



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:16 AM GMT

PDB ID : 2C91  
Title : MOUSE SUCCINIC SEMIALDEHYDE REDUCTASE, AKR7A5  
Authors : Zhu, X.; Ellis, E.M.; Lapthorn, A.J.  
Deposited on : 2005-12-08  
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  
<http://wwpdb.org/validation/2016/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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

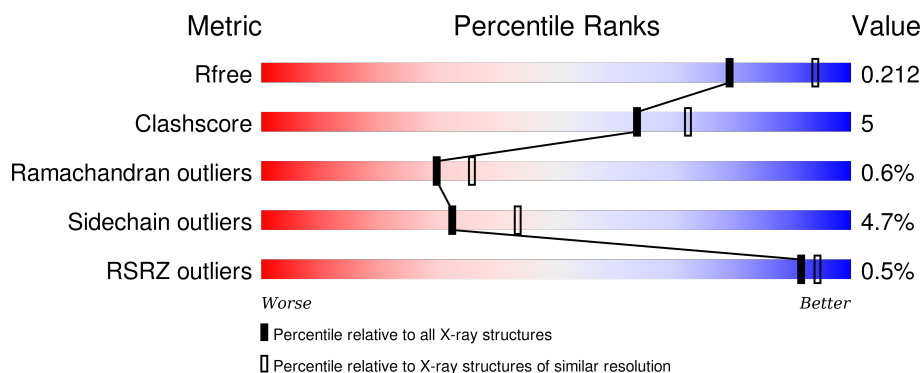
# 1 Overall quality at a glance

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))
$R_{free}$	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (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	338	 79% 15% . .
1	B	338	 81% 12% . .
1	C	338	 81% 13% . .
1	D	338	 82% 11% . .
1	E	338	 81% 12% . .

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Mol	Chain	Length	Quality of chain
1	F	338	
1	G	338	
1	H	338	
1	I	338	
1	J	338	

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	TLA	H	360	-	-	-	X
4	GOL	B	361	-	-	-	X
4	GOL	B	362	-	-	-	X
4	GOL	D	363	-	-	-	X
4	GOL	F	361	-	-	-	X
4	GOL	G	363	-	-	-	X
4	GOL	G	364	-	-	X	X
4	GOL	H	362	-	-	-	X
4	GOL	I	361	-	-	-	X
4	GOL	J	363	-	-	-	X
4	GOL	J	364	-	-	-	X
5	PO4	J	367	-	-	-	X
6	MES	B	364	-	-	-	X
6	MES	C	364	-	-	-	X
6	MES	I	363	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 28440 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 AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total	C	N	O	S	0	3	0
			2569	1617	454	480	18			
1	B	324	Total	C	N	O	S	0	0	0
			2545	1603	447	477	18			
1	C	324	Total	C	N	O	S	0	1	0
			2552	1608	447	479	18			
1	D	324	Total	C	N	O	S	0	2	0
			2564	1616	453	477	18			
1	E	324	Total	C	N	O	S	0	1	0
			2556	1611	450	477	18			
1	F	324	Total	C	N	O	S	0	0	0
			2548	1606	447	477	18			
1	G	324	Total	C	N	O	S	0	1	0
			2552	1608	447	479	18			
1	H	324	Total	C	N	O	S	0	1	0
			2538	1601	440	479	18			
1	I	324	Total	C	N	O	S	0	0	0
			2548	1606	447	477	18			
1	J	325	Total	C	N	O	S	0	1	0
			2559	1613	448	480	18			

There are 20 discrepancies between the modelled and reference sequences:

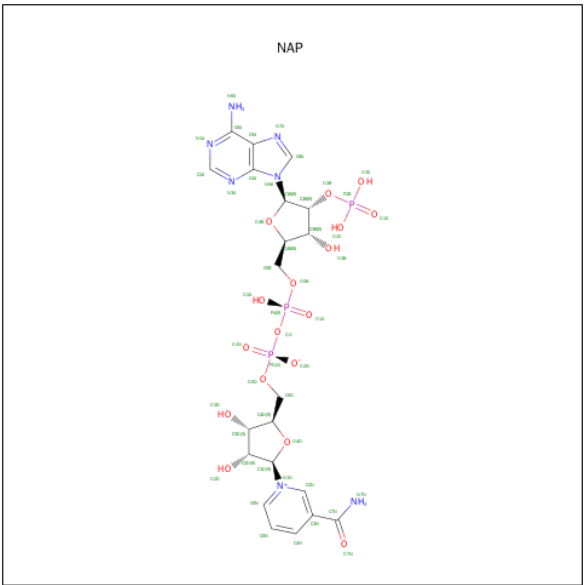
Chain	Residue	Modelled	Actual	Comment	Reference
A	87	ILE	VAL	CONFLICT	UNP Q8CG76
A	122	CYS	ARG	CONFLICT	UNP Q8CG76
B	87	ILE	VAL	CONFLICT	UNP Q8CG76
B	122	CYS	ARG	CONFLICT	UNP Q8CG76
C	87	ILE	VAL	CONFLICT	UNP Q8CG76
C	122	CYS	ARG	CONFLICT	UNP Q8CG76
D	87	ILE	VAL	CONFLICT	UNP Q8CG76
D	122	CYS	ARG	CONFLICT	UNP Q8CG76
E	87	ILE	VAL	CONFLICT	UNP Q8CG76

