Full wwPDB X-ray Structure Validation Report (i)

Oct 7, 2023 – 01:57 PM EDT

PDB ID	:	6DES
Title	:	Crystal structure of Candida albicans acetohydroxyacid synthase in complex with the herbicide propoxycarbazone
Authors	:	Garcia, M.D.; Guddat, L.W.
Deposited on	:	2018-05-12
Resolution	:	2.40 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 (i) 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 (i)) were used in the production of this report:

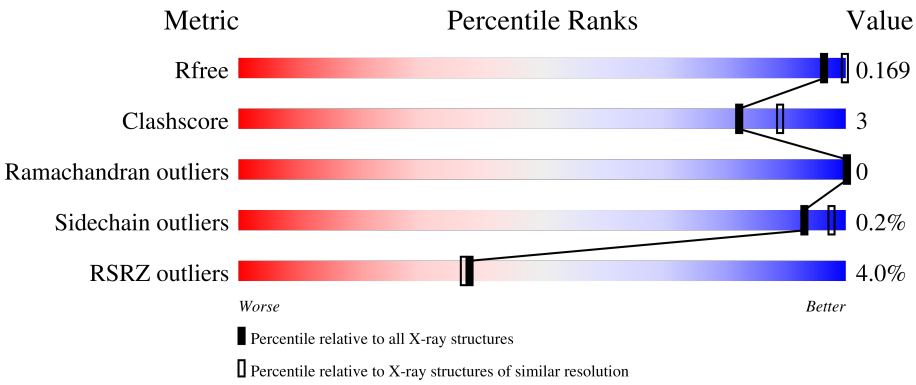
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% 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	682	4% 83% 5% 12%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5300 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	598	4664	2964	788	888	24	0	20	0

There are 45 discrepancies between the modelled and reference sequences:

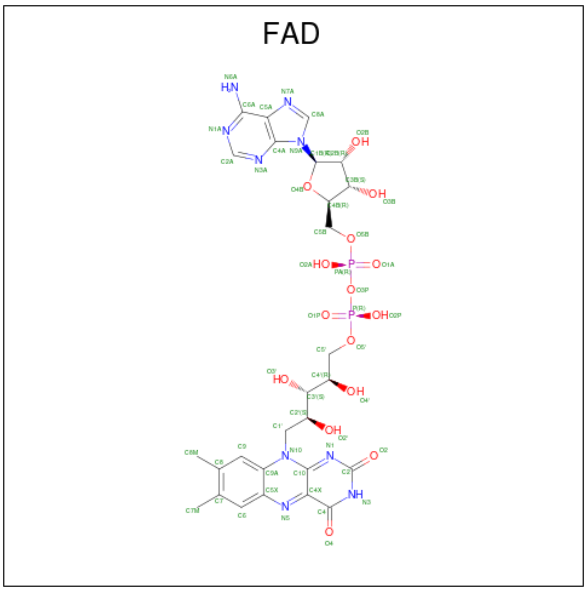
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	initiating methionine	UNP A0A1D8PJF9
A	3	HIS	-	expression tag	UNP A0A1D8PJF9
A	4	HIS	-	expression tag	UNP A0A1D8PJF9
A	5	HIS	-	expression tag	UNP A0A1D8PJF9
A	6	HIS	-	expression tag	UNP A0A1D8PJF9
A	7	HIS	-	expression tag	UNP A0A1D8PJF9
A	8	HIS	-	expression tag	UNP A0A1D8PJF9
A	9	SER	-	expression tag	UNP A0A1D8PJF9
A	10	SER	-	expression tag	UNP A0A1D8PJF9
A	11	GLY	-	expression tag	UNP A0A1D8PJF9
A	12	LEU	-	expression tag	UNP A0A1D8PJF9
A	13	VAL	-	expression tag	UNP A0A1D8PJF9
A	14	PRO	-	expression tag	UNP A0A1D8PJF9
A	15	ARG	-	expression tag	UNP A0A1D8PJF9
A	16	GLY	-	expression tag	UNP A0A1D8PJF9
A	17	SER	-	expression tag	UNP A0A1D8PJF9
A	18	GLY	-	expression tag	UNP A0A1D8PJF9
A	19	MET	-	expression tag	UNP A0A1D8PJF9
A	20	LYS	-	expression tag	UNP A0A1D8PJF9
A	21	GLU	-	expression tag	UNP A0A1D8PJF9
A	22	THR	-	expression tag	UNP A0A1D8PJF9
A	23	ALA	-	expression tag	UNP A0A1D8PJF9
A	24	ALA	-	expression tag	UNP A0A1D8PJF9
A	25	ALA	-	expression tag	UNP A0A1D8PJF9
A	26	LYS	-	expression tag	UNP A0A1D8PJF9
A	27	PHE	-	expression tag	UNP A0A1D8PJF9
A	28	GLU	-	expression tag	UNP A0A1D8PJF9

