



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2018 – 02:57 pm GMT

PDB ID : 5YB8  
Title : L-Amino acid oxidase/monooxygenase from Pseudomonas sp. AIU 813 - L-arginine complex  
Authors : Im, D.; Matsui, D.; Arakawa, T.; Isobe, K.; Asano, Y.; Fushinobu, S.  
Deposited on : 2017-09-03  
Resolution : 2.30 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.

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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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk31020  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk31020

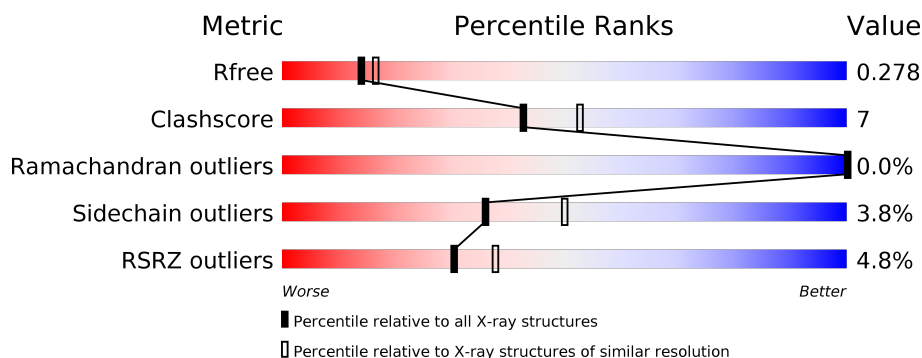
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

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. 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	580	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>13%</div> <div>5%</div> </div> </div>
1	B	580	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>13%</div> <div>5%</div> </div> </div>
1	C	580	<div> <div>5%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>5%</div> </div> </div>
1	D	580	<div> <div>8%</div> <div> <div></div> <div>81%</div> <div>13%</div> <div>5%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ARG	C	601	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17837 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-amino acid oxidase/monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	549	Total	C	N	O	S	0	0	0
			4305	2749	742	791	23			
1	B	549	Total	C	N	O	S	0	0	0
			4305	2749	742	791	23			
1	C	549	Total	C	N	O	S	0	0	0
			4305	2749	742	791	23			
1	D	549	Total	C	N	O	S	0	0	0
			4305	2749	742	791	23			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP W6JQJ6
A	-18	GLY	-	expression tag	UNP W6JQJ6
A	-17	SER	-	expression tag	UNP W6JQJ6
A	-16	SER	-	expression tag	UNP W6JQJ6
A	-15	HIS	-	expression tag	UNP W6JQJ6
A	-14	HIS	-	expression tag	UNP W6JQJ6
A	-13	HIS	-	expression tag	UNP W6JQJ6
A	-12	HIS	-	expression tag	UNP W6JQJ6
A	-11	HIS	-	expression tag	UNP W6JQJ6
A	-10	HIS	-	expression tag	UNP W6JQJ6
A	-9	SER	-	expression tag	UNP W6JQJ6
A	-8	SER	-	expression tag	UNP W6JQJ6
A	-7	GLY	-	expression tag	UNP W6JQJ6
A	-6	LEU	-	expression tag	UNP W6JQJ6
A	-5	VAL	-	expression tag	UNP W6JQJ6
A	-4	PRO	-	expression tag	UNP W6JQJ6
A	-3	ARG	-	expression tag	UNP W6JQJ6
A	-2	GLY	-	expression tag	UNP W6JQJ6
A	-1	SER	-	expression tag	UNP W6JQJ6
A	0	HIS	-	expression tag	UNP W6JQJ6
A	473	PHE	SER	conflict	UNP W6JQJ6