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Chain	Residue	Modelled	Actual	Comment	Reference
E	122	CYS	ARG	CONFLICT	UNP Q8CG76
F	87	ILE	VAL	CONFLICT	UNP Q8CG76
F	122	CYS	ARG	CONFLICT	UNP Q8CG76
G	87	ILE	VAL	CONFLICT	UNP Q8CG76
G	122	CYS	ARG	CONFLICT	UNP Q8CG76
H	87	ILE	VAL	CONFLICT	UNP Q8CG76
H	122	CYS	ARG	CONFLICT	UNP Q8CG76
I	87	ILE	VAL	CONFLICT	UNP Q8CG76
I	122	CYS	ARG	CONFLICT	UNP Q8CG76
J	87	ILE	VAL	CONFLICT	UNP Q8CG76
J	122	CYS	ARG	CONFLICT	UNP Q8CG76

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



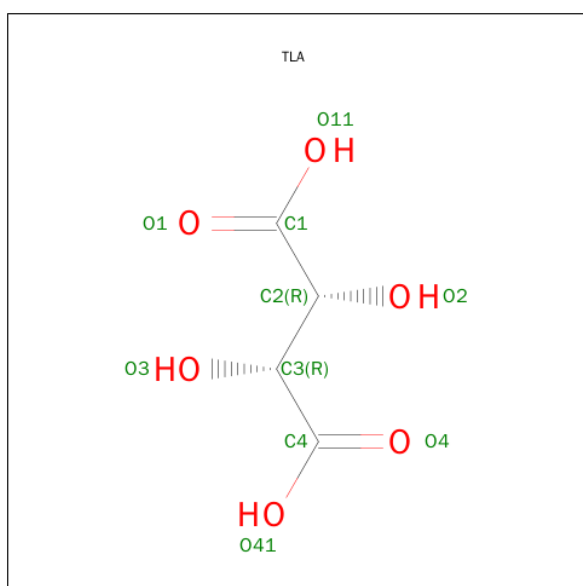
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	G	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	H	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	I	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	J	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>6</sub>).



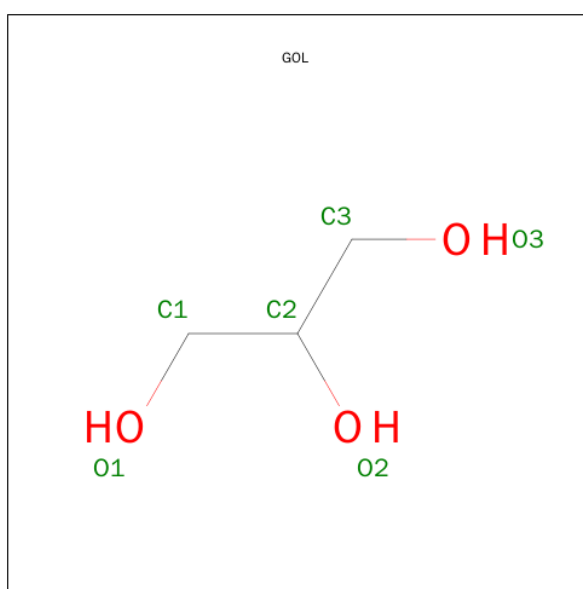
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	4	6		
3	B	1	Total	C	O	0	0
			10	4	6		
3	C	1	Total	C	O	0	0
			10	4	6		
3	D	1	Total	C	O	0	0
			10	4	6		
3	E	1	Total	C	O	0	0
			10	4	6		
3	F	1	Total	C	O	0	0
			10	4	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	C	O	0	0
			10	4	6		
3	H	1	Total	C	O	0	0
			10	4	6		
3	I	1	Total	C	O	0	0
			10	4	6		
3	J	1	Total	C	O	0	0
			10	4	6		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

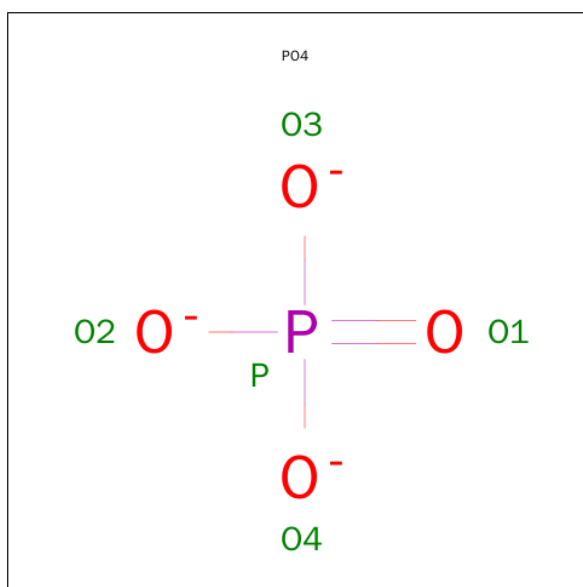
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		