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	ARG	-	expression tag	UNP A0A1D8PJF9
A	30	GLN	-	expression tag	UNP A0A1D8PJF9
A	31	HIS	-	expression tag	UNP A0A1D8PJF9
A	32	MET	-	expression tag	UNP A0A1D8PJF9
A	33	ASP	-	expression tag	UNP A0A1D8PJF9
A	34	SER	-	expression tag	UNP A0A1D8PJF9
A	35	PRO	-	expression tag	UNP A0A1D8PJF9
A	36	ASP	-	expression tag	UNP A0A1D8PJF9
A	37	LEU	-	expression tag	UNP A0A1D8PJF9
A	38	GLY	-	expression tag	UNP A0A1D8PJF9
A	39	THR	-	expression tag	UNP A0A1D8PJF9
A	40	ASP	-	expression tag	UNP A0A1D8PJF9
A	41	ASP	-	expression tag	UNP A0A1D8PJF9
A	42	ASP	-	expression tag	UNP A0A1D8PJF9
A	43	ASP	-	expression tag	UNP A0A1D8PJF9
A	44	LYS	-	expression tag	UNP A0A1D8PJF9
A	45	ALA	-	expression tag	UNP A0A1D8PJF9
A	46	MET	-	expression tag	UNP A0A1D8PJF9

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

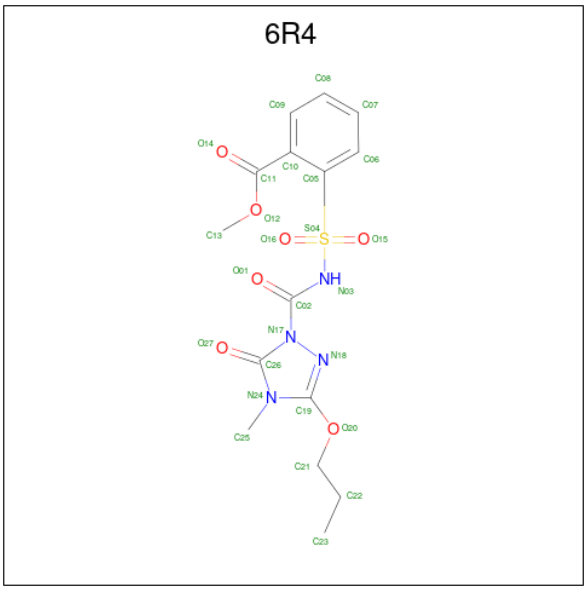
- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

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

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

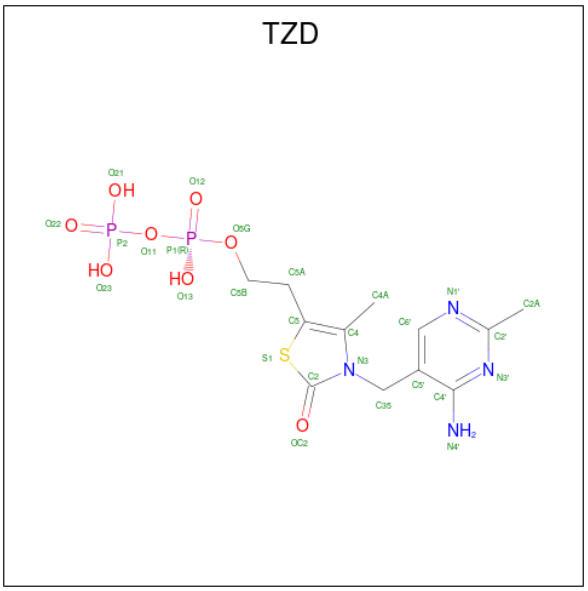
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	1	1	1	0	0

- Molecule 5 is methyl 2-[(4-methyl-5-oxidanylidene-3-propoxy-1,2,4-triazol-1-yl)carbonylsulfamoyl]benzoate (three-letter code: 6R4) (formula: $C_{15}H_{18}N_4O_7S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
5	A	1	27	15	4	7	1	0	0

- Molecule 6 is 2-{3-[(4-AMINO-2-METHYLPYRIMIDIN-5-YL)METHYL]-4-METHYL-2-OXO-2,3-DIHYDRO-1,3-THIAZOL-5-YL}ETHYL TRIHYDROGEN DIPHOSPHATE (three-letter code: TZD) (formula: $C_{12}H_{18}N_4O_8P_2S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
6	A	1	27	12	4	8	2	1	0	0

- Molecule 7 is water.