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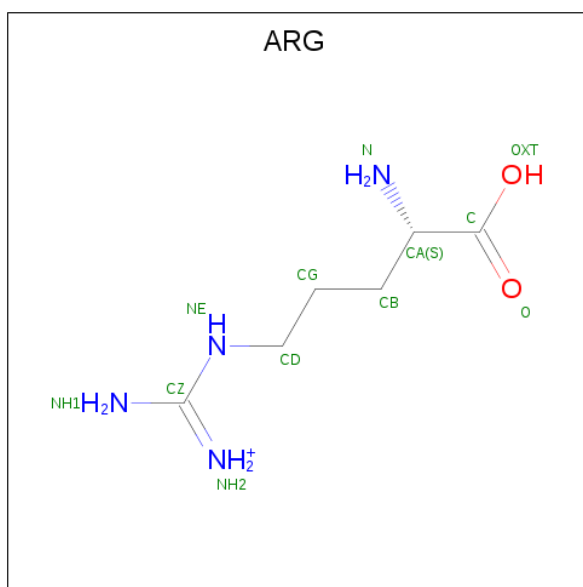
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	expression tag	UNP W6JQJ6
B	-18	GLY	-	expression tag	UNP W6JQJ6
B	-17	SER	-	expression tag	UNP W6JQJ6
B	-16	SER	-	expression tag	UNP W6JQJ6
B	-15	HIS	-	expression tag	UNP W6JQJ6
B	-14	HIS	-	expression tag	UNP W6JQJ6
B	-13	HIS	-	expression tag	UNP W6JQJ6
B	-12	HIS	-	expression tag	UNP W6JQJ6
B	-11	HIS	-	expression tag	UNP W6JQJ6
B	-10	HIS	-	expression tag	UNP W6JQJ6
B	-9	SER	-	expression tag	UNP W6JQJ6
B	-8	SER	-	expression tag	UNP W6JQJ6
B	-7	GLY	-	expression tag	UNP W6JQJ6
B	-6	LEU	-	expression tag	UNP W6JQJ6
B	-5	VAL	-	expression tag	UNP W6JQJ6
B	-4	PRO	-	expression tag	UNP W6JQJ6
B	-3	ARG	-	expression tag	UNP W6JQJ6
B	-2	GLY	-	expression tag	UNP W6JQJ6
B	-1	SER	-	expression tag	UNP W6JQJ6
B	0	HIS	-	expression tag	UNP W6JQJ6
B	473	PHE	SER	conflict	UNP W6JQJ6
C	-19	MET	-	expression tag	UNP W6JQJ6
C	-18	GLY	-	expression tag	UNP W6JQJ6
C	-17	SER	-	expression tag	UNP W6JQJ6
C	-16	SER	-	expression tag	UNP W6JQJ6
C	-15	HIS	-	expression tag	UNP W6JQJ6
C	-14	HIS	-	expression tag	UNP W6JQJ6
C	-13	HIS	-	expression tag	UNP W6JQJ6
C	-12	HIS	-	expression tag	UNP W6JQJ6
C	-11	HIS	-	expression tag	UNP W6JQJ6
C	-10	HIS	-	expression tag	UNP W6JQJ6
C	-9	SER	-	expression tag	UNP W6JQJ6
C	-8	SER	-	expression tag	UNP W6JQJ6
C	-7	GLY	-	expression tag	UNP W6JQJ6
C	-6	LEU	-	expression tag	UNP W6JQJ6
C	-5	VAL	-	expression tag	UNP W6JQJ6
C	-4	PRO	-	expression tag	UNP W6JQJ6
C	-3	ARG	-	expression tag	UNP W6JQJ6
C	-2	GLY	-	expression tag	UNP W6JQJ6
C	-1	SER	-	expression tag	UNP W6JQJ6
C	0	HIS	-	expression tag	UNP W6JQJ6
C	473	PHE	SER	conflict	UNP W6JQJ6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-19	MET	-	expression tag	UNP W6JQJ6
D	-18	GLY	-	expression tag	UNP W6JQJ6
D	-17	SER	-	expression tag	UNP W6JQJ6
D	-16	SER	-	expression tag	UNP W6JQJ6
D	-15	HIS	-	expression tag	UNP W6JQJ6
D	-14	HIS	-	expression tag	UNP W6JQJ6
D	-13	HIS	-	expression tag	UNP W6JQJ6
D	-12	HIS	-	expression tag	UNP W6JQJ6
D	-11	HIS	-	expression tag	UNP W6JQJ6
D	-10	HIS	-	expression tag	UNP W6JQJ6
D	-9	SER	-	expression tag	UNP W6JQJ6
D	-8	SER	-	expression tag	UNP W6JQJ6
D	-7	GLY	-	expression tag	UNP W6JQJ6
D	-6	LEU	-	expression tag	UNP W6JQJ6
D	-5	VAL	-	expression tag	UNP W6JQJ6
D	-4	PRO	-	expression tag	UNP W6JQJ6
D	-3	ARG	-	expression tag	UNP W6JQJ6
D	-2	GLY	-	expression tag	UNP W6JQJ6
D	-1	SER	-	expression tag	UNP W6JQJ6
D	0	HIS	-	expression tag	UNP W6JQJ6
D	473	PHE	SER	conflict	UNP W6JQJ6