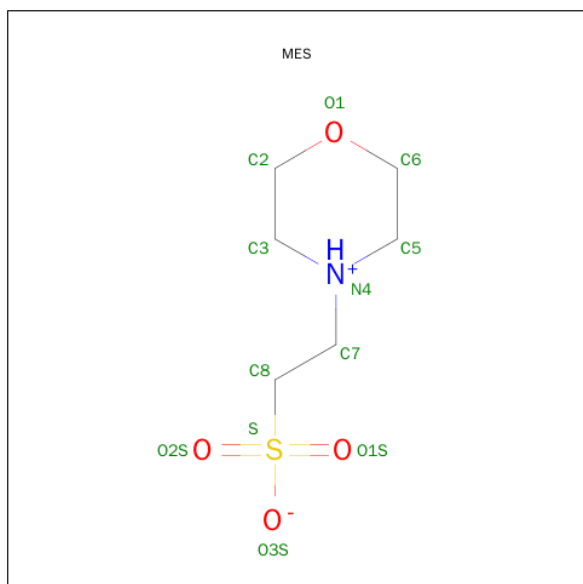
- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	J	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	I	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	J	1	Total	C	N	O	S	0	0
			12	6	1	4	1		


- Molecule 7 is water.

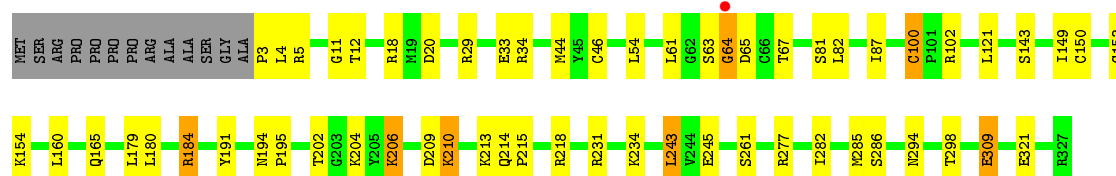
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	223	Total	O	0	0
			223	223		
7	B	131	Total	O	0	0
			131	131		
7	C	225	Total	O	0	0
			225	225		
7	D	272	Total	O	0	0
			272	272		
7	E	262	Total	O	0	0
			262	262		
7	F	214	Total	O	0	0
			214	214		
7	G	257	Total	O	0	0
			257	257		
7	H	159	Total	O	0	0
			159	159		
7	I	164	Total	O	0	0
			164	164		
7	J	202	Total	O	0	0
			202	202		

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


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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.

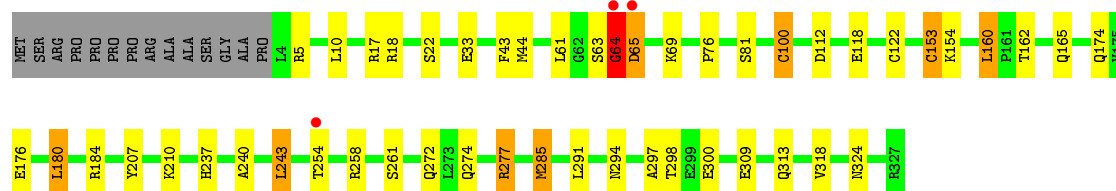
- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain A: 




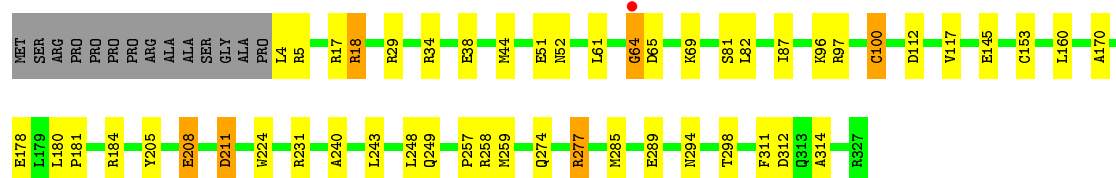
- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain B: 




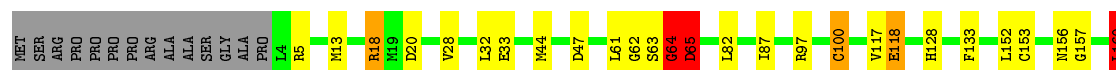
- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

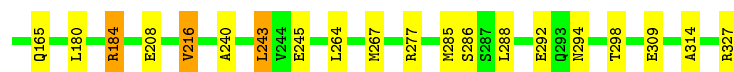
Chain C: 



- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

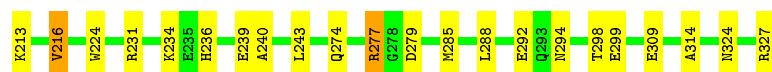
Chain D: 





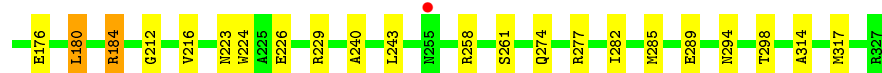
• Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain E: 81% 12%



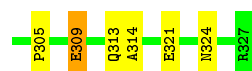
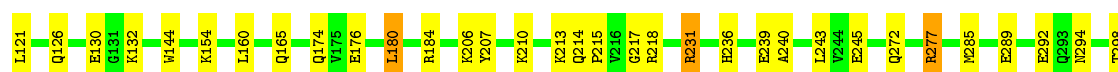
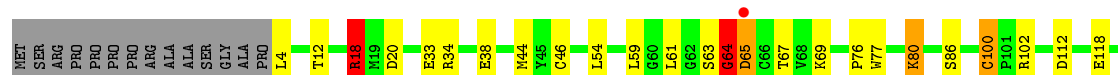
• Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain F: 81% 12%



• Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain G: 77% 16%



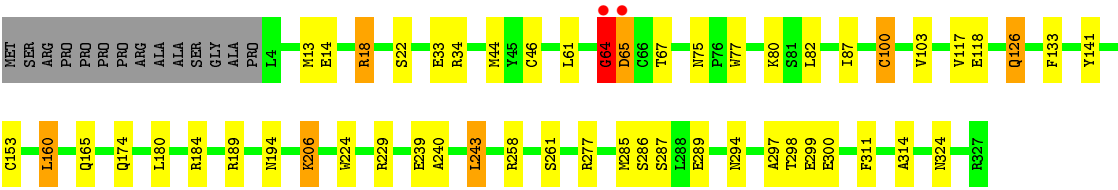
• Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain H: 81% 12%

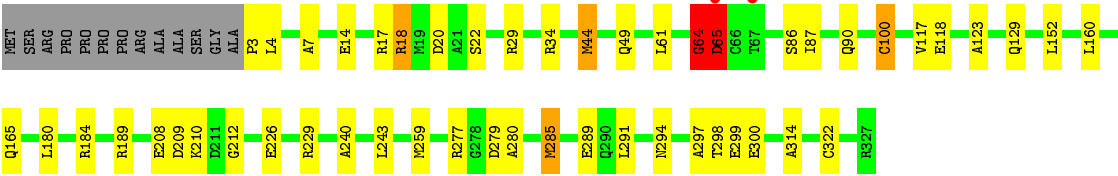
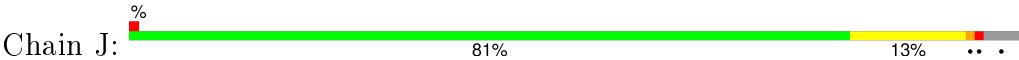


• Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain I: 80% 13%



● Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.53Å 159.24Å 96.70Å 90.02° 119.40° 78.50°	Depositor
Resolution (Å)	45.00 – 2.30 41.88 – 2.30	Depositor EDS
% Data completeness (in resolution range)	89.8 (45.00-2.30) 86.9 (41.88-2.30)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.58 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.160 , 0.208 0.170 , 0.212	Depositor DCC
$R_{free}$ test set	9982 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.3	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.458 for -h-l,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 198863 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	28440	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PO4, TLA, NAP, MES

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	1.17	13/2647 (0.5%)	0.98	9/3584 (0.3%)
1	B	1.02	5/2608 (0.2%)	0.89	4/3533 (0.1%)
1	C	1.09	6/2620 (0.2%)	0.95	10/3549 (0.3%)
1	D	1.17	7/2633 (0.3%)	1.03	15/3565 (0.4%)
1	E	1.14	4/2622 (0.2%)	1.05	19/3552 (0.5%)
1	F	1.10	5/2611 (0.2%)	0.97	9/3537 (0.3%)
1	G	1.16	8/2620 (0.3%)	1.00	10/3549 (0.3%)
1	H	1.02	4/2604 (0.2%)	0.88	7/3531 (0.2%)
1	I	1.09	8/2611 (0.3%)	0.94	5/3537 (0.1%)
1	J	1.01	4/2625 (0.2%)	0.94	13/3556 (0.4%)
All	All	1.10	64/26201 (0.2%)	0.96	101/35493 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
All	All	0	10

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	118	GLU	CG-CD	9.15	1.65	1.51
1	D	309	GLU	CG-CD	8.77	1.65	1.51
1	I	100	CYS	CB-SG	-8.64	1.67	1.82
1	F	289	GLU	CG-CD	8.10	1.64	1.51
1	D	18	ARG	CG-CD	8.08	1.72	1.51

The worst 5 of 101 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	97	ARG	NE-CZ-NH2	-10.66	114.97	120.30
1	E	184	ARG	NE-CZ-NH2	-10.20	115.20	120.30
1	G	80	LYS	CD-CE-NZ	-9.83	89.09	111.70
1	D	97	ARG	NE-CZ-NH1	9.57	125.09	120.30
1	D	18	ARG	NE-CZ-NH1	9.55	125.07	120.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	64	GLY	Peptide
1	B	64	GLY	Peptide
1	C	64	GLY	Peptide
1	D	64	GLY	Peptide
1	E	64	GLY	Peptide

