS:H	1.52	0.41
1:B:338:LEU:HD22	1:B:510:TRP:CD1	2.56	0.41
1:B:301:LYS:HG2	1:B:301:LYS:H	1.61	0.41
1:A:226:LEU:HB3	1:A:227:PRO:HD3	2.02	0.41
1:B:172:THR:HB	1:B:173:PRO:HD3	2.03	0.41
1:B:366:ASN:O	1:B:366:ASN:CG	2.58	0.41
1:B:298:LEU:CD1	1:B:298:LEU:C	2.85	0.41
1:B:366:ASN:HA	1:B:391:GLU:CB	2.49	0.41
1:B:368:ASP:CA	1:B:392:ALA:HA	2.51	0.41
1:B:576:ASN:OD1	1:B:578:GLU:HB3	2.21	0.41
1:A:571:LYS:HB3	1:A:632:PHE:CZ	2.56	0.40
1:B:301:LYS:C	1:B:447:TRP:CZ3	2.94	0.40
1:B:584:THR:HG1	1:B:594:ARG:HE	1.61	0.40
1:A:376:ARG:HD3	4:A:703:FAD:O2A	2.22	0.40
1:B:298:LEU:HD21	1:B:400:ARG:O	2.21	0.40
1:B:303:VAL:HB	1:B:370:ILE:HG22	2.03	0.40
1:B:329:ILE:HG22	1:B:330:PRO:HD2	2.03	0.40
1:B:394:ARG:HH11	1:B:400:ARG:NH1	2.20	0.40

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	539/677 (80%)	531 (98%)	8 (2%)	0	100	100
1	B	562/677 (83%)	515 (92%)	30 (5%)	17 (3%)	4	0
All	All	1101/1354 (81%)	1046 (95%)	38 (4%)	17 (2%)	10	2

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	272	ALA
1	B	300	LYS
1	B	364	VAL
1	B	367	ALA
1	B	368	ASP
1	B	385	ILE
1	B	591	TYR
1	B	270	SER
1	B	384	ASN
1	B	389	ALA
1	B	452	ASN
1	B	365	GLN
1	B	435	MET
1	B	437	LYS
1	B	273	LEU
1	B	328	GLN
1	B	366	ASN

### 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	445/556 (80%)	441 (99%)	4 (1%)	78	77
1	B	462/556 (83%)	435 (94%)	27 (6%)	20	9
All	All	907/1112 (82%)	876 (97%)	31 (3%)	37	25

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	265	LYS
1	A	281	GLN
1	A	357	CYS
1	A	614	LEU
1	B	127	ASN
1	B	151	ARG
1	B	265	LYS
1	B	271	ASN
1	B	273	LEU
1	B	274	ASN
1	B	298	LEU
1	B	300	LYS
1	B	301	LYS
1	B	302	PRO
1	B	326	ARG
1	B	329	ILE
1	B	352	LEU
1	B	362	LEU
1	B	366	ASN
1	B	370	ILE
1	B	379	ASP
1	B	390	PRO
1	B	435	MET
1	B	437	LYS
1	B	440	PRO
1	B	442	LYS
1	B	443	GLU
1	B	447	TRP
1	B	457	GLU
1	B	555	MET
1	B	600	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 21 ligands modelled in this entry, 4 are monoatomic - leaving 17 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	$\# Z  > 2$
7	OXY	A	708	-	1,1,1	0.22	0	-		
7	OXY	A	707	-	1,1,1	0.18	0	-		
5	TPP	B	704	3	22,27,27	1.90	4 (18%)	29,40,40	2.49	13 (44%)
5	TPP	A	704	3	22,27,27	1.39	5 (22%)	29,40,40	2.60	10 (34%)
4	FAD	B	702	-	51,58,58	2.32	15 (29%)	60,89,89	1.37	9 (15%)
6	PYR	A	706	-	2,5,5	0.25	0	2,6,6	1.26	0
8	PO4	B	713	-	4,4,4	1.22	0	6,6,6	0.88	0
7	OXY	B	711	-	1,1,1	0.28	0	-		
4	FAD	A	703	-	51,58,58	2.06	8 (15%)	60,89,89	2.08	14 (23%)
6	PYR	A	705	-	2,5,5	0.78	0	2,6,6	1.51	1 (50%)
6	PYR	B	705	-	2,5,5	1.35	0	2,6,6	0.76	0
7	OXY	B	712	-	1,1,1	0.35	0	-		
6	PYR	B	706	-	2,5,5	0.45	0	2,6,6	0.65	0
7	OXY	B	709	-	1,1,1	0.19	0	-		
7	OXY	B	710	-	1,1,1	0.16	0	-		
7	OXY	B	707	-	1,1,1	0.14	0	-		
7	OXY	B	708	-	1,1,1	0.21	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
5	TPP	B	704	3	-	3/16/17/17	0/2/2/2
5	TPP	A	704	3	-	1/16/17/17	0/2/2/2
4	FAD	B	702	-	-	3/30/50/50	0/6/6/6
6	PYR	A	706	-	-	0/0/4/4	-
4	FAD	A	703	-	-	2/30/50/50	0/6/6/6
6	PYR	A	705	-	-	0/0/4/4	-
6	PYR	B	705	-	-	0/0/4/4	-
6	PYR	B	706	-	-	0/0/4/4	-