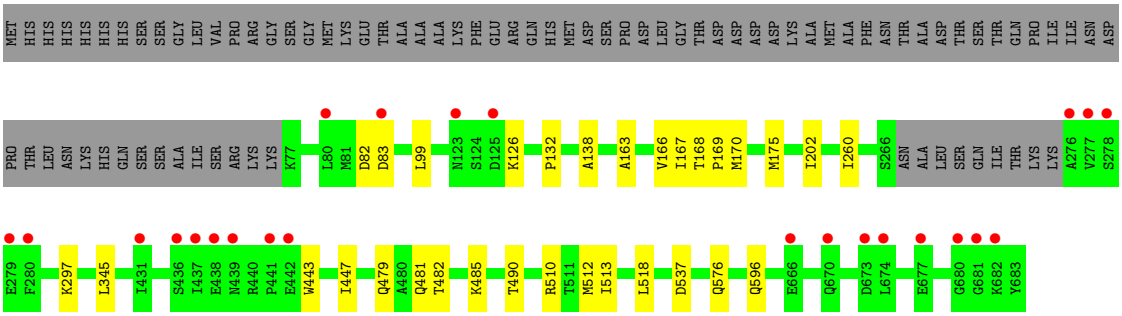
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	527	527	527	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Acetolactate synthase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α, β, γ	175.78Å 175.78Å 177.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.69 – 2.40 46.69 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (46.69-2.40) 99.6 (46.69-2.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.47 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.134 , 0.165 0.140 , 0.169	Depositor DCC
R_{free} test set	1997 reflections (3.17%)	wwPDB-VP
Wilson B-factor (Å^2)	38.3	Xtriage
Anisotropy	0.457	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 63.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	5300	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.36% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: TZD, 6R4, K, MG, FAD

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	0.30	0/4793	0.47	0/6502

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	4664	0	4703	23	0
2	A	53	0	30	1	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	27	0	0	0	0
6	A	27	0	15	1	0
7	A	527	0	0	6	0
All	All	5300	0	4748	24	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (24) 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:A:481[A]:GLN:NE2	7:A:801:HOH:O	2.22	0.73
1:A:99:LEU:HD21	1:A:126:LYS:HB3	1.75	0.68
1:A:260:ILE:HG22	7:A:802:HOH:O	1.95	0.67
1:A:82:ASP:HB2	1:A:260:ILE:HG13	1.82	0.61
1:A:132:PRO:HG3	1:A:138:ALA:HB2	1.85	0.59
1:A:596:GLN:HG3	7:A:1190:HOH:O	2.03	0.59
1:A:481[B]:GLN:NE2	7:A:810:HOH:O	2.36	0.58
1:A:167:ILE:HD13	1:A:170:MET:HE3	1.89	0.55
1:A:175[B]:MET:HE3	1:A:518:LEU:HB2	1.88	0.54
1:A:510:ARG:NH2	7:A:818:HOH:O	2.44	0.50
1:A:175[B]:MET:HE1	1:A:518:LEU:HD13	1.96	0.48
1:A:83:ASP:OD1	1:A:83:ASP:N	2.47	0.47
1:A:576:GLN:HB3	6:A:705:TZD:H5A1	1.97	0.47
1:A:166[B]:VAL:HG23	1:A:170:MET:HE1	1.98	0.45
1:A:163:ALA:HB1	1:A:202:ILE:HG12	2.00	0.44
1:A:479:GLN:O	1:A:482:THR:HG23	2.18	0.44
1:A:490:THR:HA	1:A:513:ILE:O	2.18	0.43
2:A:701:FAD:H9	2:A:701:FAD:H1'1	1.84	0.42
1:A:485:LYS:HE2	1:A:537:ASP:O	2.19	0.42
1:A:99:LEU:HD11	1:A:126:LYS:HG3	2.01	0.42
1:A:481[B]:GLN:NE2	7:A:829:HOH:O	2.53	0.41
1:A:297:LYS:HG2	1:A:443:TRP:CE3	2.56	0.41
1:A:168:THR:HB	1:A:169:PRO:HD3	2.03	0.41
1:A:345:LEU:HD21	1:A:447[A]:ILE:HG23	2.03	0.40

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	614/682 (90%)	604 (98%)	10 (2%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	506/563 (90%)	505 (100%)	1 (0%)	93 97

