



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:58 PM UTC

PDB ID : 2DKH / pdb\_00002dkh  
Title : Crystal structure of 3-hydroxybenzoate hydroxylase from Comamonas testosteroni, in complex with the substrate  
Authors : Hiromoto, T.; Fujiwara, S.; Hosokawa, K.; Yamaguchi, H.  
Deposited on : 2006-04-11  
Resolution : 1.80 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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

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

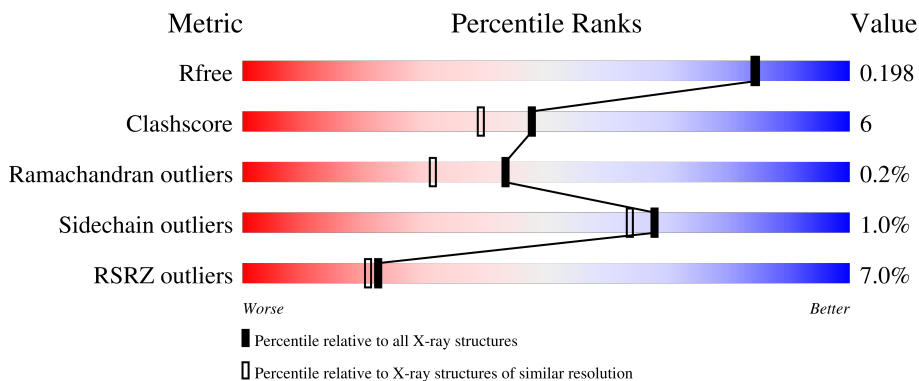
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

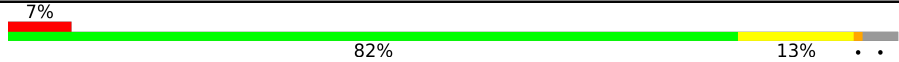
The reported resolution of this entry is 1.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	639	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5457 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 3-hydroxybenzoate hydroxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	614	4785	3030	854	877	24	0	0	0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



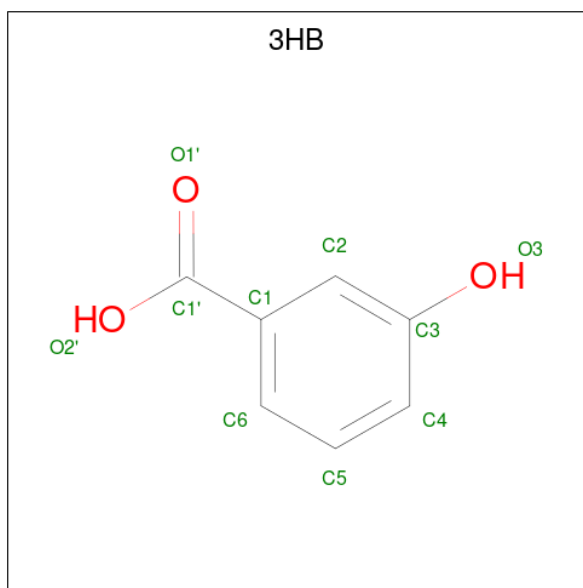
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: 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
			Total	C	N	O	P		
3	A	1	53	27	9	15	2	0	0

- Molecule 4 is 3-HYDROXYBENZOIC ACID (CCD ID: 3HB) (formula:  $C_7H_6O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	10	7	3	0	0

