



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 6, 2023 – 01:06 am GMT

PDB ID : 6F6J  
Title : Crystal structure of the Fe(II)/alpha-ketoglutarate dependent dioxygenase KDO1 with Fe(II)/succinate/(3S)-3-hydroxy-L-lysine  
Authors : Isabet, T.; Stura, E.A.; Legrand, P.; Zaparucha, A.; Bastard, K.  
Deposited on : 2017-12-05  
Resolution : 2.00 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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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

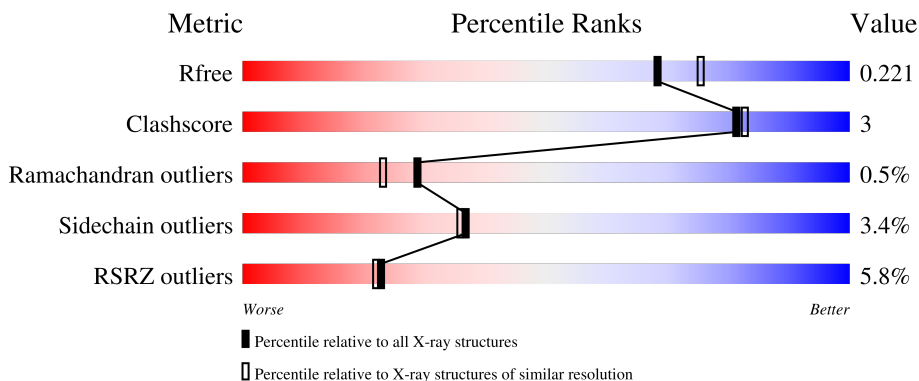
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	358	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 82%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">2%      82%      8%      9%</p>
1	B	358	<div style="display: flex; align-items: center;"> <div style="width: 10%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 84%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">10%      84%      7%      9%</p>
1	C	358	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 84%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">3%      84%      7%      9%</p>
1	D	358	<div style="display: flex; align-items: center;"> <div style="width: 6%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 85%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">6%      85%      6%      9%</p>

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
3	SIN	A	402[A]	-	X	-	-
3	SIN	A	402[B]	-	X	-	-
3	SIN	D	402	-	X	-	-
5	ACT	A	404	-	-	X	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11560 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 L-lysine 3-hydroxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	325	2558	1603	463	476	16	0	6	0
1	B	326	2562	1605	463	480	14	0	6	0
1	C	325	2539	1592	458	474	15	0	4	0
1	D	326	2526	1585	453	474	14	0	2	0

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

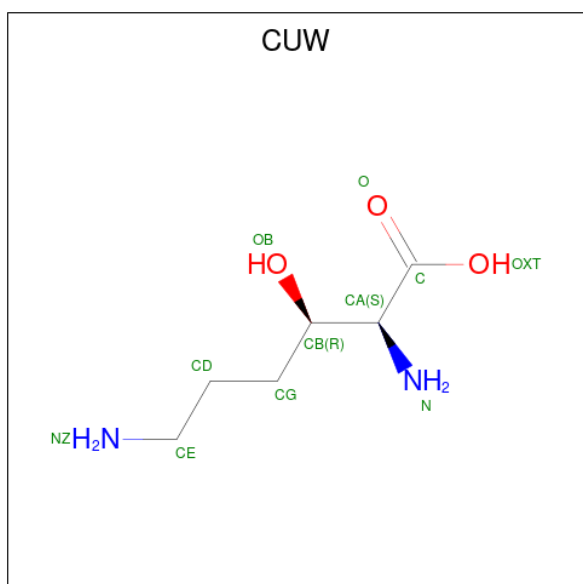
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	B	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		
2	D	1	Total	Fe	0	0
			1	1		

- Molecule 3 is SUCCINIC ACID (three-letter code: SIN) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>4</sub>).