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

Mol	Chain	Res	Type
1	A	512	MET

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 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	$\#\|Z\| > 2$
5	6R4	A	704	-	28,28,28	3.26	9 (32%)	32,40,40	4.20	10 (31%)
6	TZD	A	705	4	23,28,28	3.18	6 (26%)	28,42,42	1.86	8 (28%)
2	FAD	A	701	-	53,58,58	1.58	9 (16%)	68,89,89	1.32	11 (16%)

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	6R4	A	704	-	-	11/24/25/25	0/2/2/2
6	TZD	A	705	4	-	0/16/17/17	0/2/2/2
2	FAD	A	701	-	-	4/30/50/50	0/6/6/6

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	704	6R4	C19-N18	13.60	1.43	1.29
6	A	705	TZD	C5-S1	-10.13	1.55	1.74
6	A	705	TZD	C4-N3	7.10	1.55	1.39
6	A	705	TZD	C5A-C5	6.30	1.53	1.50
5	A	704	6R4	C19-N24	4.70	1.42	1.34
2	A	701	FAD	C10-N1	4.54	1.42	1.33
2	A	701	FAD	C4X-N5	4.45	1.39	1.30
5	A	704	6R4	O20-C19	4.37	1.40	1.33
2	A	701	FAD	C2B-C1B	-4.18	1.47	1.53
5	A	704	6R4	O12-C11	4.14	1.42	1.33
5	A	704	6R4	C02-N03	3.30	1.46	1.39
6	A	705	TZD	C4'-N4'	3.13	1.42	1.34
2	A	701	FAD	O4B-C1B	3.02	1.45	1.41
2	A	701	FAD	O3'-C3'	-2.66	1.36	1.43
6	A	705	TZD	C5'-C4'	-2.50	1.38	1.42
5	A	704	6R4	N17-N18	2.40	1.42	1.38
5	A	704	6R4	O15-S04	2.39	1.46	1.43
2	A	701	FAD	C1'-N10	-2.34	1.42	1.48
2	A	701	FAD	C2-N1	2.29	1.42	1.36
5	A	704	6R4	C05-S04	2.20	1.80	1.77
5	A	704	6R4	C26-N24	2.12	1.43	1.38
2	A	701	FAD	C1'-C2'	2.12	1.55	1.52
2	A	701	FAD	C2'-C3'	2.10	1.57	1.53
6	A	705	TZD	C35-N3	-2.08	1.44	1.48

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	704	6R4	O16-S04-O15	-14.59	101.62	119.55
5	A	704	6R4	O20-C19-N24	11.42	124.64	116.89
5	A	704	6R4	N24-C19-N18	-7.29	108.89	114.39
6	A	705	TZD	C5A-C5-C4	-6.08	122.55	127.43
5	A	704	6R4	C05-S04-N03	6.05	113.18	106.06
5	A	704	6R4	C26-N17-N18	-5.54	108.10	112.17
5	A	704	6R4	N03-C02-N17	5.37	120.00	113.43
5	A	704	6R4	O12-C11-C10	4.60	119.93	112.30
2	A	701	FAD	N3A-C2A-N1A	-4.13	122.23	128.68
6	A	705	TZD	N1'-C2'-N3'	-3.46	119.59	125.54
2	A	701	FAD	C4X-C10-N10	3.10	121.01	116.48
5	A	704	6R4	C25-N24-C26	2.93	128.18	123.43
2	A	701	FAD	C4A-C5A-N7A	-2.88	106.39	109.40
6	A	705	TZD	C6'-N1'-C2'	2.87	120.85	115.96
2	A	701	FAD	C4-N3-C2	-2.87	120.33	125.64
2	A	701	FAD	C4X-C4-N3	2.61	119.83	113.19
6	A	705	TZD	C2A-C2'-N1'	2.61	120.01	117.14
2	A	701	FAD	C4X-C10-N1	-2.54	118.84	124.73
2	A	701	FAD	O4-C4-C4X	-2.51	119.94	126.60
5	A	704	6R4	O27-C26-N17	-2.40	125.99	129.34
2	A	701	FAD	C10-C4X-N5	-2.37	119.83	124.86
6	A	705	TZD	C6'-C5'-C4'	2.32	118.88	115.72
5	A	704	6R4	C21-O20-C19	-2.32	113.19	116.28
2	A	701	FAD	C10-N1-C2	2.29	121.49	116.90
6	A	705	TZD	C5'-C6'-N1'	-2.25	120.07	123.82
2	A	701	FAD	C4-C4X-N5	2.18	121.33	118.23
2	A	701	FAD	C9A-N10-C10	-2.13	117.45	120.77
6	A	705	TZD	O21-P2-O11	2.11	111.72	104.64
6	A	705	TZD	C2A-C2'-N3'	2.08	120.40	117.15

