



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:43 PM GMT

PDB ID : 4MIG  
Title : Pyranose 2-oxidase from Phanerochaete chrysosporium, recombinant wild type  
Authors : Hassan, N.; Tan, T.C.; Spadiut, O.; Pisanelli, I.; Fusco, L.; Haltrich, D.; Peterbauer, C.; Divne, C.  
Deposited on : 2013-08-31  
Resolution : 1.80 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

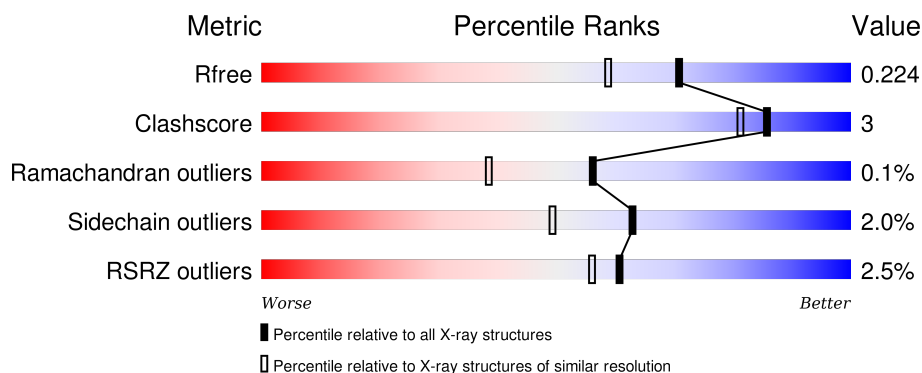
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 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))
$R_{free}$	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (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 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	648	 2% 79% 8% 12%
1	B	648	 2% 80% 9% 11%
1	C	648	 2% 81% 8% 11%
1	D	648	 2% 80% 7% 12%