## 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	2569	0	2484	35	0
1	B	2545	0	2453	24	0
1	C	2552	0	2464	21	0
1	D	2564	0	2488	21	0
1	E	2556	0	2475	26	0
1	F	2548	0	2462	29	0
1	G	2552	0	2464	37	0
1	H	2538	0	2435	22	0
1	I	2548	0	2462	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	2559	0	2470	20	0
2	A	48	0	25	2	0
2	B	48	0	25	3	0
2	C	48	0	25	0	0
2	D	48	0	25	1	0
2	E	48	0	25	1	0
2	F	48	0	25	3	0
2	G	48	0	24	1	0
2	H	48	0	25	4	0
2	I	48	0	25	3	0
2	J	48	0	25	2	0
3	A	10	0	4	0	0
3	B	10	0	4	2	0
3	C	10	0	4	3	0
3	D	10	0	4	0	0
3	E	10	0	4	1	0
3	F	10	0	4	1	0
3	G	10	0	4	0	0
3	H	10	0	4	2	0
3	I	10	0	4	1	0
3	J	10	0	4	1	0
4	A	12	0	16	2	0
4	B	18	0	24	0	0
4	C	18	0	24	0	0
4	D	18	0	24	0	0
4	E	18	0	24	0	0
4	F	6	0	8	0	0
4	G	18	0	24	5	0
4	H	12	0	16	2	0
4	I	12	0	16	1	0
4	J	18	0	24	0	0
5	A	5	0	0	0	0
5	J	5	0	0	0	0
6	B	12	0	12	0	0
6	C	12	0	12	0	0
6	D	12	0	12	0	0
6	I	12	0	12	0	0
6	J	12	0	12	0	0
7	A	223	0	0	9	0
7	B	131	0	0	3	0
7	C	225	0	0	7	0
7	D	272	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	E	262	0	0	7	0
7	F	214	0	0	9	0
7	G	257	0	0	8	0
7	H	159	0	0	2	0
7	I	164	0	0	9	0
7	J	202	0	0	8	0
All	All	28440	0	25206	267	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 5.

The worst 5 of 267 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:E:100:CYS:SG	7:E:2088:HOH:O	1.95	1.23
1:C:100:CYS:SG	7:C:2071:HOH:O	2.05	1.10
1:F:44:MET:SD	7:F:2025:HOH:O	2.10	1.08
1:A:100:CYS:SG	7:A:2061:HOH:O	2.10	1.06
1:I:13:MET:HG2	7:I:2008:HOH:O	1.61	0.99

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	326/338 (96%)	320 (98%)	4 (1%)	2 (1%)	30	36
1	B	322/338 (95%)	314 (98%)	6 (2%)	2 (1%)	30	36
1	C	323/338 (96%)	314 (97%)	7 (2%)	2 (1%)	30	36
1	D	324/338 (96%)	317 (98%)	5 (2%)	2 (1%)	30	36
1	E	323/338 (96%)	316 (98%)	6 (2%)	1 (0%)	46	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	322/338 (95%)	312 (97%)	8 (2%)	2 (1%)	30	36
1	G	323/338 (96%)	316 (98%)	5 (2%)	2 (1%)	30	36
1	H	323/338 (96%)	316 (98%)	5 (2%)	2 (1%)	30	36
1	I	322/338 (95%)	314 (98%)	6 (2%)	2 (1%)	30	36
1	J	324/338 (96%)	313 (97%)	8 (2%)	3 (1%)	21	24
All	All	3232/3380 (96%)	3152 (98%)	60 (2%)	20 (1%)	30	36

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	ASP
1	B	65	ASP
1	C	65	ASP
1	D	65	ASP
1	E	65	ASP

### 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	269/276 (98%)	260 (97%)	9 (3%)	45	61
1	B	265/276 (96%)	250 (94%)	15 (6%)	25	34
1	C	267/276 (97%)	253 (95%)	14 (5%)	29	38
1	D	268/276 (97%)	257 (96%)	11 (4%)	37	50
1	E	267/276 (97%)	258 (97%)	9 (3%)	44	59
1	F	266/276 (96%)	251 (94%)	15 (6%)	26	35
1	G	267/276 (97%)	254 (95%)	13 (5%)	31	41
1	H	264/276 (96%)	249 (94%)	15 (6%)	25	34
1	I	266/276 (96%)	251 (94%)	15 (6%)	26	35
1	J	267/276 (97%)	255 (96%)	12 (4%)	34	46
All	All	2666/2760 (97%)	2538 (95%)	128 (5%)	32	42

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	285	MET
1	F	261	SER
1	J	22	SER
1	F	5	ARG
1	F	117	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	274	GLN
1	F	49	GLN
1	I	272	GLN
1	E	49	GLN
1	E	129	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](#)