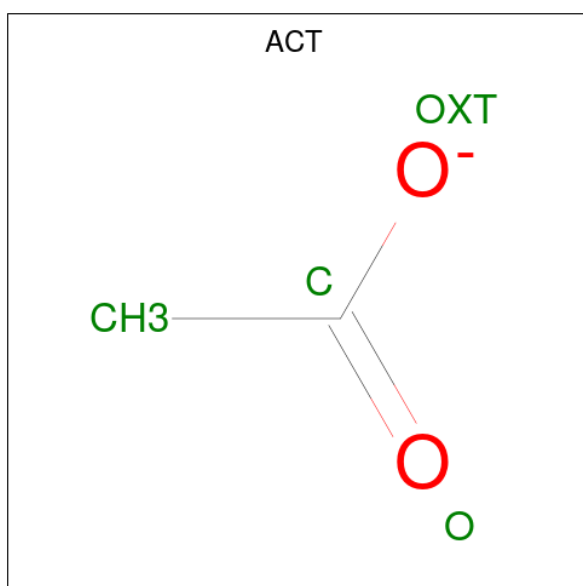
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C O	0	1
			16	8 8		
3	B	1	Total	C O	0	0
			8	4 4		
3	C	1	Total	C O	0	1
			16	8 8		
3	D	1	Total	C O	0	0
			8	4 4		

- Molecule 4 is (2 {S},3 {R})-2,6-bis(azanyl)-3-oxidanyl-hexanoic acid (three-letter code: CUW) (formula: C<sub>6</sub>H<sub>14</sub>N<sub>2</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			11	6	2	3		
4	B	1	Total	C	N	O	0	0
			11	6	2	3		
4	C	1	Total	C	N	O	0	0
			11	6	2	3		
4	D	1	Total	C	N	O	0	0
			11	6	2	3		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



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

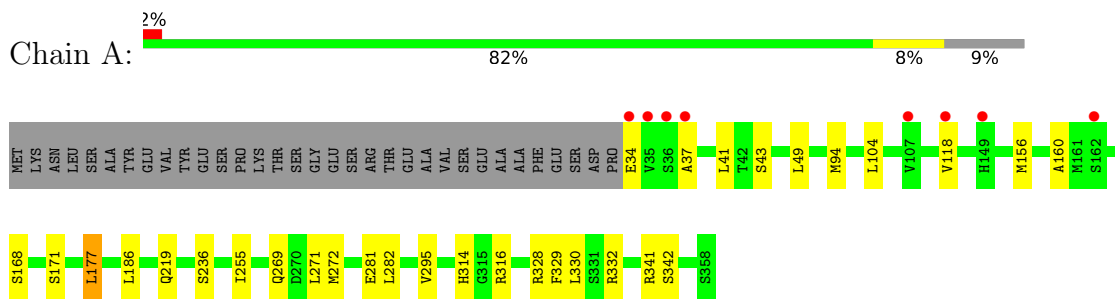
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	353	Total	O	0	4
			354	354		
6	B	277	Total	O	0	0
			277	277		
6	C	345	Total	O	0	1
			345	345		
6	D	295	Total	O	0	0
			295	295		