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	702	FAD	C1'-N10	-7.87	1.40	1.48
5	B	704	TPP	C6-C5	6.53	1.53	1.50
4	A	703	FAD	C4-C4X	6.19	1.52	1.41
4	B	702	FAD	C10-N1	6.07	1.41	1.33
4	B	702	FAD	C2B-C1B	-5.99	1.44	1.53
4	A	703	FAD	C1'-N10	-5.82	1.42	1.48
4	A	703	FAD	C10-N1	5.65	1.40	1.33
4	A	703	FAD	C4X-N5	5.08	1.40	1.33
4	A	703	FAD	C4-N3	4.29	1.40	1.33
4	A	703	FAD	C2B-C1B	-4.22	1.47	1.53
4	B	702	FAD	C4X-C10	-3.94	1.34	1.38
4	B	702	FAD	C4-C4X	3.70	1.47	1.41
4	B	702	FAD	O3'-C3'	-3.51	1.34	1.43
5	A	704	TPP	C4'-N4'	3.15	1.42	1.34
5	B	704	TPP	C2'-N1'	2.98	1.39	1.34
4	B	702	FAD	O4-C4	-2.94	1.17	1.24
5	B	704	TPP	C4-N3	-2.92	1.37	1.39
4	B	702	FAD	C2B-C3B	-2.86	1.45	1.53
5	A	704	TPP	C6'-N1'	2.83	1.40	1.34
4	A	703	FAD	C2'-C3'	2.55	1.58	1.53
4	B	702	FAD	PA-O2A	-2.44	1.43	1.55
4	B	702	FAD	C2A-N1A	-2.43	1.29	1.33
4	B	702	FAD	O4B-C4B	-2.40	1.39	1.45
5	B	704	TPP	C7'-C5'	2.31	1.56	1.51
4	B	702	FAD	C4X-N5	2.28	1.36	1.33
4	B	702	FAD	P-O2P	-2.25	1.44	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	704	TPP	C4-N3	-2.25	1.37	1.39
4	B	702	FAD	C9A-C5X	-2.14	1.38	1.42
5	A	704	TPP	C7'-C5'	2.12	1.55	1.51
4	A	703	FAD	C7M-C7	2.10	1.55	1.51
4	B	702	FAD	C8A-N7A	-2.02	1.31	1.34
5	A	704	TPP	PB-O2B	-2.02	1.47	1.54

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	703	FAD	C1'-N10-C9A	8.45	124.94	118.29
5	B	704	TPP	CM2-C2'-N1'	6.96	124.80	117.14
5	A	704	TPP	CM2-C2'-N1'	6.65	124.45	117.14
5	A	704	TPP	C6-C5-C4	6.08	132.31	127.43
4	A	703	FAD	C4-N3-C2	5.68	119.94	115.14
4	B	702	FAD	C4-N3-C2	4.61	119.03	115.14
4	A	703	FAD	C4-C4X-N5	4.59	123.84	118.60
5	B	704	TPP	N1'-C2'-N3'	-4.50	117.80	125.54
5	A	704	TPP	N1'-C2'-N3'	-4.38	118.00	125.54
5	A	704	TPP	C7'-N3-C2	-4.31	117.56	125.35
5	B	704	TPP	C6'-N1'-C2'	4.03	122.81	115.96
5	B	704	TPP	C7'-N3-C2	-3.79	118.50	125.35
4	B	702	FAD	C4A-C5A-N7A	-3.78	105.46	109.40
4	A	703	FAD	C4-C4X-C10	-3.76	117.46	119.95
5	B	704	TPP	C5-C4-N3	3.76	115.09	107.57
5	A	704	TPP	C6'-N1'-C2'	3.74	122.33	115.96
5	A	704	TPP	CM4-C4-C5	-3.74	119.42	127.60
4	A	703	FAD	C10-C4X-N5	-3.72	118.68	121.26
5	B	704	TPP	CM4-C4-C5	-3.56	119.83	127.60
4	A	703	FAD	C5'-C4'-C3'	-3.52	105.40	112.20
5	A	704	TPP	CM4-C4-N3	3.33	126.78	122.53
5	A	704	TPP	C5-C4-N3	3.11	113.80	107.57
4	B	702	FAD	C9A-N10-C10	-3.05	117.92	121.91
4	A	703	FAD	N3A-C2A-N1A	-2.97	124.04	128.68
4	B	702	FAD	C1'-N10-C10	-2.83	115.87	118.41
4	A	703	FAD	C9A-N10-C10	-2.83	118.20	121.91
5	A	704	TPP	PA-O3A-PB	-2.80	123.20	132.83
4	A	703	FAD	C4X-N5-C5X	2.79	119.56	116.77
5	B	704	TPP	C6-C5-C4	2.72	129.62	127.43
4	B	702	FAD	C1'-N10-C9A	2.58	120.33	118.29
5	B	704	TPP	O3B-PB-O2B	2.56	117.43	107.64
4	A	703	FAD	C4A-C5A-N7A	-2.53	106.76	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	702	FAD	N3A-C2A-N1A	-2.53	124.73	128.68
4	A	703	FAD	C5X-C9A-N10	2.51	119.53	117.72
5	B	704	TPP	N4'-C4'-N3'	-2.50	113.50	117.03
4	B	702	FAD	C4-C4X-C10	-2.43	118.34	119.95
4	A	703	FAD	C4X-C4-N3	-2.32	120.25	123.43
5	B	704	TPP	PA-O3A-PB	-2.31	124.89	132.83
5	A	704	TPP	C5'-C6'-N1'	-2.29	120.01	123.82
4	A	703	FAD	C4X-C10-N10	2.27	122.63	120.30
4	A	703	FAD	O4B-C4B-C5B	-2.24	101.99	109.37
4	B	702	FAD	O2'-C2'-C1'	-2.21	104.27	109.59
4	B	702	FAD	O4B-C1B-C2B	-2.18	103.74	106.93
6	A	705	PYR	O3-C2-C3	2.12	124.93	120.17
5	B	704	TPP	C5'-C4'-N3'	2.05	124.46	121.24
5	B	704	TPP	C5'-C6'-N1'	-2.01	120.46	123.82
5	B	704	TPP	C5'-C7'-N3	-2.01	109.93	113.28