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	704	6R4	N18-C19-O20-C21
5	A	704	6R4	N24-C19-O20-C21
5	A	704	6R4	C02-N03-S04-O15
5	A	704	6R4	C06-C05-S04-O16
5	A	704	6R4	C10-C05-S04-O16
5	A	704	6R4	C10-C05-S04-N03
2	A	701	FAD	P-O3P-PA-O5B

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
5	A	704	6R4	C06-C05-S04-N03
5	A	704	6R4	C09-C10-C11-O12
2	A	701	FAD	O4B-C4B-C5B-O5B
2	A	701	FAD	O3'-C3'-C4'-C5'
5	A	704	6R4	O20-C21-C22-C23
2	A	701	FAD	C2'-C3'-C4'-C5'
5	A	704	6R4	C05-C10-C11-O14
5	A	704	6R4	C05-C10-C11-O12

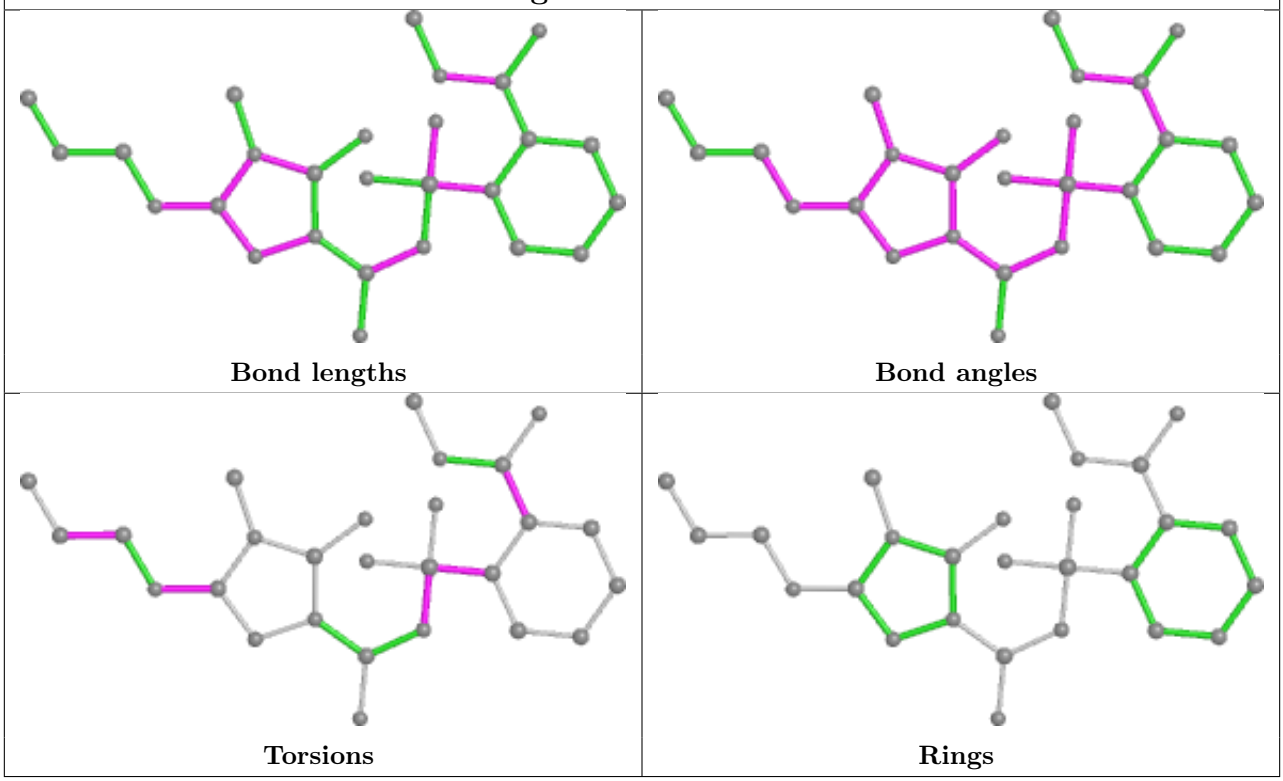
There are no ring outliers.