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 20096 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 Pyranose 2-oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	570	Total	C	N	O	S	0	5	0
			4524	2879	781	838	26			
1	B	574	Total	C	N	O	S	0	3	0
			4543	2889	783	845	26			
1	C	579	Total	C	N	O	S	0	6	0
			4598	2923	796	853	26			
1	D	570	Total	C	N	O	S	0	4	0
			4519	2876	780	837	26			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	INITIATING METHIONINE	UNP Q6QWR1
A	-12	ALA	-	EXPRESSION TAG	UNP Q6QWR1
A	-11	SER	-	EXPRESSION TAG	UNP Q6QWR1
A	-10	MET	-	EXPRESSION TAG	UNP Q6QWR1
A	-9	THR	-	EXPRESSION TAG	UNP Q6QWR1
A	-8	GLY	-	EXPRESSION TAG	UNP Q6QWR1
A	-7	GLY	-	EXPRESSION TAG	UNP Q6QWR1
A	-6	GLN	-	EXPRESSION TAG	UNP Q6QWR1
A	-5	GLN	-	EXPRESSION TAG	UNP Q6QWR1
A	-4	MET	-	EXPRESSION TAG	UNP Q6QWR1
A	-3	GLY	-	EXPRESSION TAG	UNP Q6QWR1
A	-2	ARG	-	EXPRESSION TAG	UNP Q6QWR1
A	-1	GLY	-	EXPRESSION TAG	UNP Q6QWR1
A	0	SER	-	EXPRESSION TAG	UNP Q6QWR1
A	622	LYS	-	EXPRESSION TAG	UNP Q6QWR1
A	623	LEU	-	EXPRESSION TAG	UNP Q6QWR1
A	624	ALA	-	EXPRESSION TAG	UNP Q6QWR1
A	625	ALA	-	EXPRESSION TAG	UNP Q6QWR1
A	626	ALA	-	EXPRESSION TAG	UNP Q6QWR1
A	627	LEU	-	EXPRESSION TAG	UNP Q6QWR1
A	628	GLU	-	EXPRESSION TAG	UNP Q6QWR1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	629	HIS	-	EXPRESSION TAG	UNP Q6QWR1
A	630	HIS	-	EXPRESSION TAG	UNP Q6QWR1
A	631	HIS	-	EXPRESSION TAG	UNP Q6QWR1
A	632	HIS	-	EXPRESSION TAG	UNP Q6QWR1
A	633	HIS	-	EXPRESSION TAG	UNP Q6QWR1
A	634	HIS	-	EXPRESSION TAG	UNP Q6QWR1
B	-13	MET	-	INITIATING METHIONINE	UNP Q6QWR1
B	-12	ALA	-	EXPRESSION TAG	UNP Q6QWR1
B	-11	SER	-	EXPRESSION TAG	UNP Q6QWR1
B	-10	MET	-	EXPRESSION TAG	UNP Q6QWR1
B	-9	THR	-	EXPRESSION TAG	UNP Q6QWR1
B	-8	GLY	-	EXPRESSION TAG	UNP Q6QWR1
B	-7	GLY	-	EXPRESSION TAG	UNP Q6QWR1
B	-6	GLN	-	EXPRESSION TAG	UNP Q6QWR1
B	-5	GLN	-	EXPRESSION TAG	UNP Q6QWR1
B	-4	MET	-	EXPRESSION TAG	UNP Q6QWR1
B	-3	GLY	-	EXPRESSION TAG	UNP Q6QWR1
B	-2	ARG	-	EXPRESSION TAG	UNP Q6QWR1
B	-1	GLY	-	EXPRESSION TAG	UNP Q6QWR1
B	0	SER	-	EXPRESSION TAG	UNP Q6QWR1
B	622	LYS	-	EXPRESSION TAG	UNP Q6QWR1
B	623	LEU	-	EXPRESSION TAG	UNP Q6QWR1
B	624	ALA	-	EXPRESSION TAG	UNP Q6QWR1
B	625	ALA	-	EXPRESSION TAG	UNP Q6QWR1
B	626	ALA	-	EXPRESSION TAG	UNP Q6QWR1
B	627	LEU	-	EXPRESSION TAG	UNP Q6QWR1
B	628	GLU	-	EXPRESSION TAG	UNP Q6QWR1
B	629	HIS	-	EXPRESSION TAG	UNP Q6QWR1
B	630	HIS	-	EXPRESSION TAG	UNP Q6QWR1
B	631	HIS	-	EXPRESSION TAG	UNP Q6QWR1
B	632	HIS	-	EXPRESSION TAG	UNP Q6QWR1
B	633	HIS	-	EXPRESSION TAG	UNP Q6QWR1
B	634	HIS	-	EXPRESSION TAG	UNP Q6QWR1
C	-13	MET	-	INITIATING METHIONINE	UNP Q6QWR1
C	-12	ALA	-	EXPRESSION TAG	UNP Q6QWR1
C	-11	SER	-	EXPRESSION TAG	UNP Q6QWR1
C	-10	MET	-	EXPRESSION TAG	UNP Q6QWR1
C	-9	THR	-	EXPRESSION TAG	UNP Q6QWR1
C	-8	GLY	-	EXPRESSION TAG	UNP Q6QWR1
C	-7	GLY	-	EXPRESSION TAG	UNP Q6QWR1
C	-6	GLN	-	EXPRESSION TAG	UNP Q6QWR1
C	-5	GLN	-	EXPRESSION TAG	UNP Q6QWR1