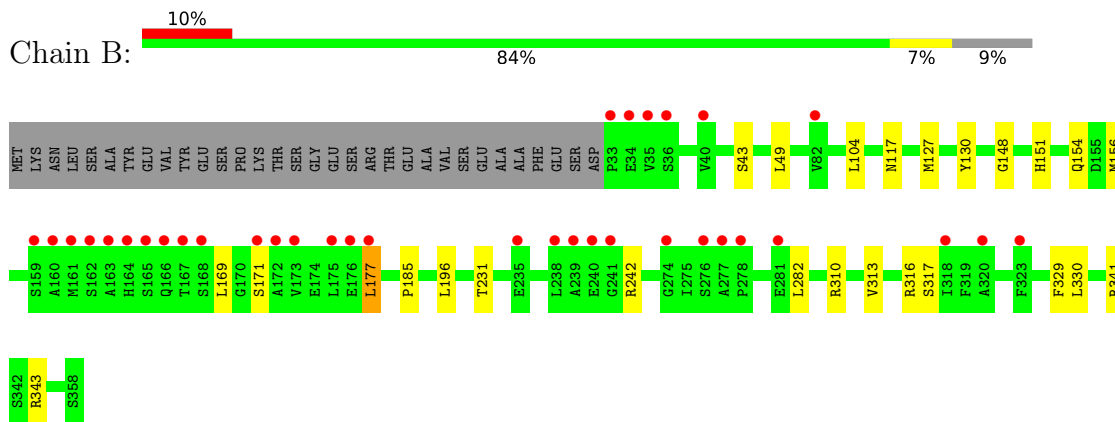
### 3 Residue-property plots [i](#)

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.

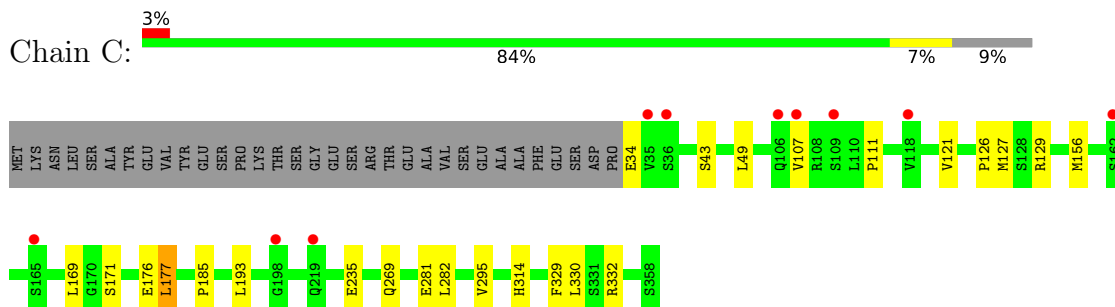
- Molecule 1: L-lysine 3-hydroxylase



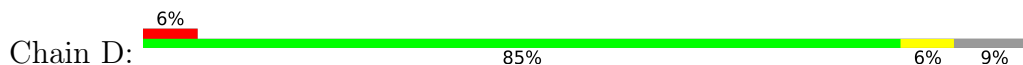
- Molecule 1: L-lysine 3-hydroxylase

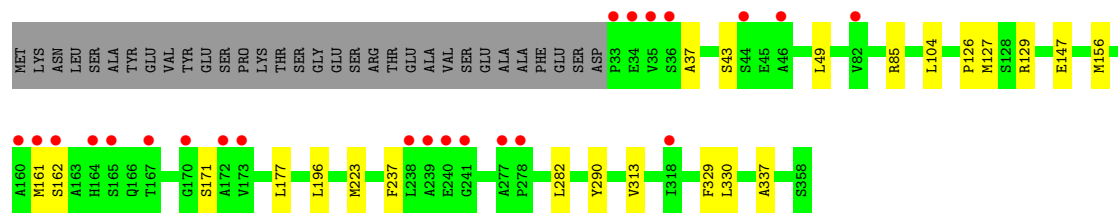


- Molecule 1: L-lysine 3-hydroxylase



- Molecule 1: L-lysine 3-hydroxylase







## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.95Å 67.39Å 110.65Å 107.55° 102.87° 93.58°	Depositor
Resolution (Å)	40.00 – 2.00 48.14 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (40.00-2.00) 99.1 (48.14-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.54 (at 2.00Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.194 , 0.225 0.190 , 0.221	Depositor DCC
$R_{free}$ test set	5027 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.5	Xtrriage
Anisotropy	0.486	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 54.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.006 for -h,-k,h+k+l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11560	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.12% 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: CUW, FE, ACT, SIN