- Molecule 2 is ARGinine (three-letter code: ARG) (formula:  $C_6H_{15}N_4O_2$ ).



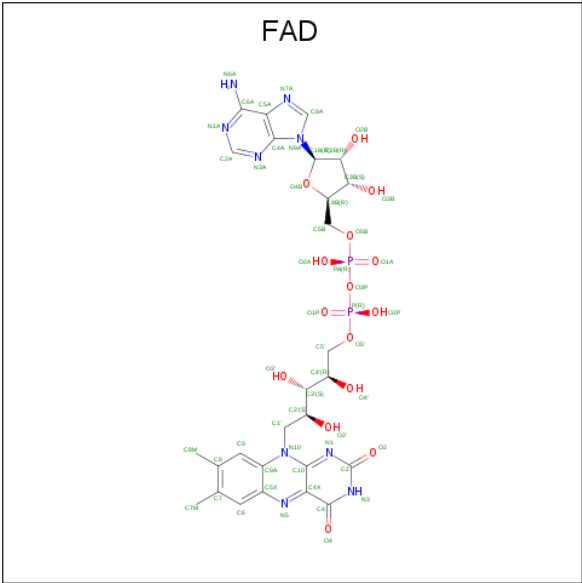
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			12	6	4	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			12	6	4	2		
2	A	1	Total	C	N	O	0	0
			12	6	4	2		
2	B	1	Total	C	N	O	0	0
			12	6	4	2		
2	B	1	Total	C	N	O	0	0
			12	6	4	2		
2	C	1	Total	C	N	O	0	0
			12	6	4	2		
2	C	1	Total	C	N	O	0	0
			12	6	4	2		
2	D	1	Total	C	N	O	0	0
			12	6	4	2		

- Molecule 3 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
3	A	1	Total	C	N	O	P	0
			53	27	9	15	2	
3	B	1	Total	C	N	O	P	0
			53	27	9	15	2	
3	C	1	Total	C	N	O	P	0
			53	27	9	15	2	
3	D	1	Total	C	N	O	P	0
			53	27	9	15	2	

- Molecule 4 is water.