2 monomers are involved in 2 short contacts:

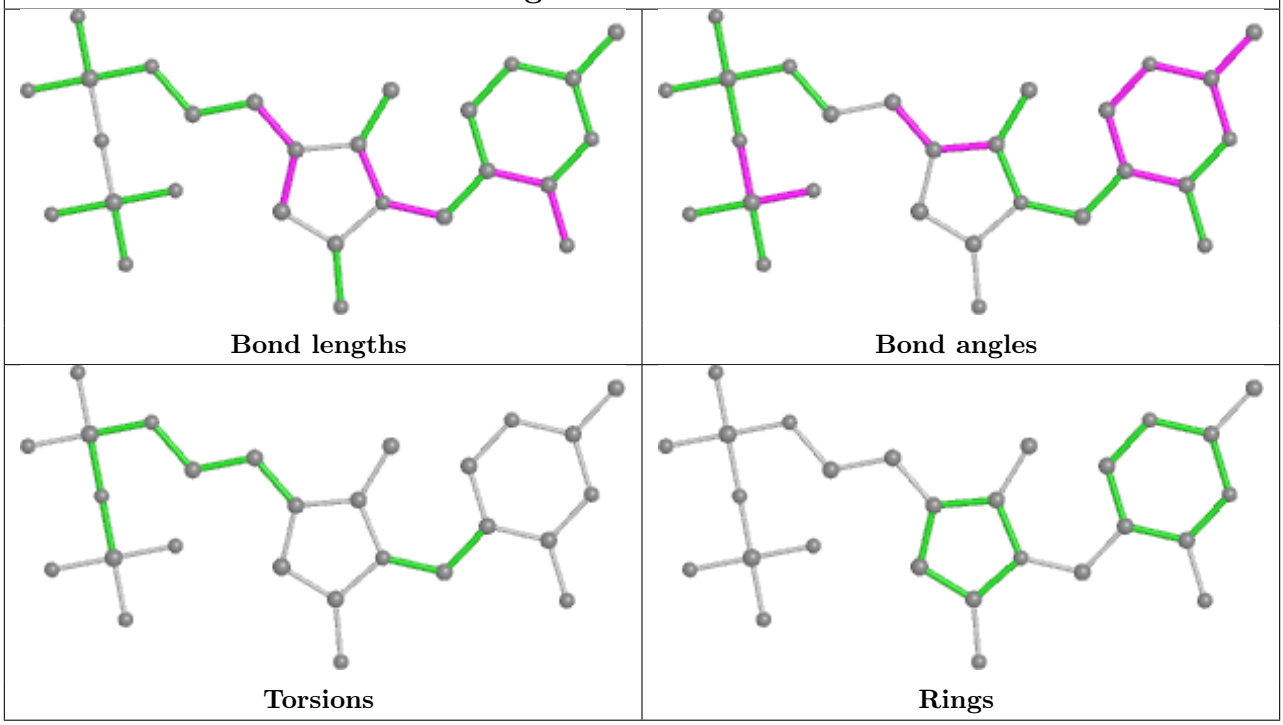
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	705	TZD	1	0
2	A	701	FAD	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