52 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	NAP	A	350	-	42,52,52	1.84	8 (19%)	54,80,80	1.82	6 (11%)
3	TLA	A	360	-	3,9,9	0.44	0	6,12,12	0.97	0
4	GOL	A	361	-	5,5,5	0.49	0	5,5,5	0.71	0
4	GOL	A	363	-	5,5,5	0.80	0	5,5,5	0.91	0
5	PO4	A	364	-	4,4,4	0.72	0	6,6,6	0.43	0
2	NAP	B	350	-	42,52,52	1.68	7 (16%)	54,80,80	2.63	12 (22%)
3	TLA	B	360	-	3,9,9	2.64	1 (33%)	6,12,12	1.51	2 (33%)
4	GOL	B	361	-	5,5,5	0.53	0	5,5,5	0.57	0
4	GOL	B	362	-	5,5,5	0.73	0	5,5,5	1.28	1 (20%)
4	GOL	B	363	-	5,5,5	0.70	0	5,5,5	0.91	0
6	MES	B	364	-	11,12,12	0.81	0	14,16,16	4.13	9 (64%)
2	NAP	C	350	-	42,52,52	1.49	4 (9%)	54,80,80	1.93	7 (12%)
3	TLA	C	360	-	3,9,9	1.46	1 (33%)	6,12,12	0.91	0
4	GOL	C	361	-	5,5,5	0.66	0	5,5,5	1.35	0
4	GOL	C	362	-	5,5,5	0.52	0	5,5,5	1.17	1 (20%)
4	GOL	C	363	-	5,5,5	0.80	0	5,5,5	1.36	0
6	MES	C	364	-	11,12,12	0.78	0	14,16,16	2.34	7 (50%)
2	NAP	D	350	-	42,52,52	1.62	5 (11%)	54,80,80	1.93	6 (11%)
3	TLA	D	360	-	3,9,9	1.67	1 (33%)	6,12,12	2.12	3 (50%)
4	GOL	D	361	-	5,5,5	0.59	0	5,5,5	0.30	0
4	GOL	D	362	-	5,5,5	0.49	0	5,5,5	0.78	0
4	GOL	D	363	-	5,5,5	1.42	0	5,5,5	1.73	1 (20%)
6	MES	D	364	-	11,12,12	1.06	1 (9%)	14,16,16	3.22	7 (50%)
2	NAP	E	350	-	42,52,52	1.67	5 (11%)	54,80,80	2.43	9 (16%)
3	TLA	E	360	-	3,9,9	0.94	0	6,12,12	0.94	0
4	GOL	E	361	-	5,5,5	0.54	0	5,5,5	0.94	0
4	GOL	E	362	-	5,5,5	0.62	0	5,5,5	0.70	0
4	GOL	E	363	-	5,5,5	0.73	0	5,5,5	0.95	0
2	NAP	F	350	-	42,52,52	1.79	4 (9%)	54,80,80	2.15	10 (18%)
3	TLA	F	360	-	3,9,9	0.41	0	6,12,12	1.19	0
4	GOL	F	361	-	5,5,5	0.72	0	5,5,5	1.56	2 (40%)
2	NAP	G	350	-	42,52,52	1.89	9 (21%)	54,80,80	1.88	8 (14%)
3	TLA	G	360	-	3,9,9	1.22	0	6,12,12	1.17	0
4	GOL	G	362	-	5,5,5	0.58	0	5,5,5	1.24	1 (20%)
4	GOL	G	363	-	5,5,5	0.59	0	5,5,5	1.23	1 (20%)
4	GOL	G	364	-	5,5,5	0.95	0	5,5,5	1.58	2 (40%)
2	NAP	H	350	-	42,52,52	1.79	5 (11%)	54,80,80	2.15	14 (25%)
3	TLA	H	360	-	3,9,9	1.59	1 (33%)	6,12,12	1.01	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GOL	H	361	-	5,5,5	0.38	0	5,5,5	0.66	0
4	GOL	H	362	-	5,5,5	0.68	0	5,5,5	1.09	0
2	NAP	I	350	-	42,52,52	1.66	3 (7%)	54,80,80	1.82	9 (16%)
3	TLA	I	360	-	3,9,9	1.97	1 (33%)	6,12,12	1.57	1 (16%)
4	GOL	I	361	-	5,5,5	0.48	0	5,5,5	0.86	0
4	GOL	I	362	-	5,5,5	0.67	0	5,5,5	1.40	1 (20%)
6	MES	I	363	-	11,12,12	1.33	3 (27%)	14,16,16	2.56	5 (35%)
2	NAP	J	350	-	42,52,52	1.52	5 (11%)	54,80,80	2.28	12 (22%)
3	TLA	J	360	-	3,9,9	0.70	0	6,12,12	1.00	0
4	GOL	J	363	-	5,5,5	0.39	0	5,5,5	1.02	0
4	GOL	J	364	-	5,5,5	0.52	0	5,5,5	0.72	0
4	GOL	J	366	-	5,5,5	0.85	0	5,5,5	0.97	0
5	PO4	J	367	-	4,4,4	0.31	0	6,6,6	0.27	0
6	MES	J	368	-	11,12,12	1.08	1 (9%)	14,16,16	2.44	4 (28%)