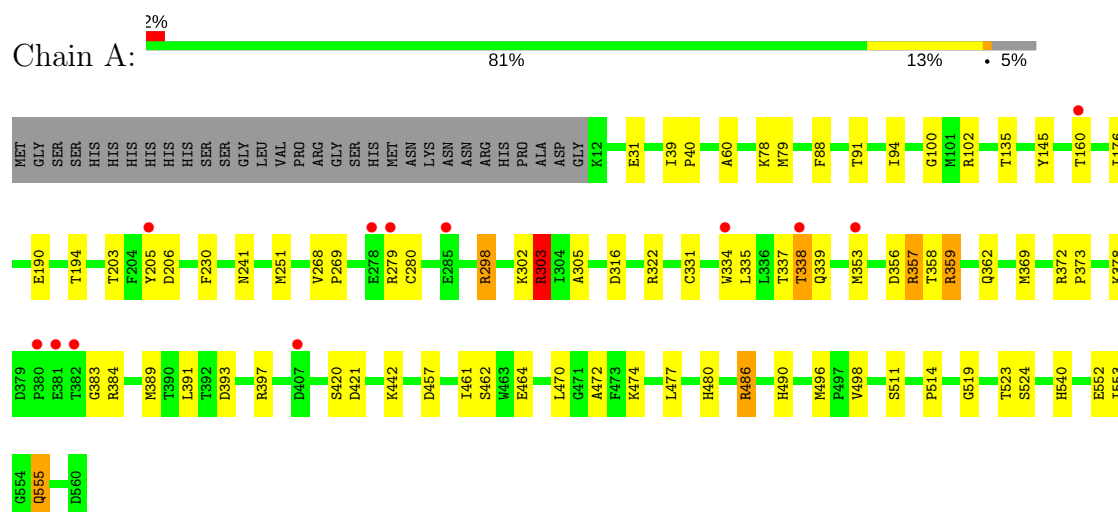
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	98	Total 98	O 98	0	0
4	B	108	Total 108	O 108	0	0
4	C	53	Total 53	O 53	0	0
4	D	50	Total 50	O 50	0	0



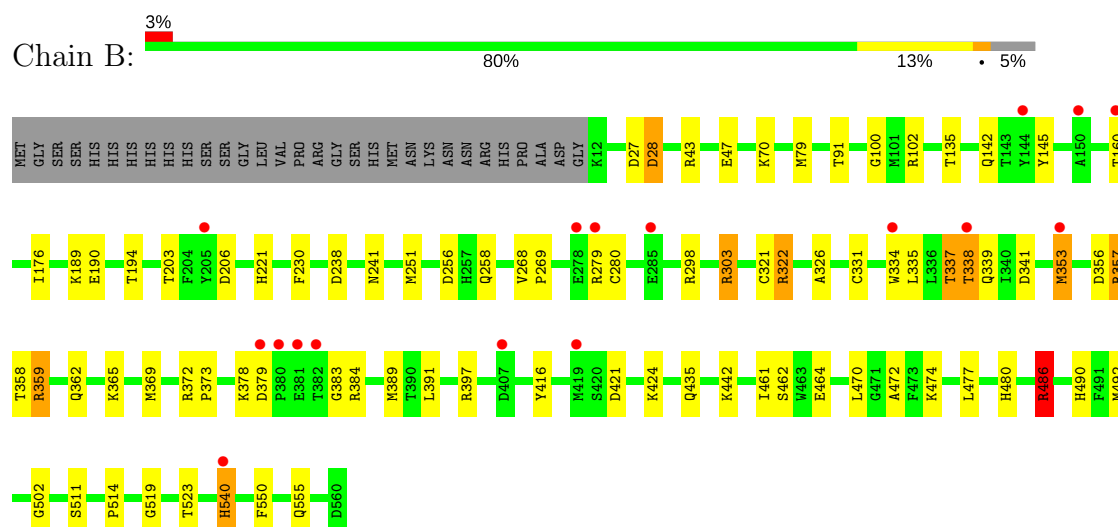
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

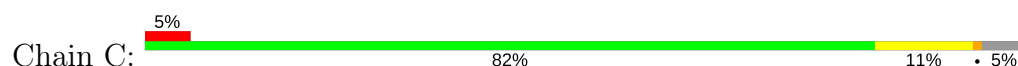
- Molecule 1: L-amino acid oxidase/monooxygenase