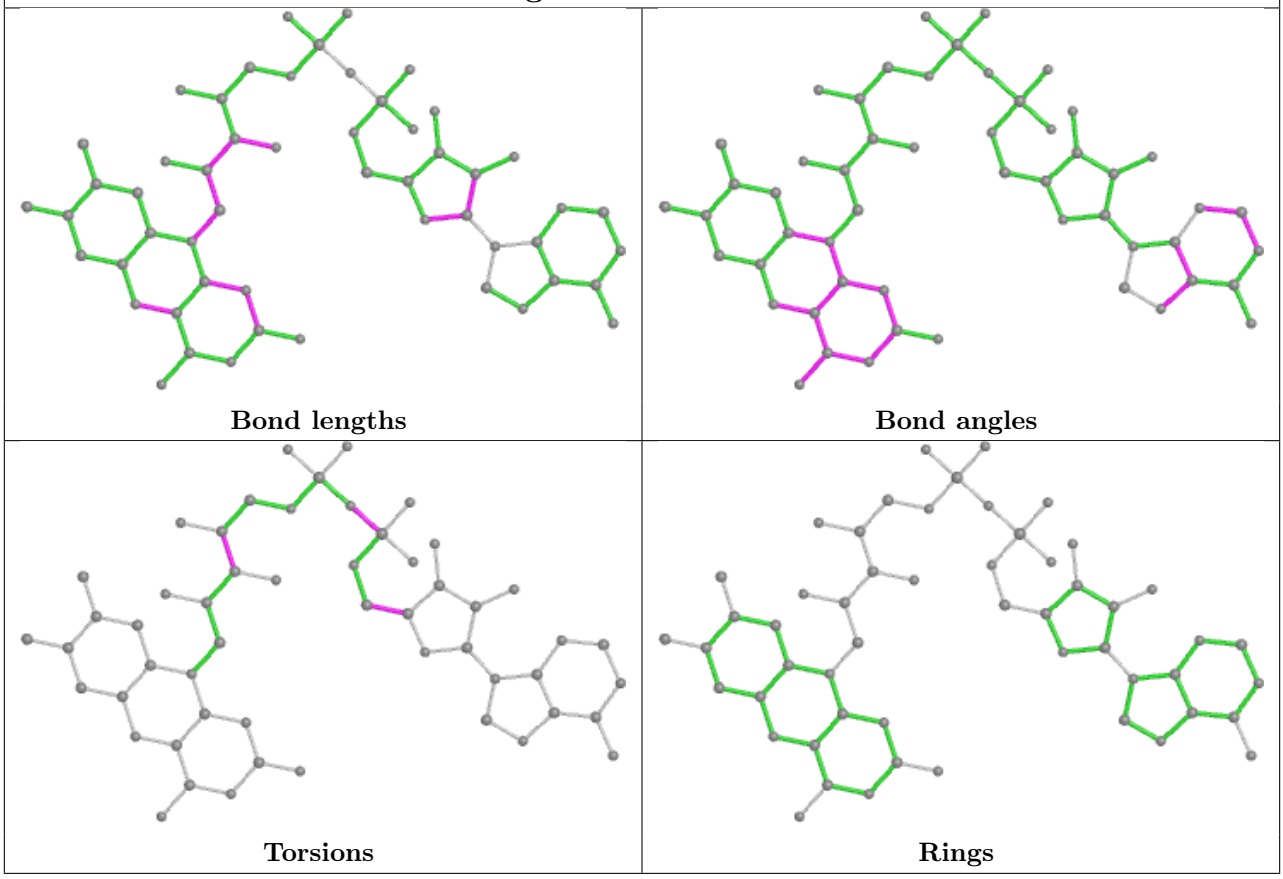
Ligand 6R4 A 704



Ligand TZD A 705



Ligand FAD A 701



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, 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	598/682 (87%)	-0.37	24 (4%) 38 37	24, 38, 64, 108	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	277	VAL	4.7
1	A	680	GLY	3.6
1	A	681	GLY	3.4
1	A	279	GLU	3.3
1	A	276	ALA	3.0
1	A	436[A]	SER	3.0
1	A	682	LYS	2.8
1	A	677	GLU	2.7
1	A	674	LEU	2.7
1	A	439	ASN	2.6
1	A	437	ILE	2.6
1	A	666	GLU	2.6
1	A	673	ASP	2.6
1	A	438	GLU	2.6
1	A	280	PHE	2.5
1	A	442	GLU	2.4
1	A	670	GLN	2.4
1	A	80	LEU	2.4
1	A	125	ASP	2.3
1	A	441	PRO	2.3
1	A	123	ASN	2.2
1	A	431	ILE	2.2
1	A	83	ASP	2.1
1	A	278	SER	2.1

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

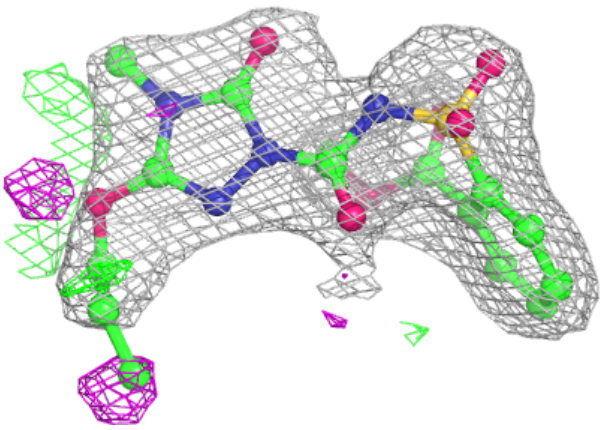
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

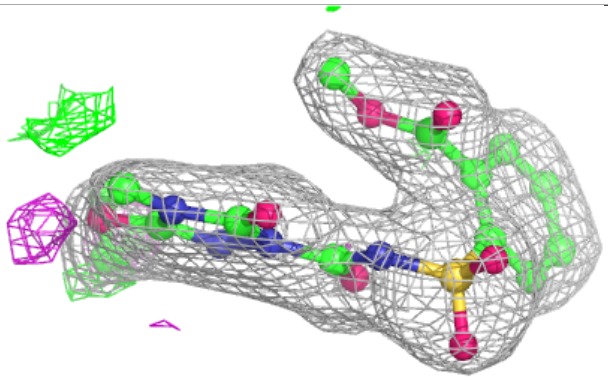
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	6R4	A	704	27/27	0.97	0.16	30,39,54,84	27
3	K	A	702	1/1	0.99	0.08	36,36,36,36	0
4	MG	A	703	1/1	0.99	0.13	21,21,21,21	0
2	FAD	A	701	53/53	0.99	0.11	23,30,36,41	0
6	TZD	A	705	27/27	0.99	0.14	22,29,37,49	0