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	NAP	A	350	-	-	0/27/67/67	0/5/5/5
3	TLA	A	360	-	-	0/4/12/12	0/0/0/0
4	GOL	A	361	-	-	0/4/4/4	0/0/0/0
4	GOL	A	363	-	-	0/4/4/4	0/0/0/0
5	PO4	A	364	-	-	0/0/0/0	0/0/0/0
2	NAP	B	350	-	-	0/27/67/67	0/5/5/5
3	TLA	B	360	-	-	0/4/12/12	0/0/0/0
4	GOL	B	361	-	-	0/4/4/4	0/0/0/0
4	GOL	B	362	-	-	0/4/4/4	0/0/0/0
4	GOL	B	363	-	-	0/4/4/4	0/0/0/0
6	MES	B	364	-	-	0/6/14/14	0/1/1/1
2	NAP	C	350	-	-	0/27/67/67	0/5/5/5
3	TLA	C	360	-	-	0/4/12/12	0/0/0/0
4	GOL	C	361	-	-	0/4/4/4	0/0/0/0
4	GOL	C	362	-	-	0/4/4/4	0/0/0/0
4	GOL	C	363	-	-	0/4/4/4	0/0/0/0
6	MES	C	364	-	-	0/6/14/14	0/1/1/1
2	NAP	D	350	-	-	0/27/67/67	0/5/5/5
3	TLA	D	360	-	-	0/4/12/12	0/0/0/0
4	GOL	D	361	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	D	362	-	-	0/4/4/4	0/0/0/0
4	GOL	D	363	-	-	0/4/4/4	0/0/0/0
6	MES	D	364	-	-	0/6/14/14	0/1/1/1
2	NAP	E	350	-	-	0/27/67/67	0/5/5/5
3	TLA	E	360	-	-	0/4/12/12	0/0/0/0
4	GOL	E	361	-	-	0/4/4/4	0/0/0/0
4	GOL	E	362	-	-	0/4/4/4	0/0/0/0
4	GOL	E	363	-	-	0/4/4/4	0/0/0/0
2	NAP	F	350	-	-	0/27/67/67	0/5/5/5
3	TLA	F	360	-	-	0/4/12/12	0/0/0/0
4	GOL	F	361	-	-	0/4/4/4	0/0/0/0
2	NAP	G	350	-	-	0/27/67/67	0/5/5/5
3	TLA	G	360	-	-	0/4/12/12	0/0/0/0
4	GOL	G	362	-	-	0/4/4/4	0/0/0/0
4	GOL	G	363	-	-	0/4/4/4	0/0/0/0
4	GOL	G	364	-	-	0/4/4/4	0/0/0/0
2	NAP	H	350	-	-	0/27/67/67	0/5/5/5
3	TLA	H	360	-	-	0/4/12/12	0/0/0/0
4	GOL	H	361	-	-	0/4/4/4	0/0/0/0
4	GOL	H	362	-	-	0/4/4/4	0/0/0/0
2	NAP	I	350	-	-	0/27/67/67	0/5/5/5
3	TLA	I	360	-	-	0/4/12/12	0/0/0/0
4	GOL	I	361	-	-	0/4/4/4	0/0/0/0
4	GOL	I	362	-	-	0/4/4/4	0/0/0/0
6	MES	I	363	-	-	0/6/14/14	0/1/1/1
2	NAP	J	350	-	-	0/27/67/67	0/5/5/5
3	TLA	J	360	-	-	0/4/12/12	0/0/0/0
4	GOL	J	363	-	-	0/4/4/4	0/0/0/0
4	GOL	J	364	-	-	0/4/4/4	0/0/0/0
4	GOL	J	366	-	-	0/4/4/4	0/0/0/0
5	PO4	J	367	-	-	0/0/0/0	0/0/0/0
6	MES	J	368	-	-	0/6/14/14	0/1/1/1

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	350	NAP	C3N-C7N	-2.83	1.46	1.50
2	G	350	NAP	O4B-C4B	-2.69	1.38	1.45
2	G	350	NAP	O3B-C3B	-2.59	1.36	1.43
2	A	350	NAP	PN-O2N	-2.36	1.44	1.54
2	H	350	NAP	O2B-C2B	-2.27	1.37	1.44

The worst 5 of 141 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	350	NAP	N3A-C2A-N1A	-14.64	117.69	128.89
2	E	350	NAP	N3A-C2A-N1A	-14.54	117.76	128.89
2	J	350	NAP	N3A-C2A-N1A	-12.57	119.27	128.89
2	F	350	NAP	N3A-C2A-N1A	-11.90	119.78	128.89
2	D	350	NAP	N3A-C2A-N1A	-11.24	120.29	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

20 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	350	NAP	2	0
4	A	361	GOL	2	0
2	B	350	NAP	3	0
3	B	360	TLA	2	0
3	C	360	TLA	3	0
2	D	350	NAP	1	0
2	E	350	NAP	1	0
3	E	360	TLA	1	0
2	F	350	NAP	3	0
3	F	360	TLA	1	0
2	G	350	NAP	1	0
4	G	364	GOL	5	0
2	H	350	NAP	4	0
3	H	360	TLA	2	0
4	H	361	GOL	2	0
2	I	350	NAP	3	0
3	I	360	TLA	1	0
4	I	362	GOL	1	0
2	J	350	NAP	2	0
3	J	360	TLA	1	0

## 5.7 Other polymers

There are no such residues in this entry.



## 5.8 Polymer linkage issues ⓘ

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	325/338 (96%)	-0.38	1 (0%) 94 96	30, 36, 47, 72	0
1	B	324/338 (95%)	-0.26	3 (0%) 85 89	29, 36, 47, 71	0
1	C	324/338 (95%)	-0.41	1 (0%) 94 96	30, 36, 47, 72	0
1	D	324/338 (95%)	-0.33	0 100 100	30, 36, 47, 73	0
1	E	324/338 (95%)	-0.38	0 100 100	30, 36, 47, 72	0
1	F	324/338 (95%)	-0.38	3 (0%) 85 89	30, 36, 47, 72	0
1	G	324/338 (95%)	-0.34	1 (0%) 94 96	30, 36, 47, 72	0
1	H	324/338 (95%)	-0.25	2 (0%) 90 93	30, 36, 46, 71	0
1	I	324/338 (95%)	-0.35	2 (0%) 90 93	29, 36, 47, 72	0
1	J	325/338 (96%)	-0.34	2 (0%) 90 93	30, 36, 47, 72	0
All	All	3242/3380 (95%)	-0.34	15 (0%) 91 94	29, 36, 47, 73	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	64	GLY	4.6
1	H	64	GLY	3.9
1	F	65	ASP	3.7
1	A	64	GLY	3.6
1	I	65	ASP	3.1