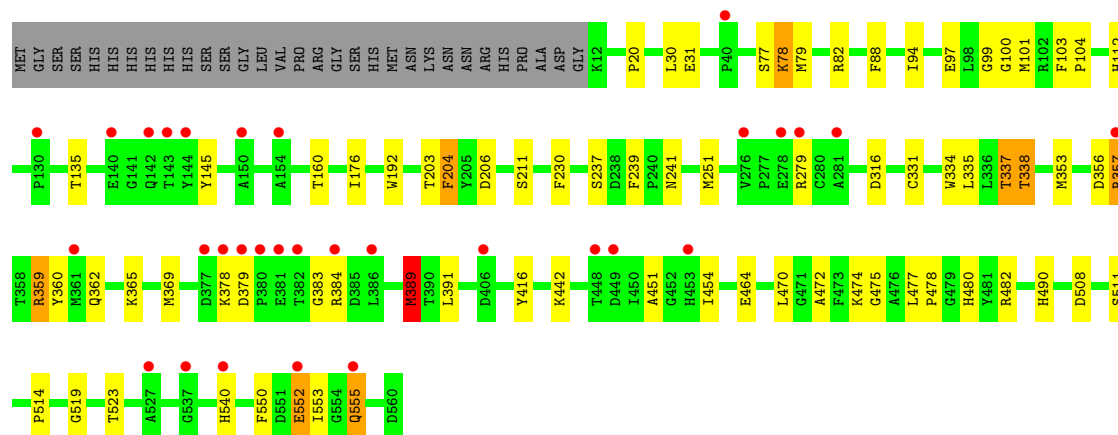


- Molecule 1: L-amino acid oxidase/monooxygenase

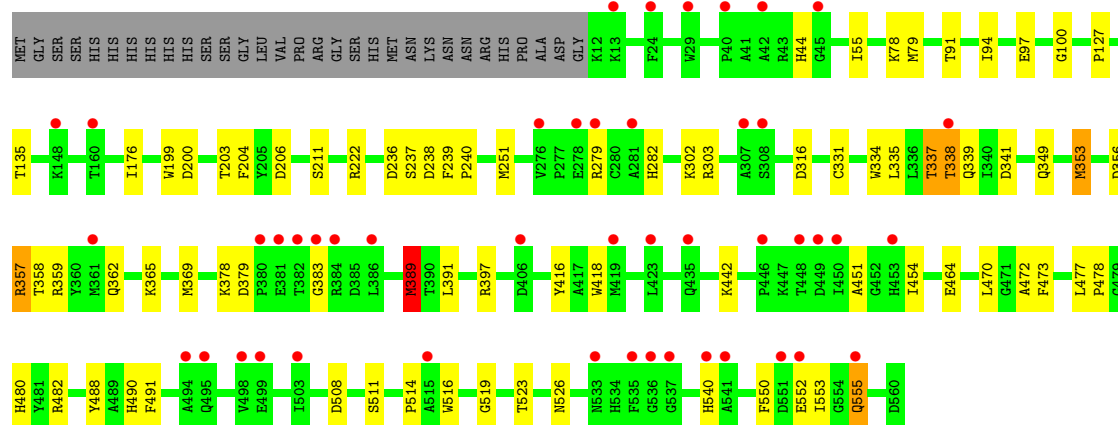
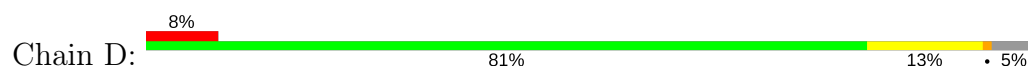


- Molecule 1: L-amino acid oxidase/monooxygenase





• Molecule 1: L-amino acid oxidase/monooxygenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.20Å 133.00Å 101.50Å 90.00° 112.00° 90.00°	Depositor
Resolution (Å)	94.11 – 2.30 45.52 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (94.11-2.30) 99.8 (45.52-2.30)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.80 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, $R_{free}$	0.220 , 0.273 0.226 , 0.278	Depositor DCC
$R_{free}$ test set	2009 reflections (1.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.3	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 40.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.138 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	17837	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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