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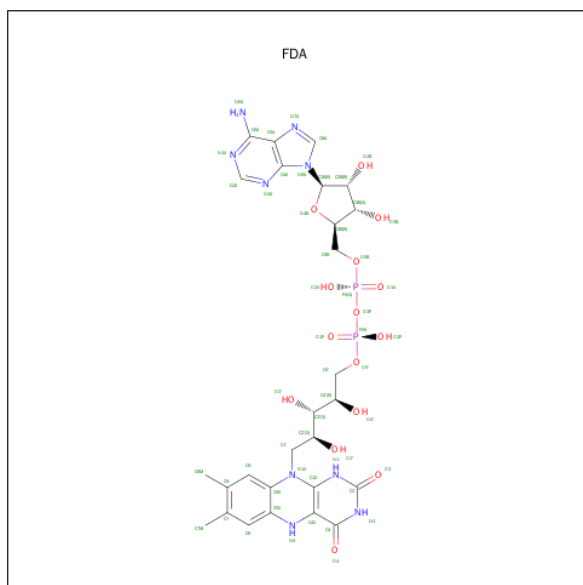
Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	MET	-	EXPRESSION TAG	UNP Q6QWR1
C	-3	GLY	-	EXPRESSION TAG	UNP Q6QWR1
C	-2	ARG	-	EXPRESSION TAG	UNP Q6QWR1
C	-1	GLY	-	EXPRESSION TAG	UNP Q6QWR1
C	0	SER	-	EXPRESSION TAG	UNP Q6QWR1
C	622	LYS	-	EXPRESSION TAG	UNP Q6QWR1
C	623	LEU	-	EXPRESSION TAG	UNP Q6QWR1
C	624	ALA	-	EXPRESSION TAG	UNP Q6QWR1
C	625	ALA	-	EXPRESSION TAG	UNP Q6QWR1
C	626	ALA	-	EXPRESSION TAG	UNP Q6QWR1
C	627	LEU	-	EXPRESSION TAG	UNP Q6QWR1
C	628	GLU	-	EXPRESSION TAG	UNP Q6QWR1
C	629	HIS	-	EXPRESSION TAG	UNP Q6QWR1
C	630	HIS	-	EXPRESSION TAG	UNP Q6QWR1
C	631	HIS	-	EXPRESSION TAG	UNP Q6QWR1
C	632	HIS	-	EXPRESSION TAG	UNP Q6QWR1
C	633	HIS	-	EXPRESSION TAG	UNP Q6QWR1
C	634	HIS	-	EXPRESSION TAG	UNP Q6QWR1
D	-13	MET	-	INITIATING METHIONINE	UNP Q6QWR1
D	-12	ALA	-	EXPRESSION TAG	UNP Q6QWR1
D	-11	SER	-	EXPRESSION TAG	UNP Q6QWR1
D	-10	MET	-	EXPRESSION TAG	UNP Q6QWR1
D	-9	THR	-	EXPRESSION TAG	UNP Q6QWR1
D	-8	GLY	-	EXPRESSION TAG	UNP Q6QWR1
D	-7	GLY	-	EXPRESSION TAG	UNP Q6QWR1
D	-6	GLN	-	EXPRESSION TAG	UNP Q6QWR1
D	-5	GLN	-	EXPRESSION TAG	UNP Q6QWR1
D	-4	MET	-	EXPRESSION TAG	UNP Q6QWR1
D	-3	GLY	-	EXPRESSION TAG	UNP Q6QWR1
D	-2	ARG	-	EXPRESSION TAG	UNP Q6QWR1
D	-1	GLY	-	EXPRESSION TAG	UNP Q6QWR1
D	0	SER	-	EXPRESSION TAG	UNP Q6QWR1
D	622	LYS	-	EXPRESSION TAG	UNP Q6QWR1
D	623	LEU	-	EXPRESSION TAG	UNP Q6QWR1
D	624	ALA	-	EXPRESSION TAG	UNP Q6QWR1
D	625	ALA	-	EXPRESSION TAG	UNP Q6QWR1
D	626	ALA	-	EXPRESSION TAG	UNP Q6QWR1
D	627	LEU	-	EXPRESSION TAG	UNP Q6QWR1
D	628	GLU	-	EXPRESSION TAG	UNP Q6QWR1
D	629	HIS	-	EXPRESSION TAG	UNP Q6QWR1
D	630	HIS	-	EXPRESSION TAG	UNP Q6QWR1
D	631	HIS	-	EXPRESSION TAG	UNP Q6QWR1