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	704	TPP	C4-C5-C6-C7
5	B	704	TPP	PA-O3A-PB-O2B
5	A	704	TPP	C4-C5-C6-C7
4	B	702	FAD	P-O3P-PA-O5B
4	A	703	FAD	P-O3P-PA-O5B
5	B	704	TPP	PA-O3A-PB-O1B
4	A	703	FAD	O4B-C4B-C5B-O5B
4	B	702	FAD	C5'-O5'-P-O1P
4	B	702	FAD	O4B-C4B-C5B-O5B

There are no ring outliers.

8 monomers are involved in 14 short contacts:

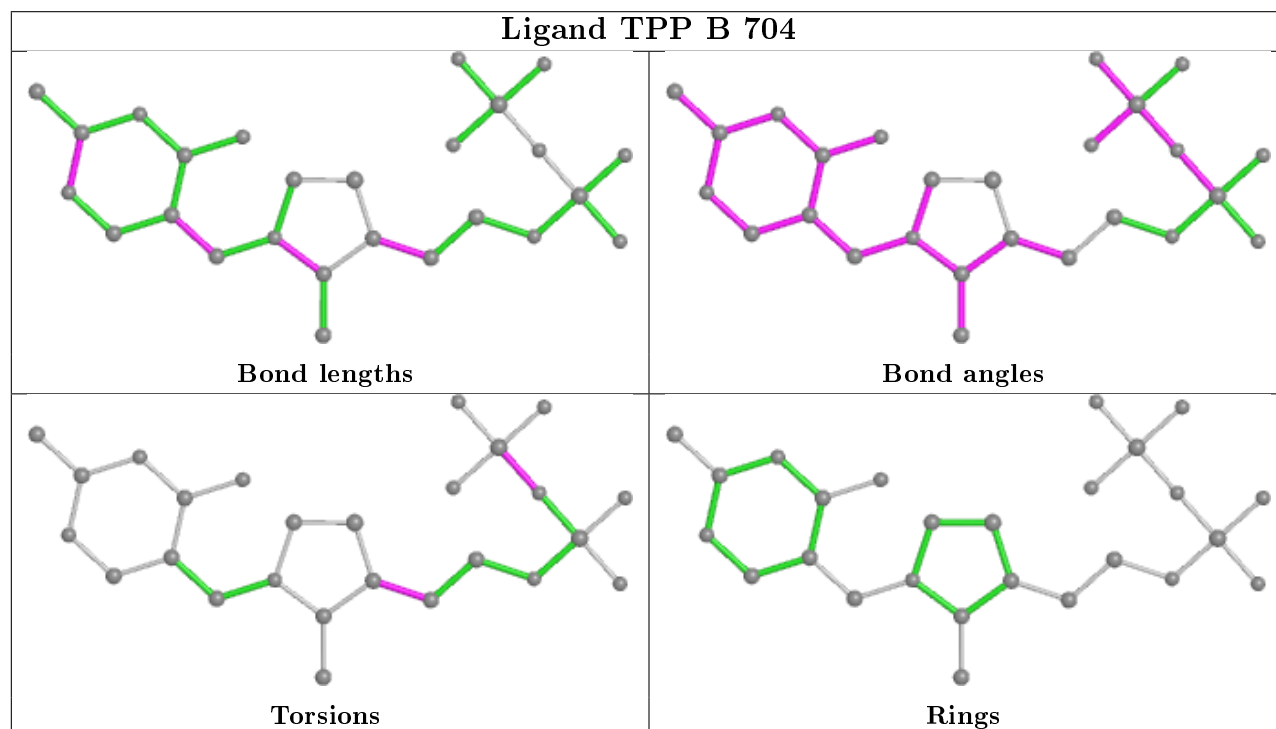
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	708	OXY	1	0
5	B	704	TPP	6	0
5	A	704	TPP	2	0
4	B	702	FAD	2	0
4	A	703	FAD	1	0
6	A	705	PYR	7	0
6	B	705	PYR	3	0