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	0.82	0/4428	0.88	5/6019 (0.1%)
1	B	0.82	0/4428	0.91	5/6019 (0.1%)
1	C	0.69	0/4428	0.81	4/6019 (0.1%)
1	D	0.69	0/4428	0.81	4/6019 (0.1%)
All	All	0.76	0/17712	0.85	18/24076 (0.1%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	486	ARG	NE-CZ-NH1	8.41	124.50	120.30
1	B	353	MET	CG-SD-CE	8.09	113.14	100.20
1	D	482	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	A	486	ARG	NE-CZ-NH1	6.99	123.79	120.30
1	C	482	ARG	NE-CZ-NH2	-6.52	117.04	120.30

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	4305	0	4166	74	0
1	B	4305	0	4164	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4305	0	4166	66	0
1	D	4305	0	4166	69	0
2	A	36	0	36	1	0
2	B	24	0	24	2	0
2	C	24	0	24	1	0
2	D	12	0	12	2	0
3	A	53	0	31	5	0
3	B	53	0	31	6	0
3	C	53	0	31	5	0
3	D	53	0	31	6	0
4	A	98	0	0	4	0
4	B	108	0	0	10	0
4	C	53	0	0	1	0
4	D	50	0	0	1	0
All	All	17837	0	16882	253	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 7.

The worst 5 of 253 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:D:472:ALA:HB1	3:D:602:FAD:HM83	1.45	0.97
1:D:203:THR:OG1	1:D:206:ASP:OD2	1.84	0.95
1:B:472:ALA:HB1	3:B:603:FAD:HM83	1.47	0.95
1:C:472:ALA:HB1	3:C:603:FAD:HM83	1.49	0.94
1:A:303:ARG:HH11	1:A:303:ARG:HG3	1.29	0.94

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	547/580 (94%)	531 (97%)	16 (3%)	0	100	100
1	B	547/580 (94%)	530 (97%)	17 (3%)	0	100	100
1	C	547/580 (94%)	537 (98%)	10 (2%)	0	100	100
1	D	547/580 (94%)	533 (97%)	13 (2%)	1 (0%)	49	61
All	All	2188/2320 (94%)	2131 (97%)	56 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	397	ARG

### 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	448/474 (94%)	431 (96%)	17 (4%)	36	50
1	B	448/474 (94%)	432 (96%)	16 (4%)	38	52
1	C	448/474 (94%)	432 (96%)	16 (4%)	38	52
1	D	448/474 (94%)	433 (97%)	15 (3%)	41	56
All	All	1792/1896 (94%)	1728 (96%)	64 (4%)	36	52

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	442	LYS
1	C	79	MET
1	D	442	LYS
1	B	486	ARG
1	B	555	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	490	HIS
1	C	428	HIS
1	D	480	HIS
1	C	267	GLN
1	C	362	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

12 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
2	ARG	A	601	-	6,11,11	0.42	0	5,13,13	0.41	0
2	ARG	A	602	-	6,11,11	0.59	0	5,13,13	0.80	0
2	ARG	A	603	-	6,11,11	0.36	0	5,13,13	0.64	0
3	FAD	A	604	-	51,58,58	1.36	7 (13%)	57,89,89	3.21	19 (33%)
2	ARG	B	601	-	6,11,11	0.47	0	5,13,13	0.63	0
2	ARG	B	602	-	6,11,11	0.45	0	5,13,13	0.80	0
3	FAD	B	603	-	51,58,58	1.66	10 (19%)	57,89,89	3.62	18 (31%)
2	ARG	C	601	-	6,11,11	0.71	0	5,13,13	0.55	0
2	ARG	C	602	-	6,11,11	0.42	0	5,13,13	0.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	FAD	C	603	-	51,58,58	1.53	6 (11%)	57,89,89	2.80	22 (38%)
2	ARG	D	601	-	6,11,11	0.45	0	5,13,13	0.66	0
3	FAD	D	602	-	51,58,58	1.54	7 (13%)	57,89,89	2.66	17 (29%)