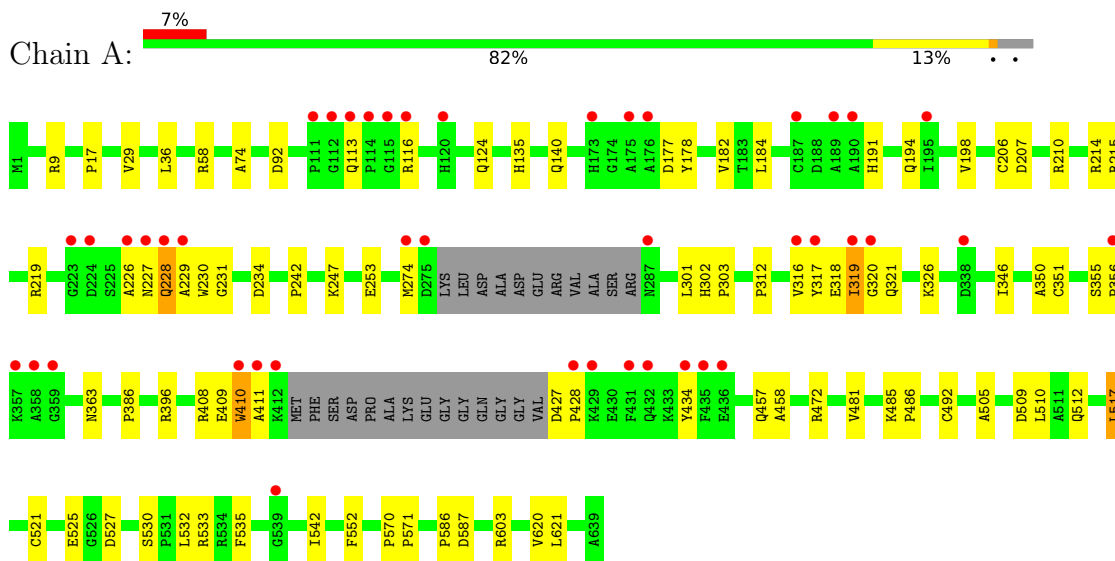
- Molecule 5 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	A	594	Total 594	O 594	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: 3-hydroxybenzoate hydroxylase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.59Å 73.59Å 224.77Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.00 – 1.80 45.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.5 (45.00-1.80) 98.5 (45.00-1.80)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.35 (at 1.79Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.173 , 0.198 0.173 , 0.198	Depositor DCC
$R_{free}$ test set	6646 reflections (10.13%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.3	Xtrriage
Anisotropy	0.227	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 41.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5457	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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: FAD, SO4, 3HB

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	0.40	0/4902	0.93	23/6661 (0.3%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	570	PRO	N-CA-C	8.40	120.95	110.70
1	A	247	LYS	N-CA-C	-7.95	97.12	109.76
1	A	492	CYS	N-CA-C	-6.67	104.40	112.54
1	A	207	ASP	N-CA-C	6.29	119.98	112.93
1	A	206	CYS	N-CA-C	-6.17	102.48	111.30
1	A	535	PHE	N-CA-C	6.03	121.39	113.30
1	A	481	VAL	N-CA-C	5.67	116.44	110.72
1	A	242	PRO	N-CA-C	5.65	121.19	113.84
1	A	571	PRO	N-CA-C	-5.49	102.52	111.68
1	A	124	GLN	N-CA-C	-5.42	101.83	109.96
1	A	113	GLN	CA-C-N	5.41	125.33	119.76
1	A	113	GLN	C-N-CA	5.41	125.33	119.76
1	A	512	GLN	CA-C-N	5.40	125.07	119.56
1	A	512	GLN	C-N-CA	5.40	125.07	119.56
1	A	620	VAL	N-CA-C	-5.38	98.20	107.24
1	A	135	HIS	N-CA-C	-5.36	100.56	109.46
1	A	587	ASP	N-CA-C	-5.34	100.40	108.67
1	A	517	LEU	N-CA-C	5.19	117.34	111.11
1	A	410	TRP	N-CA-C	-5.15	106.69	112.87
1	A	363	ASN	N-CA-C	5.12	116.55	111.07
1	A	509	ASP	N-CA-C	5.12	116.86	111.28
1	A	396	ARG	N-CA-C	5.10	116.92	111.36
1	A	603	ARG	N-CA-C	5.07	116.81	111.28

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	4785	0	4689	52	0
2	A	15	0	0	0	0
3	A	53	0	31	2	0
4	A	10	0	5	0	0
5	A	594	0	0	4	0
All	All	5457	0	4725	54	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 6.