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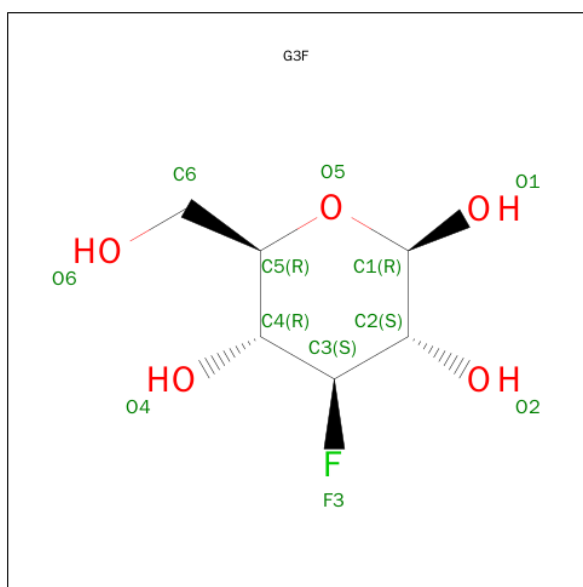
Chain	Residue	Modelled	Actual	Comment	Reference
D	632	HIS	-	EXPRESSION TAG	UNP Q6QWR1
D	633	HIS	-	EXPRESSION TAG	UNP Q6QWR1
D	634	HIS	-	EXPRESSION TAG	UNP Q6QWR1

- Molecule 2 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (three-letter code: FDA) (formula:  $C_{27}H_{35}N_9O_{15}P_2$ ).



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

- Molecule 3 is 3-DEOXY-3-FLUORO-BETA-D-GLUCOPYRANOSE (three-letter code: G3F) (formula:  $C_6H_{11}FO_5$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	F	O	0	0
			12	6	1	5		
3	B	1	Total	C	F	O	0	0
			12	6	1	5		
3	C	1	Total	C	F	O	0	0
			12	6	1	5		
3	D	1	Total	C	F	O	0	0
			12	6	1	5		

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mn	0	0
			1	1		
4	A	3	Total	Mn	0	0
			3	3		
4	D	3	Total	Mn	0	0
			3	3		
4	C	1	Total	Mn	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	467	Total	O	0	0
			467	467		

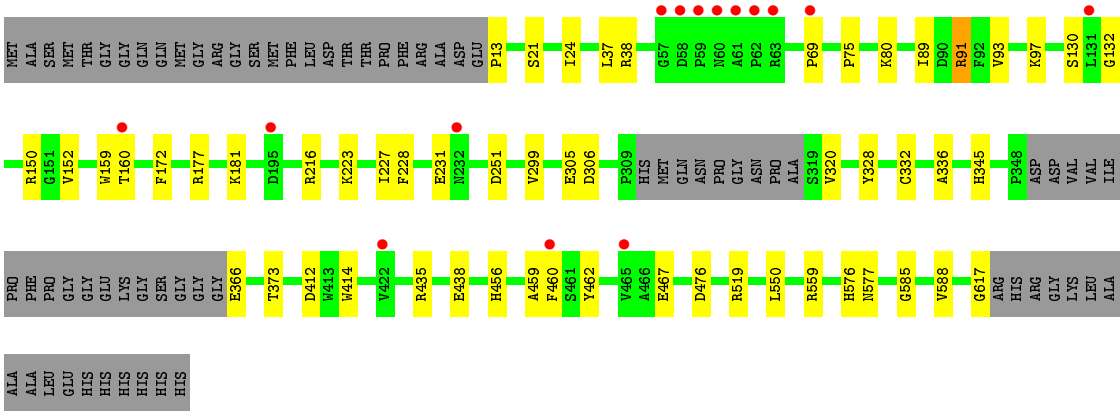
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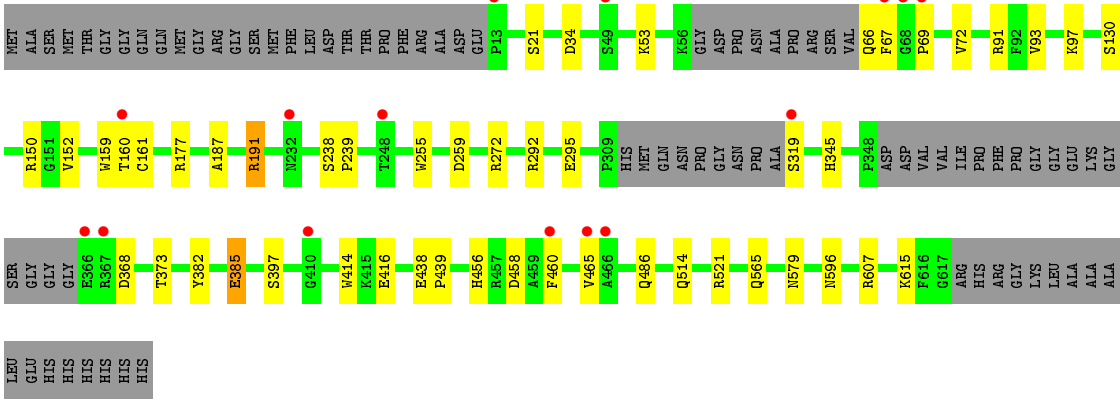
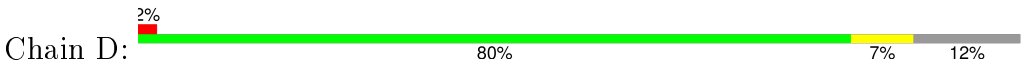
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	380	Total 380	O 380	0	0
5	C	340	Total 340	O 340	0	0
5	D	457	Total 457	O 457	0	0