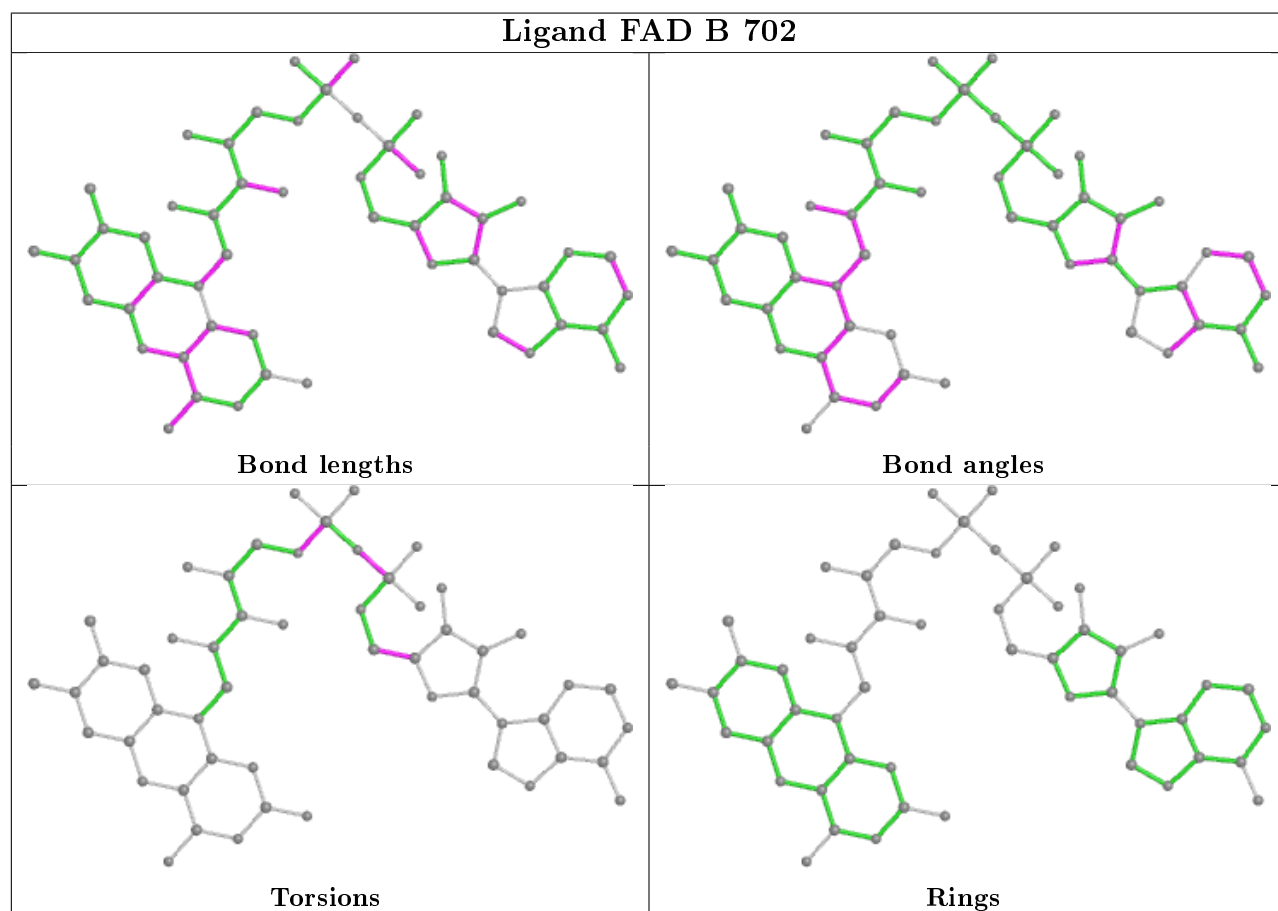
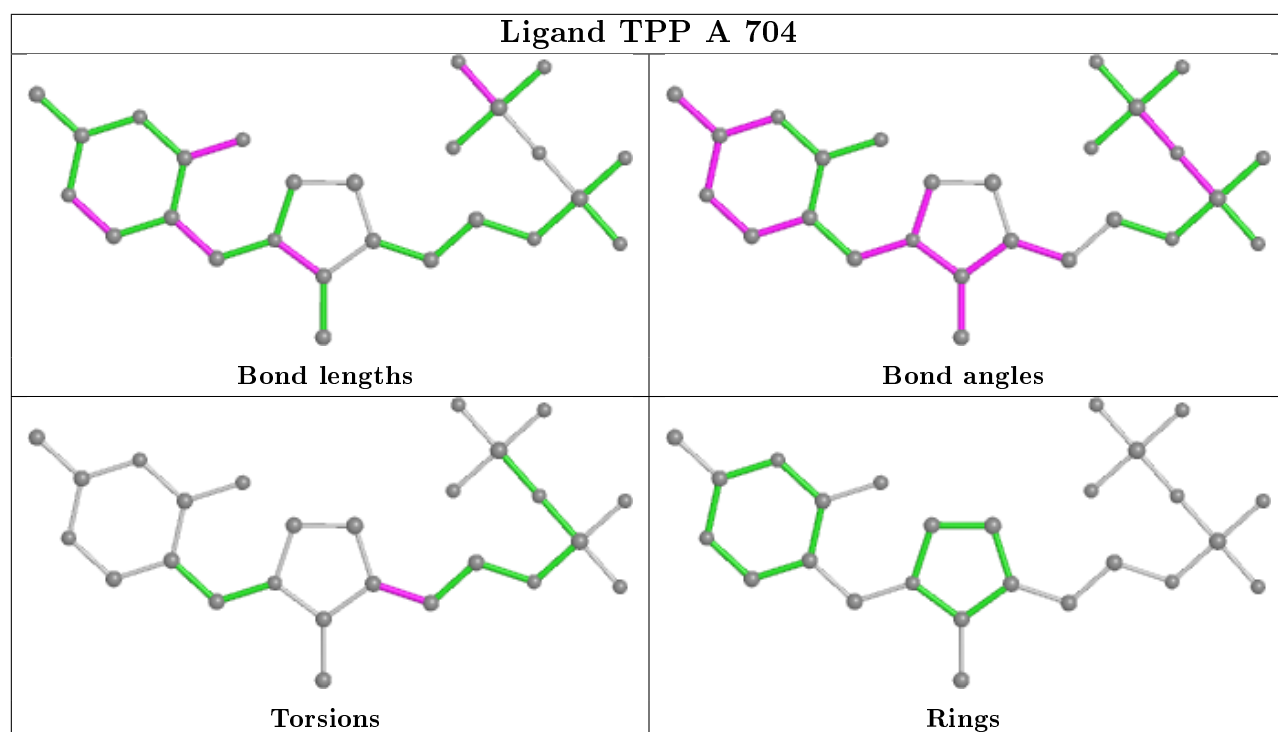
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