All (54) 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:227:ASN:HB3	1:A:228:GLN:HE21	1.06	1.11
1:A:227:ASN:HB3	1:A:228:GLN:NE2	1.88	0.88
1:A:116:ARG:HG2	1:A:303:PRO:HD3	1.77	0.66
1:A:319:ILE:N	1:A:319:ILE:HD13	2.16	0.60
1:A:29:VAL:HG11	1:A:198:VAL:HG21	1.84	0.59
1:A:621:LEU:HD23	5:A:860:HOH:O	2.02	0.59
1:A:521:CYS:O	1:A:525:GLU:HG2	2.03	0.58
1:A:231:GLY:N	1:A:274:MET:HE2	2.18	0.58
1:A:505:ALA:HB2	1:A:517:LEU:HD13	1.86	0.57
1:A:427:ASP:N	1:A:428:PRO:HD2	2.21	0.56
1:A:319:ILE:HD13	1:A:319:ILE:H	1.69	0.55
1:A:386:PRO:HG3	5:A:928:HOH:O	2.06	0.55
3:A:640:FAD:O1A	3:A:640:FAD:O4'	2.22	0.55
1:A:321:GLN:HG3	1:A:355:SER:HB3	1.89	0.54
1:A:214:ARG:HD3	1:A:350:ALA:O	2.08	0.54
1:A:210:ARG:HB3	1:A:215:ARG:NH2	2.23	0.53
1:A:527:ASP:O	1:A:530:SER:HB3	2.08	0.53
1:A:234:ASP:O	1:A:312:PRO:HD2	2.09	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:MET:HE1	1:A:316:VAL:HG13	1.89	0.53
1:A:321:GLN:HG2	1:A:355:SER:H	1.74	0.52
1:A:510:LEU:HD13	1:A:552:PHE:CE1	2.46	0.50
1:A:177:ASP:O	1:A:178:TYR:C	2.56	0.49
1:A:409:GLU:C	1:A:411:ALA:H	2.21	0.49
1:A:229:ALA:HB2	1:A:318:GLU:OE2	2.13	0.48
1:A:219:ARG:CZ	1:A:326:LYS:HB3	2.44	0.48
1:A:319:ILE:HD11	1:A:356:PRO:HG3	1.96	0.47
1:A:321:GLN:CG	1:A:355:SER:H	2.27	0.47
1:A:410:TRP:CZ3	1:A:434:TYR:HB3	2.50	0.47
1:A:230:TRP:C	1:A:274:MET:HE2	2.40	0.46
1:A:409:GLU:C	1:A:411:ALA:N	2.70	0.46
1:A:36:LEU:HD23	1:A:182:VAL:HG21	1.98	0.45
1:A:253:GLU:HA	1:A:253:GLU:OE2	2.17	0.44
1:A:9:ARG:HD2	1:A:17:PRO:HG3	2.00	0.43
1:A:116:ARG:CG	1:A:303:PRO:HD3	2.46	0.43
1:A:320:GLY:HA2	5:A:1219:HOH:O	2.17	0.43
1:A:525:GLU:O	1:A:533:ARG:HD3	2.19	0.43
1:A:457:GLN:O	1:A:458:ALA:HB3	2.18	0.42
1:A:319:ILE:N	1:A:319:ILE:CD1	2.80	0.42
1:A:552:PHE:O	1:A:586:PRO:HD3	2.18	0.42
1:A:317:TYR:CE1	1:A:319:ILE:HD12	2.54	0.42
1:A:532:LEU:HD21	1:A:542:ILE:HG13	2.01	0.42
1:A:74:ALA:O	1:A:140:GLN:HB2	2.19	0.42
1:A:36:LEU:CD2	1:A:182:VAL:HG21	2.50	0.41
1:A:301:LEU:O	1:A:302:HIS:C	2.63	0.41
3:A:640:FAD:H9	3:A:640:FAD:H1'1	1.88	0.41
1:A:58:ARG:NE	1:A:58:ARG:HA	2.35	0.41
1:A:116:ARG:NE	1:A:303:PRO:HG3	2.36	0.41
1:A:346:ILE:HD12	1:A:351:CYS:HB3	2.03	0.41
1:A:116:ARG:HD3	5:A:1179:HOH:O	2.20	0.40
1:A:184:LEU:HD12	1:A:184:LEU:N	2.36	0.40
1:A:532:LEU:HD23	1:A:532:LEU:O	2.20	0.40
1:A:191:HIS:HA	1:A:194:GLN:NE2	2.36	0.40
1:A:227:ASN:CB	1:A:228:GLN:HE21	2.00	0.40
1:A:485:LYS:HA	1:A:486:PRO:HD3	1.94	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	608/639 (95%)	593 (98%)	14 (2%)	1 (0%)	43 31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	226	ALA