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
2	ARG	A	601	-	-	0/7/11/11	0/0/0/0
2	ARG	A	602	-	-	0/7/11/11	0/0/0/0
2	ARG	A	603	-	-	0/7/11/11	0/0/0/0
3	FAD	A	604	-	-	0/28/50/50	0/6/6/6
2	ARG	B	601	-	-	0/7/11/11	0/0/0/0
2	ARG	B	602	-	-	0/7/11/11	0/0/0/0
3	FAD	B	603	-	-	0/28/50/50	0/6/6/6
2	ARG	C	601	-	-	0/7/11/11	0/0/0/0
2	ARG	C	602	-	-	0/7/11/11	0/0/0/0
3	FAD	C	603	-	-	0/28/50/50	0/6/6/6
2	ARG	D	601	-	-	0/7/11/11	0/0/0/0
3	FAD	D	602	-	-	0/28/50/50	0/6/6/6

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	603	FAD	C8A-N9A	-3.80	1.32	1.36
3	C	603	FAD	C6-C5X	-3.80	1.35	1.41
3	B	603	FAD	C2-N1	-3.00	1.32	1.38
3	D	602	FAD	C6-C5X	-2.98	1.37	1.41
3	B	603	FAD	C5A-N7A	-2.60	1.30	1.39

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	603	FAD	C4B-O4B-C1B	-17.50	91.58	109.83
3	A	604	FAD	C4B-O4B-C1B	-11.32	98.03	109.83
3	A	604	FAD	N3A-C2A-N1A	-7.78	122.20	128.86
3	D	602	FAD	N3A-C2A-N1A	-7.69	122.28	128.86
3	B	603	FAD	N3A-C2A-N1A	-7.13	122.76	128.86

There are no chirality outliers.



There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	603	ARG	1	0
3	A	604	FAD	5	0
2	B	601	ARG	1	0
2	B	602	ARG	1	0
3	B	603	FAD	6	0
2	C	602	ARG	1	0
3	C	603	FAD	5	0
2	D	601	ARG	2	0
3	D	602	FAD	6	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	549/580 (94%)	0.19	12 (2%) 62 69	14, 29, 53, 85	0
1	B	549/580 (94%)	0.18	17 (3%) 49 56	15, 29, 51, 83	0
1	C	549/580 (94%)	0.55	31 (5%) 24 31	20, 39, 62, 112	0
1	D	549/580 (94%)	0.58	46 (8%) 11 15	22, 38, 60, 91	0
All	All	2196/2320 (94%)	0.38	106 (4%) 30 38	14, 35, 58, 112	0

The worst 5 of 106 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	380	PRO	4.9
1	C	279	ARG	4.6
1	B	279	ARG	4.6
1	C	381	GLU	4.3
1	A	279	ARG	4.1

### 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 carbohydrates 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
2	ARG	C	601	12/12	0.54	0.42	58,68,78,80	0
2	ARG	C	602	12/12	0.65	0.32	68,77,78,80	0
2	ARG	A	601	12/12	0.69	0.34	59,70,85,86	0
2	ARG	D	601	12/12	0.72	0.37	55,64,78,80	0
2	ARG	A	603	12/12	0.74	0.26	69,78,82,83	0
2	ARG	A	602	12/12	0.76	0.25	40,51,53,55	0
2	ARG	B	601	12/12	0.76	0.29	57,61,74,75	0
2	ARG	B	602	12/12	0.76	0.29	45,55,63,63	0
3	FAD	D	602	53/53	0.94	0.15	21,30,37,38	0
3	FAD	C	603	53/53	0.94	0.15	23,29,32,34	0
3	FAD	A	604	53/53	0.96	0.14	17,21,27,31	0
3	FAD	B	603	53/53	0.96	0.13	15,21,29,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.