● Molecule 1: Pyranose 2-oxidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.54Å 166.45Å 91.84Å 90.00° 106.41° 90.00°	Depositor
Resolution (Å)	44.05 – 1.80 44.05 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (44.05-1.80) 99.0 (44.05-1.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.30 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.173 , 0.214 0.183 , 0.224	Depositor DCC
$R_{free}$ test set	1514 reflections (0.65%)	DCC
Wilson B-factor (Å <sup>2</sup> )	16.1	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 47.1	EDS
Estimated twinning fraction	0.107 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 235359 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20096	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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: FDA, MN, G3F

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	1.08	4/4661 (0.1%)	1.02	18/6342 (0.3%)
1	B	1.00	1/4674 (0.0%)	0.98	10/6360 (0.2%)
1	C	0.99	2/4741 (0.0%)	0.96	10/6453 (0.2%)
1	D	1.09	3/4653 (0.1%)	1.01	10/6331 (0.2%)
All	All	1.04	10/18729 (0.1%)	0.99	48/25486 (0.2%)

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	2
1	C	0	1
All	All	0	3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	385	GLU	CD-OE2	-9.93	1.14	1.25
1	A	255	TRP	NE1-CE2	-5.80	1.30	1.37
1	C	412	ASP	CB-CG	5.52	1.63	1.51
1	A	385	GLU	CD-OE2	5.51	1.31	1.25
1	D	255	TRP	CD2-CE2	5.34	1.47	1.41

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	191	ARG	NE-CZ-NH2	-8.41	116.09	120.30
1	D	191	ARG	NE-CZ-NH1	8.05	124.32	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	191	ARG	NE-CZ-NH1	8.01	124.31	120.30
1	C	91	ARG	NE-CZ-NH1	7.91	124.26	120.30
1	A	368	ASP	CB-CG-OD1	7.80	125.32	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	326	ARG	Sidechain
1	A	69	PRO	Peptide
1	C	132	GLY	Peptide

## 5.2 Too-close contacts

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	4524	0	4424	27	0
1	B	4543	0	4430	26	0
1	C	4598	0	4496	24	0
1	D	4519	0	4418	19	0
2	A	53	0	32	2	0
2	B	53	0	29	1	0
2	C	53	0	30	3	0
2	D	53	0	31	3	0
3	A	12	0	11	1	0
3	B	12	0	11	3	0
3	C	12	0	11	1	0
3	D	12	0	11	3	0
4	A	3	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	3	0	0	0	0
5	A	467	0	0	8	0
5	B	380	0	0	7	0
5	C	340	0	0	5	0
5	D	457	0	0	7	0
All	All	20096	0	17934	100	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 100 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:160[B]:THR:HG22	5:A:1007:HOH:O	1.57	1.03
1:B:160[B]:THR:HG22	5:B:1257:HOH:O	1.59	1.01
1:D:160[B]:THR:HG22	5:D:1044:HOH:O	1.74	0.87
1:A:15:ASP:HA	1:A:326:ARG:HG3	1.64	0.76
1:A:419:ALA:O	1:A:423:GLU:HG2	1.84	0.76