### 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	499/517 (96%)	494 (99%)	5 (1%)	68 64

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	ASP
1	A	228	GLN
1	A	319	ILE
1	A	408	ARG
1	A	472	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	ASN
1	A	113	GLN
1	A	194	GLN
1	A	227	ASN
1	A	251	GLN
1	A	287	ASN
1	A	298	GLN
1	A	321	GLN
1	A	438	HIS
1	A	508	ASN
1	A	512	GLN
1	A	554	GLN
1	A	574	GLN

### 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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	FAD	A	640	-	58,58,58	1.54	7 (12%)	85,89,89	0.90	2 (2%)
2	SO4	A	644	-	4,4,4	0.25	0	6,6,6	0.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	3HB	A	641	-	10,10,10	2.08	4 (40%)	13,13,13	1.10	1 (7%)
2	SO4	A	642	-	4,4,4	0.33	0	6,6,6	0.11	0
2	SO4	A	643	-	4,4,4	0.35	0	6,6,6	0.12	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	3HB	A	641	-	-	4/4/4/4	0/1/1/1
3	FAD	A	640	-	-	5/34/50/50	0/6/6/6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	640	FAD	C4X-N5	5.49	1.42	1.30
3	A	640	FAD	C9-C8	4.14	1.45	1.39
3	A	640	FAD	C9A-N10	3.75	1.47	1.41
3	A	640	FAD	C4A-N3A	3.66	1.41	1.34
4	A	641	3HB	C5-C4	3.49	1.44	1.38
4	A	641	3HB	C6-C1	3.18	1.44	1.39
4	A	641	3HB	C2-C1	3.00	1.44	1.39
3	A	640	FAD	C6-C5X	2.97	1.44	1.40
3	A	640	FAD	C10-N1	2.65	1.38	1.33
3	A	640	FAD	C9A-C5X	2.60	1.45	1.41
4	A	641	3HB	O2'-C1'	-2.12	1.24	1.30

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	640	FAD	C5'-C4'-C3'	-3.46	105.69	112.22
4	A	641	3HB	O2'-C1'-C1	2.63	121.58	114.84
3	A	640	FAD	O2'-C2'-C3'	2.04	114.03	109.25

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	640	FAD	PA-O3P-P-O5'