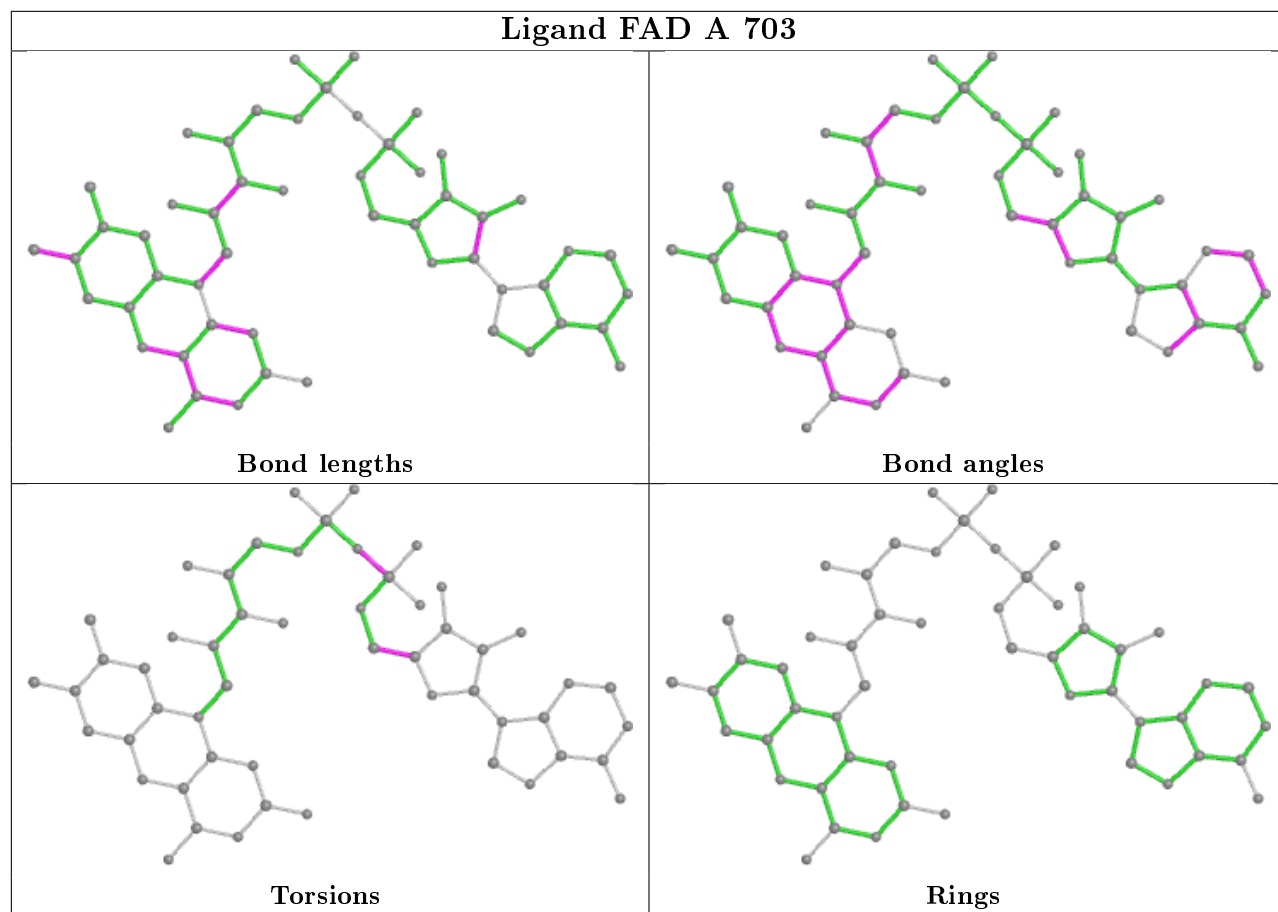
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	706	PYR	1	0