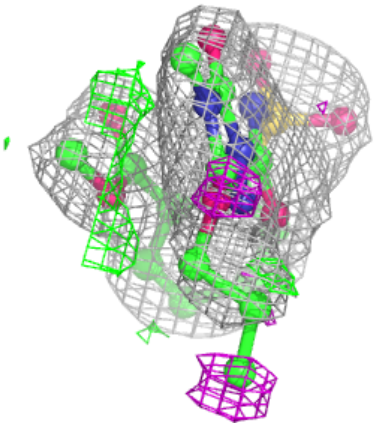
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 6R4 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)

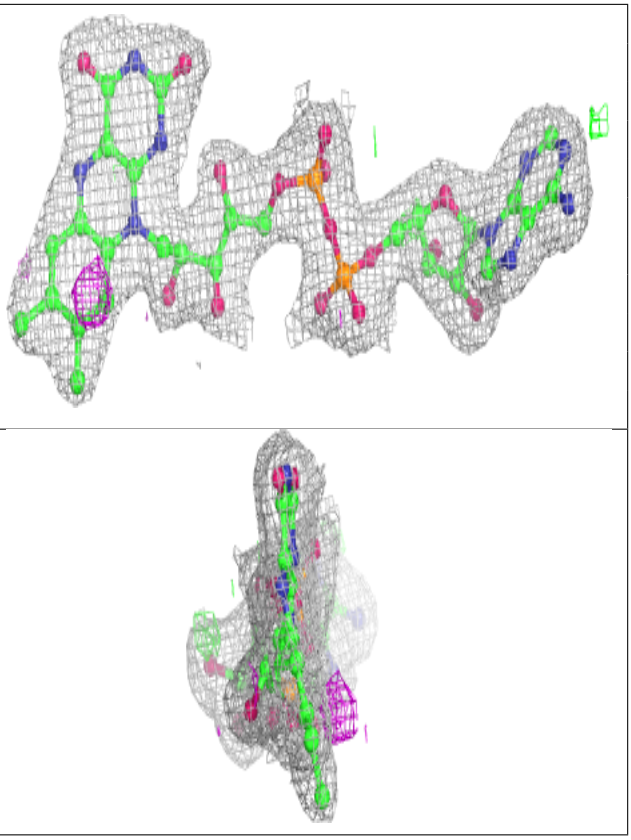






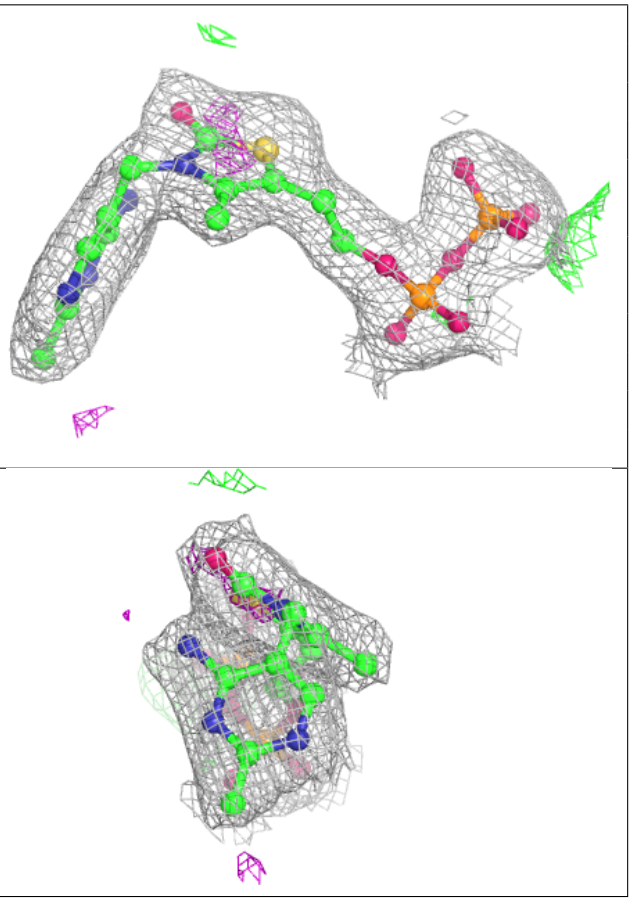
Electron density around FAD A 701:

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



Electron density around TZD A 705:

$2mF_o$-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.