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	0.55	0/2613	0.64	0/3545
1	B	0.49	0/2617	0.63	0/3552
1	C	0.52	0/2594	0.63	0/3521
1	D	0.49	0/2581	0.63	0/3505
All	All	0.51	0/10405	0.63	0/14123

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	2558	0	2514	17	0
1	B	2562	0	2513	15	0
1	C	2539	0	2494	14	0
1	D	2526	0	2483	10	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	16	0	8	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	8	0	4	0	0
3	C	16	0	8	3	0
3	D	8	0	4	0	0
4	A	11	0	0	0	0
4	B	11	0	0	0	0
4	C	11	0	0	0	0
4	D	11	0	0	0	0
5	A	4	0	3	2	0
5	D	4	0	3	0	0
6	A	354	0	0	1	0
6	B	277	0	0	3	0
6	C	345	0	0	1	0
6	D	295	0	0	1	0
All	All	11560	0	10034	53	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.

The worst 5 of 53 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:328:ARG:HH12	3:A:402[B]:SIN:H21	1.50	0.76
1:D:177:LEU:HD13	1:D:290:TYR:CE1	2.27	0.69
1:A:177:LEU:HD23	1:A:269:GLN:OE1	1.93	0.67
1:D:177:LEU:HD11	1:D:313:VAL:HG23	1.78	0.65
1:A:41:LEU:CD1	1:A:104:LEU:HD23	2.27	0.65

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	329/358 (92%)	325 (99%)	2 (1%)	2 (1%)	25	19
1	B	330/358 (92%)	327 (99%)	2 (1%)	1 (0%)	41	37
1	C	327/358 (91%)	323 (99%)	3 (1%)	1 (0%)	41	37
1	D	326/358 (91%)	321 (98%)	3 (1%)	2 (1%)	25	19
All	All	1312/1432 (92%)	1296 (99%)	10 (1%)	6 (0%)	29	23

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	ALA
1	A	171	SER
1	C	171	SER
1	D	171	SER
1	B	171	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	271/293 (92%)	259 (96%)	12 (4%)	28	25
1	B	271/293 (92%)	261 (96%)	10 (4%)	34	32
1	C	269/293 (92%)	261 (97%)	8 (3%)	41	41
1	D	268/293 (92%)	260 (97%)	8 (3%)	41	41
All	All	1079/1172 (92%)	1041 (96%)	38 (4%)	37	35

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	282	LEU
1	D	162	SER
1	C	329	PHE
1	D	85	ARG
1	D	329	PHE

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

Mol	Chain	Res	Type
1	A	283	GLN
1	B	283	GLN
1	C	269	GLN
1	C	314	HIS
1	D	283	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 monosaccharides in this entry.

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

Of 16 ligands modelled in this entry, 4 are monoatomic - leaving 12 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	CUW	D	403	-	8,10,10	0.23	0	8,12,12	0.26	0
3	SIN	A	402[A]	2	7,7,7	2.13	4 (57%)	8,8,8	2.09	4 (50%)
5	ACT	A	404	-	3,3,3	1.05	0	3,3,3	0.71	0
3	SIN	A	402[B]	-	7,7,7	2.07	4 (57%)	8,8,8	1.96	4 (50%)
3	SIN	D	402	2	7,7,7	1.44	2 (28%)	8,8,8	1.53	2 (25%)
4	CUW	A	403	2	8,10,10	1.43	2 (25%)	8,12,12	1.18	2 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	ACT	D	404	-	3,3,3	0.85	0	3,3,3	0.99	0
3	SIN	C	402[B]	2	7,7,7	0.22	0	8,8,8	0.23	0
4	CUW	B	403	-	8,10,10	0.37	0	8,12,12	0.60	0
3	SIN	C	402[A]	-	7,7,7	0.15	0	8,8,8	0.32	0
4	CUW	C	403	-	8,10,10	0.22	0	8,12,12	0.44	0
3	SIN	B	402	2	7,7,7	0.29	0	8,8,8	0.25	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CUW	D	403	-	-	1/12/12/12	-
3	SIN	A	402[A]	2	-	5/5/5/5	-
3	SIN	A	402[B]	-	-	4/5/5/5	-
3	SIN	D	402	2	-	4/5/5/5	-
4	CUW	A	403	2	-	4/12/12/12	-
3	SIN	C	402[B]	2	-	3/5/5/5	-
4	CUW	B	403	-	-	4/12/12/12	-
3	SIN	C	402[A]	-	-	2/5/5/5	-
4	CUW	C	403	-	-	1/12/12/12	-
3	SIN	B	402	2	-	4/5/5/5	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402[A]	SIN	O3-C4	3.16	1.32	1.22
3	A	402[A]	SIN	O4-C4	-2.92	1.20	1.30
4	A	403	CUW	O-C	2.90	1.31	1.22
3	A	402[B]	SIN	O4-C4	-2.89	1.21	1.30
3	A	402[B]	SIN	O1-C1	2.83	1.31	1.22