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 ⓘ

### 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, 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	542/677 (80%)	0.17	39 (7%) 15 17	19, 29, 66, 115	0
1	B	564/677 (83%)	0.95	125 (22%) 0 0	18, 40, 122, 152	0
All	All	1106/1354 (81%)	0.57	164 (14%) 2 2	18, 32, 108, 152	0

All (164) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	273	LEU	13.7
1	B	458	TYR	12.1
1	B	591	TYR	9.9
1	B	272	ALA	8.9
1	B	454	TRP	8.3
1	B	590	PHE	7.5
1	B	461	ALA	7.3
1	B	451	ILE	6.9
1	B	449	ALA	6.7
1	B	371	ILE	6.4
1	B	304	LEU	6.0
1	B	397	ALA	6.0
1	A	271	ASN	6.0
1	A	597	HIS	6.0
1	B	396	ALA	5.8
1	B	462	TYR	5.8
1	B	439	PHE	5.8
1	A	463	MET	5.7
1	B	127	ASN	5.7
1	A	83	PRO	5.6
1	A	467	PRO	5.6
1	B	460	TYR	5.6
1	B	83	PRO	5.5
1	B	274	ASN	5.5

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Mol	Chain	Res	Type	RSRZ
1	B	390	PRO	5.4
1	B	436	SER	5.3
1	B	387	LYS	5.3
1	B	372	ALA	5.3
1	B	463	MET	5.2
1	B	306	VAL	5.2
1	B	386	SER	5.1
1	B	303	VAL	5.1
1	B	467	PRO	5.0
1	B	276	LEU	5.0
1	A	596	SER	5.0
1	B	447	TRP	4.9
1	B	438	ILE	4.9
1	B	459	PRO	4.9
1	B	279	ARG	4.7
1	B	392	ALA	4.7
1	B	384	ASN	4.7
1	B	271	ASN	4.6
1	B	456	LYS	4.5
1	B	385	ILE	4.5
1	B	400	ARG	4.5
1	A	268	LEU	4.4
1	A	280	ALA	4.4
1	B	293	ALA	4.4
1	B	595	TYR	4.4
1	B	284	PHE	4.3
1	B	448	PHE	4.1
1	B	401	GLY	4.1
1	B	370	ILE	4.1
1	B	589	LEU	4.0
1	B	305	TYR	4.0
1	B	442	LYS	4.0
1	B	453	LYS	4.0
1	A	466	THR	4.0
1	A	599	HIS	4.0
1	A	647	LYS	4.0
1	B	445	SER	3.9
1	B	416	VAL	3.9
1	B	369	LEU	3.9
1	B	373	VAL	3.9
1	B	468	GLY	3.8
1	B	383	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	365	GLN	3.8
1	B	287	GLN	3.8
1	B	466	THR	3.7
1	B	326	ARG	3.6
1	B	332	THR	3.6
1	B	441	VAL	3.6
1	B	277	THR	3.6
1	A	281	GLN	3.5
1	A	265	LYS	3.5
1	B	275	GLN	3.5
1	B	283	GLU	3.5
1	B	280	ALA	3.5
1	B	285	VAL	3.4
1	B	362	LEU	3.4
1	B	394	ARG	3.4
1	B	395	ALA	3.4
1	A	270	SER	3.3
1	A	458	TYR	3.3
1	B	278	SER	3.3
1	A	283	GLU	3.2
1	B	457	GLU	3.2
1	B	298	LEU	3.2
1	B	300	LYS	3.1
1	A	468	GLY	3.0
1	A	461	ALA	3.0
1	B	418	GLN	3.0
1	A	456	LYS	3.0
1	B	415	LYS	3.0
1	B	334	THR	2.9
1	A	84	ASP	2.9
1	B	443	GLU	2.9
1	B	393	ARG	2.9
1	B	435	MET	2.9
1	B	411	LYS	2.9
1	B	197	GLY	2.9
1	B	399	GLY	2.9
1	B	270	SER	2.9
1	A	648	LYS	2.9
1	B	333	THR	2.9
1	B	290	ASN	2.9
1	B	404	ILE	2.8
1	A	387	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	592	GLU	2.8
1	B	586	TRP	2.8
1	B	307	GLY	2.8
1	B	294	ASP	2.8
1	A	282	ASP	2.7
1	B	398	GLU	2.7
1	B	440	PRO	2.7
1	A	462	TYR	2.7
1	B	450	GLN	2.7
1	A	198	THR	2.7
1	B	375	ALA	2.6
1	B	389	ALA	2.6
1	A	197	GLY	2.6
1	A	304	LEU	2.6
1	B	286	MET	2.6
1	A	195	ALA	2.6
1	B	452	ASN	2.6
1	B	315	ASP	2.5
1	A	469	SER	2.5
1	B	455	LYS	2.5
1	B	358	ALA	2.5
1	B	301	LYS	2.4
1	B	419	THR	2.4
1	A	284	PHE	2.4
1	B	292	ALA	2.4
1	B	331	VAL	2.4
1	B	296	ILE	2.4
1	B	379	ASP	2.3
1	B	391	GLU	2.3
1	A	371	ILE	2.3
1	B	464	GLU	2.2
1	B	297	ASN	2.2
1	B	593	HIS	2.2
1	B	581	GLY	2.2
1	A	453	LYS	2.2
1	B	446	GLU	2.2
1	B	313	HIS	2.2
1	A	269	PRO	2.1
1	A	384	ASN	2.1
1	B	87	THR	2.1
1	B	374	GLY	2.1
1	B	335	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	587	GLN	2.1
1	B	318	ARG	2.1
1	A	572	ILE	2.1
1	B	338	LEU	2.1
1	B	314	ALA	2.1
1	B	367	ALA	2.1
1	B	329	ILE	2.1
1	A	386	SER	2.0
1	A	196	ILE	2.0
1	A	373	VAL	2.0
1	B	444	ARG	2.0
1	A	200	ALA	2.0
1	B	366	ASN	2.0
1	B	596	SER	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

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(Å <sup>2</sup> )	Q<0.9
6	PYR	B	706	6/6	0.74	0.24	87,89,91,91	0
6	PYR	A	706	6/6	0.77	0.26	110,110,111,111	0
6	PYR	A	705	6/6	0.81	0.25	41,58,60,72	0
7	OXY	B	712	2/2	0.81	0.25	54,54,54,56	0
7	OXY	B	711	2/2	0.81	0.34	60,60,60,62	0
7	OXY	A	708	2/2	0.82	0.29	61,61,61,63	0
7	OXY	B	710	2/2	0.89	0.45	67,67,67,67	0
6	PYR	B	705	6/6	0.92	0.14	53,54,65,68	0
7	OXY	B	709	2/2	0.92	0.15	57,57,57,60	0