*Continued on next page...*

*Continued from previous page...*

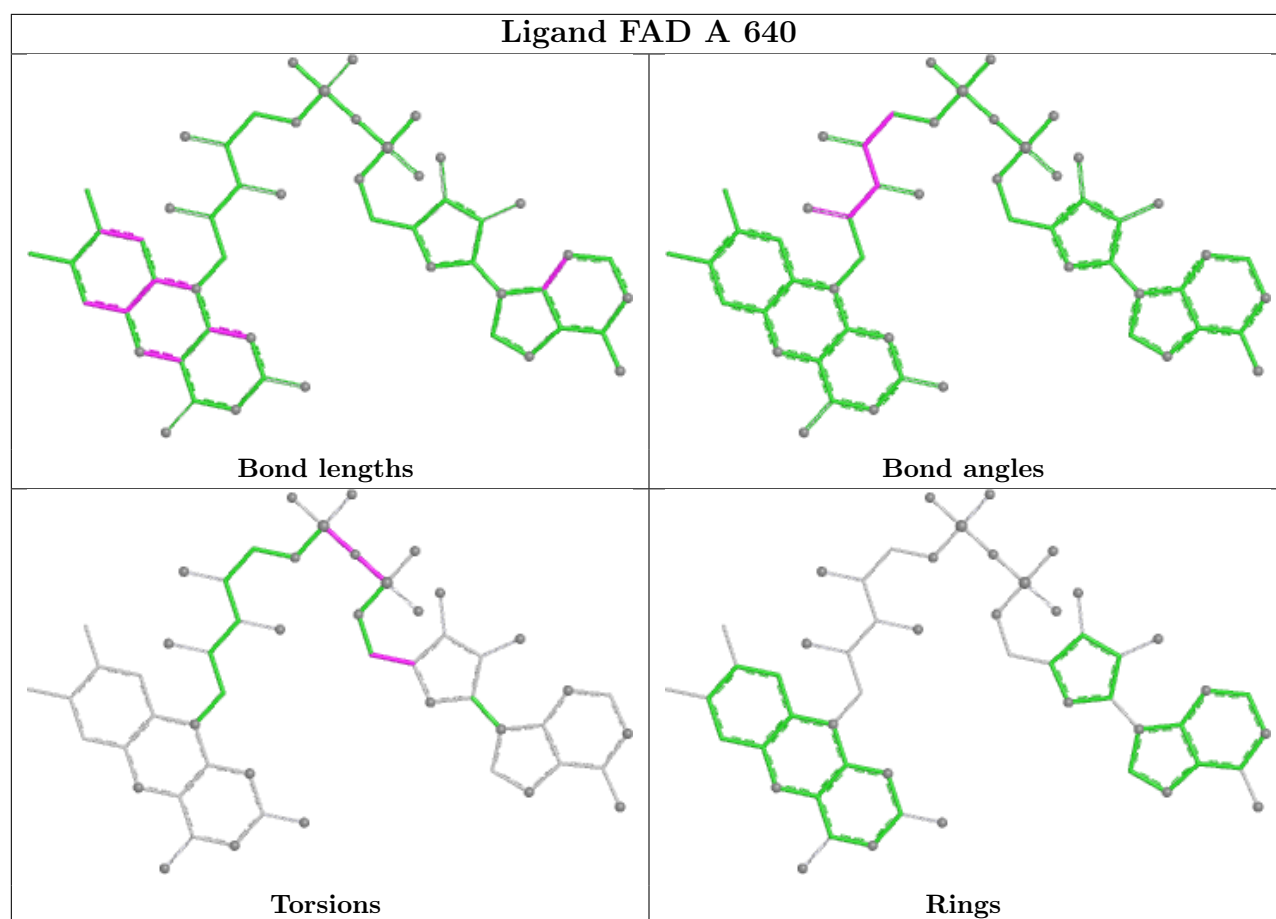
Mol	Chain	Res	Type	Atoms
4	A	641	3HB	C2-C1-C1'-O1'
4	A	641	3HB	C2-C1-C1'-O2'
4	A	641	3HB	C6-C1-C1'-O2'
4	A	641	3HB	C6-C1-C1'-O1'
3	A	640	FAD	P-O3P-PA-O1A
3	A	640	FAD	P-O3P-PA-O2A
3	A	640	FAD	PA-O3P-P-O2P
3	A	640	FAD	O4B-C4B-C5B-O5B

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	640	FAD	2	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	614/639 (96%)	0.20	43 (7%) <span style="border: 1px solid red; padding: 2px;">22</span> <span style="border: 1px solid red; padding: 2px;">21</span>	20, 30, 62, 90	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	358	ALA	5.9
1	A	410	TRP	5.2
1	A	114	PRO	5.0
1	A	317	TYR	4.9
1	A	275	ASP	4.1
1	A	435	PHE	4.1
1	A	431	PHE	4.0
1	A	434	TYR	4.0
1	A	175	ALA	3.9
1	A	176	ALA	3.7
1	A	356	PRO	3.6
1	A	436	GLU	3.5
1	A	411	ALA	3.5
1	A	316	VAL	3.4
1	A	112	GLY	3.3
1	A	227	ASN	3.2
1	A	428	PRO	3.2
1	A	287	ASN	3.1
1	A	223	GLY	3.1
1	A	432	GLN	2.9
1	A	228	GLN	2.9
1	A	319	ILE	2.8
1	A	357	LYS	2.7
1	A	115	GLY	2.7
1	A	195	ILE	2.6
1	A	359	GLY	2.6
1	A	274	MET	2.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	429	LYS	2.5
1	A	412	LYS	2.5
1	A	338	ASP	2.5
1	A	539	GLY	2.4
1	A	173	HIS	2.4
1	A	320	GLY	2.4
1	A	226	ALA	2.4
1	A	189	ALA	2.3
1	A	190	ALA	2.2
1	A	229	ALA	2.2
1	A	187	CYS	2.2
1	A	113	GLN	2.2
1	A	224	ASP	2.1
1	A	120	HIS	2.1
1	A	111	PRO	2.1
1	A	116	ARG	2.0