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	GOL	D	363	6/6	0.77	0.21	10.37	48,53,55,55	0
4	GOL	H	362	6/6	0.98	0.17	9.65	30,34,36,36	0
6	MES	I	363	12/12	0.96	0.22	8.02	55,60,61,61	0
4	GOL	G	364	6/6	0.88	0.29	6.93	58,62,62,64	0
4	GOL	J	363	6/6	0.95	0.15	5.63	39,42,42,46	0
4	GOL	I	361	6/6	0.97	0.18	4.96	44,47,48,48	0
4	GOL	B	361	6/6	0.97	0.14	4.90	33,40,42,42	0
4	GOL	G	363	6/6	0.98	0.15	3.79	34,36,36,38	0
4	GOL	B	362	6/6	0.91	0.26	3.61	57,61,62,63	0
4	GOL	F	361	6/6	0.97	0.15	3.27	36,39,41,42	0
6	MES	B	364	12/12	0.98	0.15	2.97	50,61,65,65	0
6	MES	C	364	12/12	0.98	0.14	2.77	57,62,64,64	0
3	TLA	H	360	10/10	0.99	0.13	2.64	30,36,41,43	0
5	PO4	J	367	5/5	0.98	0.14	2.62	60,60,65,67	0
4	GOL	J	364	6/6	0.98	0.14	2.29	45,48,49,50	0
6	MES	J	368	12/12	0.97	0.16	1.61	53,57,59,60	0
4	GOL	E	363	6/6	0.98	0.14	1.59	28,31,31,32	0
3	TLA	C	360	10/10	0.97	0.11	1.37	29,33,38,41	0
4	GOL	H	361	6/6	0.96	0.13	1.11	37,44,45,46	0
4	GOL	E	361	6/6	0.98	0.13	1.05	33,36,36,37	0
4	GOL	E	362	6/6	0.98	0.12	0.74	31,33,36,36	0
4	GOL	A	363	6/6	0.96	0.12	0.58	39,42,42,43	0
4	GOL	C	363	6/6	0.88	0.14	0.44	49,60,61,62	0
4	GOL	J	366	6/6	0.89	0.12	0.38	51,53,53,54	0
4	GOL	I	362	6/6	0.98	0.12	0.28	33,34,36,39	0
3	TLA	F	360	10/10	0.97	0.10	0.14	31,36,39,39	0
5	PO4	A	364	5/5	0.95	0.10	-0.18	59,59,63,65	0
4	GOL	C	361	6/6	0.97	0.10	-0.19	38,45,47,50	0
4	GOL	C	362	6/6	0.98	0.11	-0.36	33,36,39,39	0
4	GOL	A	361	6/6	0.95	0.10	-0.42	37,40,45,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	TLA	D	360	10/10	0.98	0.10	-0.62	25,31,34,36	0
4	GOL	B	363	6/6	0.98	0.10	-0.85	30,33,34,35	0
2	NAP	B	350	48/48	0.98	0.09	-1.03	27,32,38,43	0
3	TLA	A	360	10/10	0.97	0.09	-1.12	28,33,35,35	0
2	NAP	F	350	48/48	0.99	0.08	-1.21	23,29,34,36	0
3	TLA	I	360	10/10	0.97	0.09	-1.39	27,35,37,40	0
6	MES	D	364	12/12	0.97	0.09	-1.39	48,62,66,67	0
2	NAP	E	350	48/48	0.99	0.08	-1.54	20,27,31,36	0
4	GOL	D	362	6/6	0.97	0.08	-1.55	33,34,35,36	0
2	NAP	D	350	48/48	0.99	0.09	-1.60	20,25,32,37	0
2	NAP	H	350	48/48	0.98	0.08	-1.66	24,33,37,43	0
4	GOL	D	361	6/6	0.96	0.09	-1.75	29,29,33,33	0
3	TLA	B	360	10/10	0.96	0.09	-1.92	34,37,41,42	0
2	NAP	J	350	48/48	0.99	0.07	-1.93	23,30,35,40	0
4	GOL	G	362	6/6	0.97	0.09	-1.99	31,36,37,39	0
2	NAP	I	350	48/48	0.99	0.07	-2.03	22,31,35,36	0
2	NAP	C	350	48/48	0.99	0.07	-2.07	23,29,35,37	0
2	NAP	A	350	48/48	0.99	0.08	-2.15	21,26,31,35	0
3	TLA	G	360	10/10	0.97	0.09	-2.16	31,33,35,35	0
2	NAP	G	350	48/48	0.99	0.08	-2.29	19,27,31,35	0
3	TLA	J	360	10/10	0.98	0.08	-3.12	29,33,34,37	0
3	TLA	E	360	10/10	0.99	0.09	-3.61	26,31,35,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.