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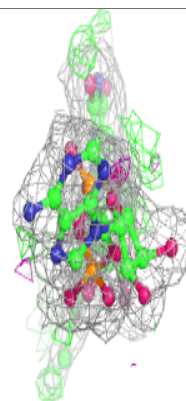
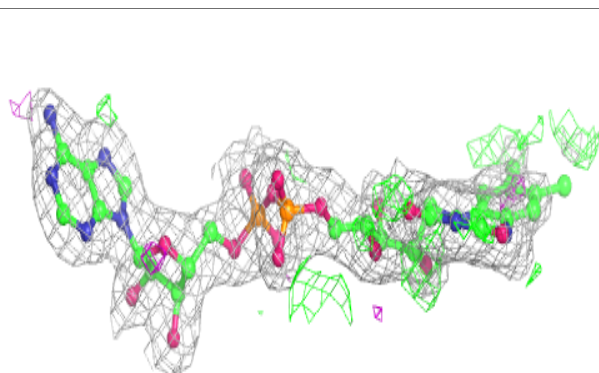
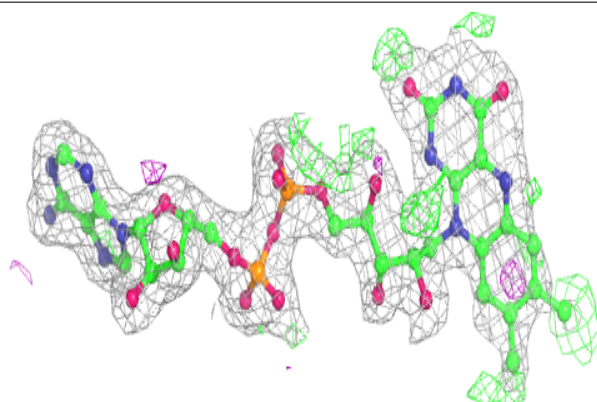
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	OXY	A	707	2/2	0.94	0.30	74,74,74,76	0
7	OXY	B	708	2/2	0.94	0.26	56,56,56,59	0
7	OXY	B	707	2/2	0.95	0.29	68,68,68,70	0
4	FAD	B	702	53/53	0.96	0.11	33,42,69,74	0
8	PO4	B	713	5/5	0.96	0.15	74,75,77,79	0
3	MG	A	702	1/1	0.97	0.03	29,29,29,29	0
5	TPP	A	704	26/26	0.98	0.08	20,26,29,31	0
5	TPP	B	704	26/26	0.98	0.08	18,23,26,28	0
4	FAD	A	703	53/53	0.98	0.09	22,31,73,75	0
3	MG	B	703	1/1	0.98	0.04	27,27,27,27	0
2	K	B	701	1/1	0.99	0.07	39,39,39,39	0
2	K	A	701	1/1	0.99	0.05	31,31,31,31	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.

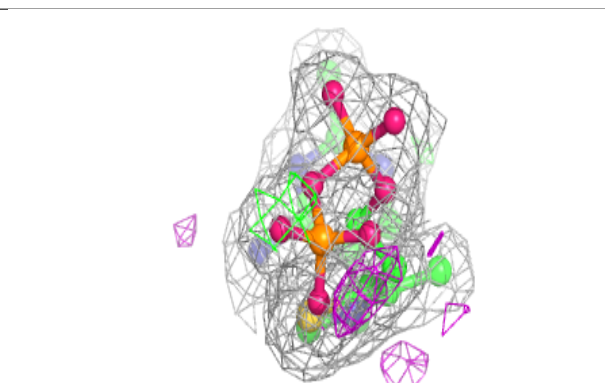
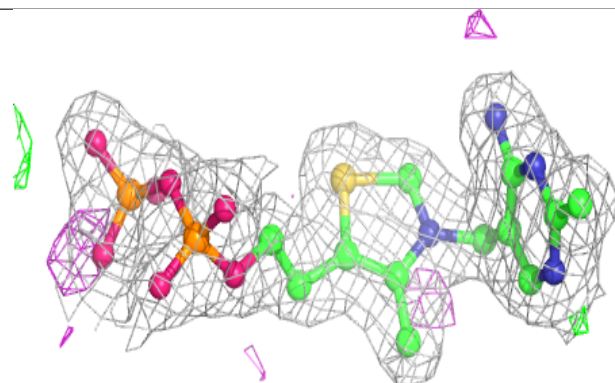
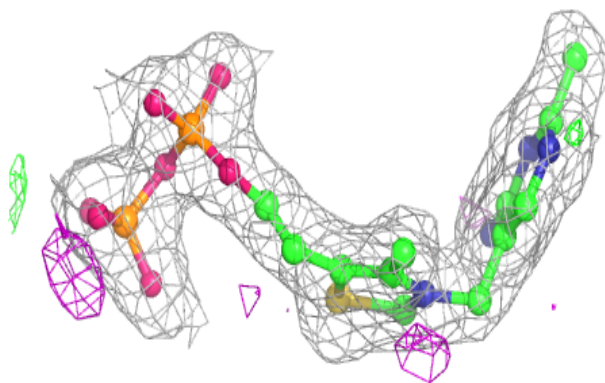
#### Electron density around FAD B 702:

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

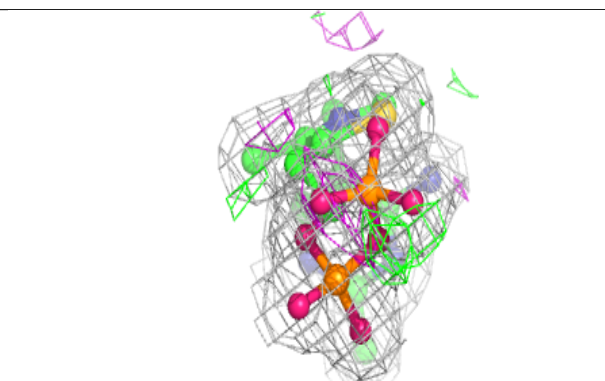
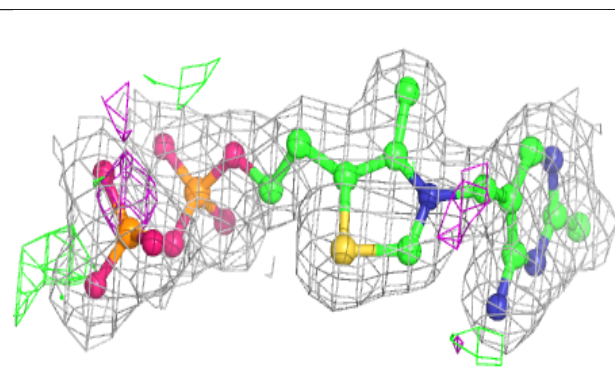
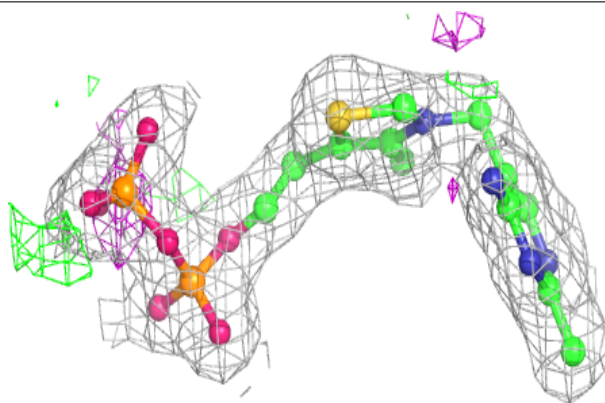


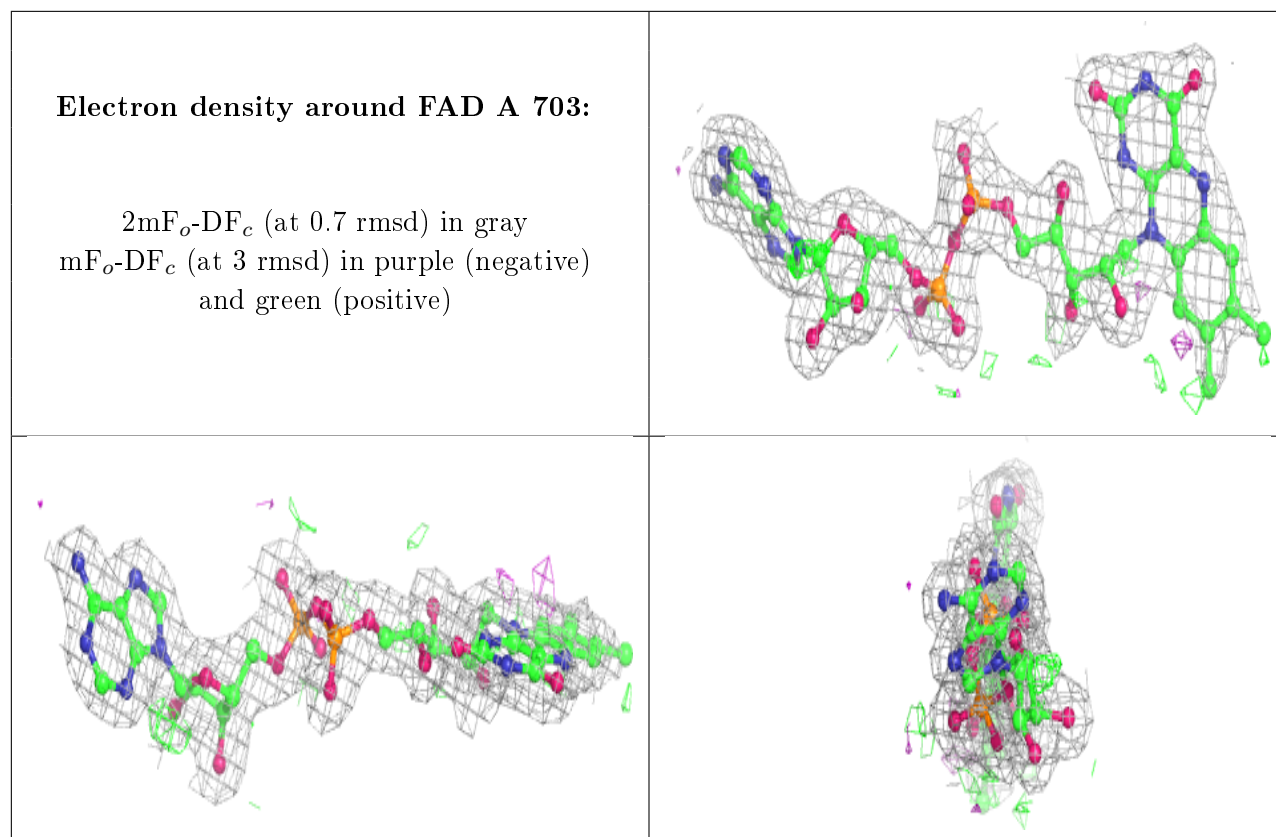
**Electron density around TPP A 704:**

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

**Electron density around TPP B 704:**

$2mF_o-DF_c$  (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.