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402[A]	SIN	O1-C1-C2	-3.31	112.44	123.08
3	D	402	SIN	O3-C4-C3	-3.16	112.93	123.08
3	A	402[A]	SIN	O2-C1-C2	3.07	123.90	114.03
3	D	402	SIN	O4-C4-C3	2.95	123.50	114.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402[B]	SIN	O3-C4-C3	-2.92	113.72	123.08

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	CUW	CA-CB-CG-CD
4	B	403	CUW	OXT-C-CA-CB
4	B	403	CUW	O-C-CA-CB
3	C	402[B]	SIN	C1-C2-C3-C4
3	A	402[A]	SIN	C1-C2-C3-C4

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	404	ACT	2	0
3	A	402[B]	SIN	2	0
3	C	402[B]	SIN	2	0
3	C	402[A]	SIN	1	0

## 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	325/358 (90%)	-0.00	8 (2%) 57 56	30, 44, 69, 90	0
1	B	326/358 (91%)	0.41	35 (10%) 6 5	35, 52, 79, 105	0
1	C	325/358 (90%)	0.12	10 (3%) 49 48	31, 47, 72, 99	0
1	D	326/358 (91%)	0.36	23 (7%) 16 15	35, 52, 80, 108	0
All	All	1302/1432 (90%)	0.22	76 (5%) 23 22	30, 49, 76, 108	0

The worst 5 of 76 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	35	VAL	7.6
1	D	34	GLU	7.5
1	B	172	ALA	6.2
1	C	36	SER	6.2
1	B	241	GLY	5.9

### 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
4	CUW	C	403	11/11	0.59	0.27	64,68,72,74	0
4	CUW	A	403	11/11	0.64	0.24	80,84,85,87	0
3	SIN	C	402[A]	8/8	0.68	0.26	38,48,50,51	8
3	SIN	C	402[B]	8/8	0.68	0.26	65,68,70,72	8
4	CUW	B	403	11/11	0.69	0.34	75,80,84,86	0
3	SIN	B	402	8/8	0.73	0.22	66,74,79,81	0
4	CUW	D	403	11/11	0.76	0.27	54,62,68,71	0
3	SIN	A	402[B]	8/8	0.84	0.23	82,83,84,84	8
3	SIN	A	402[A]	8/8	0.84	0.23	32,47,55,58	8
5	ACT	D	404	4/4	0.84	0.21	43,48,51,53	0
2	FE	B	401	1/1	0.88	0.18	103,103,103,103	0
3	SIN	D	402	8/8	0.91	0.20	59,75,83,86	0
5	ACT	A	404	4/4	0.91	0.16	56,57,57,60	0
2	FE	C	401	1/1	0.91	0.07	78,78,78,78	1
2	FE	D	401	1/1	0.97	0.12	103,103,103,103	0
2	FE	A	401	1/1	0.98	0.07	76,76,76,76	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.