## 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 oligosaccharides in this entry.

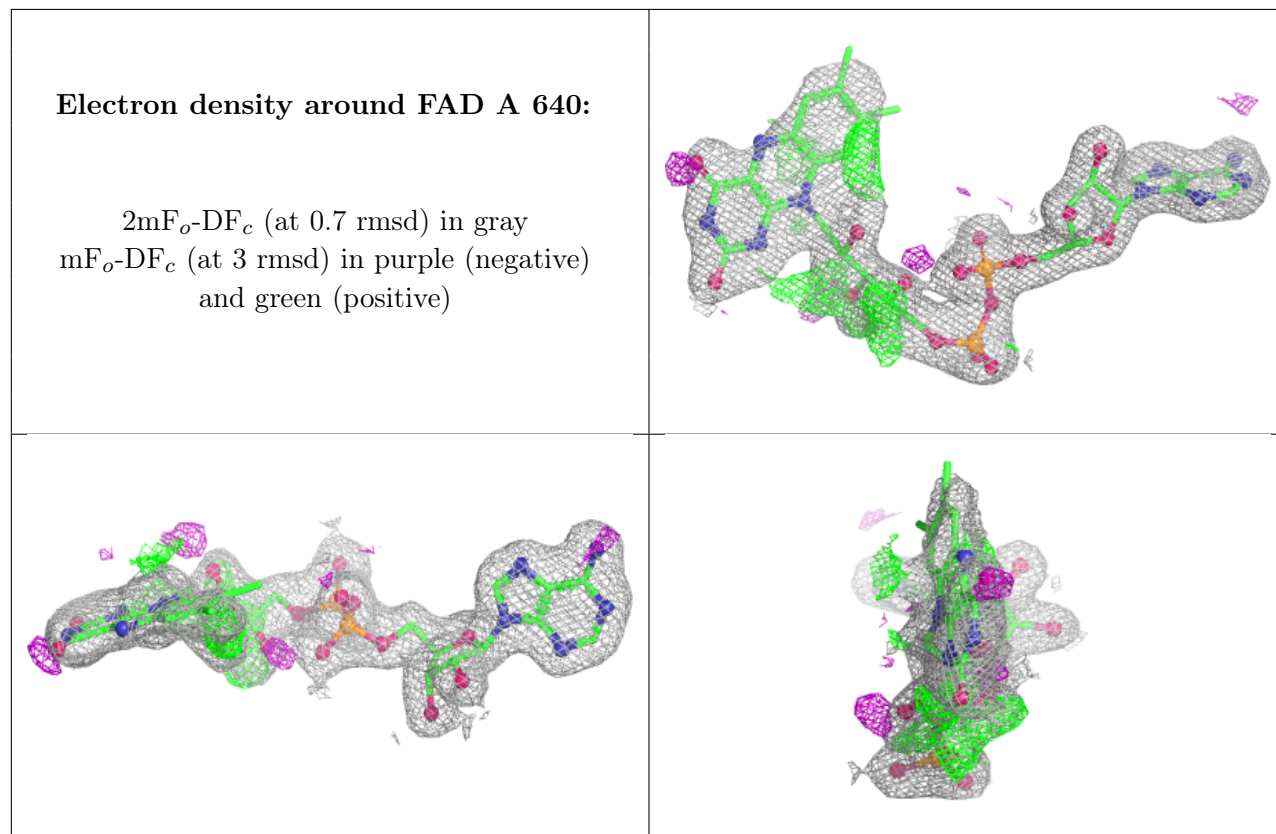
## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
4	3HB	A	641	10/10	0.92	0.09	34,37,41,42	0
3	FAD	A	640	53/53	0.94	0.12	24,34,73,76	0
2	SO4	A	644	5/5	0.95	0.09	27,33,35,42	0
2	SO4	A	642	5/5	0.95	0.08	33,41,47,50	0
2	SO4	A	643	5/5	0.95	0.08	29,40,48,50	0

The following is a graphical depiction of the model fit to experimental electron density of all

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.