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	567/648 (88%)	553 (98%)	14 (2%)	0	100	100
1	B	569/648 (88%)	556 (98%)	12 (2%)	1 (0%)	52	35
1	C	579/648 (89%)	565 (98%)	14 (2%)	0	100	100
1	D	566/648 (87%)	553 (98%)	11 (2%)	2 (0%)	39	23
All	All	2281/2592 (88%)	2227 (98%)	51 (2%)	3 (0%)	56	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	465	VAL
1	D	69	PRO
1	D	67	PHE

### 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	495/548 (90%)	485 (98%)	10 (2%)	63	49
1	B	495/548 (90%)	483 (98%)	12 (2%)	57	41
1	C	503/548 (92%)	495 (98%)	8 (2%)	70	59
1	D	494/548 (90%)	483 (98%)	11 (2%)	60	45
All	All	1987/2192 (91%)	1946 (98%)	41 (2%)	63	47

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	414	TRP
1	C	24	ILE
1	D	456	HIS
1	B	456	HIS
1	B	460	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	HIS
1	B	66	GLN
1	B	405	ASN
1	D	427	ASN

### 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](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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$
2	FDA	A	801	1	48,58,58	1.65	11 (22%)	54,89,89	3.11	18 (33%)
3	G3F	A	802	-	12,12,12	1.43	2 (16%)	15,17,17	3.19	3 (20%)
2	FDA	B	801	1	48,58,58	1.78	11 (22%)	54,89,89	3.93	16 (29%)
3	G3F	B	802	-	12,12,12	1.38	2 (16%)	15,17,17	2.41	4 (26%)
2	FDA	C	801	1	48,58,58	1.64	12 (25%)	54,89,89	3.44	18 (33%)
3	G3F	C	802	-	12,12,12	1.45	1 (8%)	15,17,17	3.44	6 (40%)
2	FDA	D	801	1	48,58,58	1.48	9 (18%)	54,89,89	3.55	16 (29%)
3	G3F	D	802	-	12,12,12	1.15	1 (8%)	15,17,17	2.39	6 (40%)

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	FDA	A	801	1	-	0/30/50/50	0/6/6/6
3	G3F	A	802	-	-	0/2/22/22	0/1/1/1
2	FDA	B	801	1	-	0/30/50/50	0/6/6/6
3	G3F	B	802	-	-	0/2/22/22	0/1/1/1
2	FDA	C	801	1	-	0/30/50/50	0/6/6/6
3	G3F	C	802	-	-	0/2/22/22	0/1/1/1
2	FDA	D	801	1	-	0/30/50/50	0/6/6/6
3	G3F	D	802	-	-	0/2/22/22	0/1/1/1

The worst 5 of 49 bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	FDA	C2B-C3B	-3.78	1.43	1.53
2	B	801	FDA	O2B-C2B	-3.54	1.34	1.43
2	D	801	FDA	C10-N10	-3.05	1.35	1.39
2	A	801	FDA	C10-N10	-3.04	1.35	1.39
2	A	801	FDA	O4B-C4B	-2.76	1.38	1.45

The worst 5 of 87 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	FDA	N3A-C2A-N1A	-16.26	116.44	128.89
2	B	801	FDA	N3A-C2A-N1A	-14.98	117.43	128.89
2	C	801	FDA	N3A-C2A-N1A	-13.52	118.54	128.89
2	A	801	FDA	N3A-C2A-N1A	-12.37	119.42	128.89
2	C	801	FDA	C4-C4X-C10	-12.32	112.05	119.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	FDA	2	0
3	A	802	G3F	1	0
2	B	801	FDA	1	0
3	B	802	G3F	3	0
2	C	801	FDA	3	0
3	C	802	G3F	1	0
2	D	801	FDA	3	0
3	D	802	G3F	3	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 [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	570/648 (87%)	-0.36	12 (2%) 67 62	9, 16, 39, 69	4 (0%)
1	B	574/648 (88%)	-0.23	15 (2%) 59 54	10, 20, 42, 72	3 (0%)
1	C	579/648 (89%)	-0.17	15 (2%) 59 54	11, 20, 45, 71	6 (1%)
1	D	570/648 (87%)	-0.37	15 (2%) 59 54	9, 16, 37, 78	3 (0%)
All	All	2293/2592 (88%)	-0.28	57 (2%) 61 56	9, 18, 41, 78	16 (0%)

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	57	GLY	6.4
1	C	59	PRO	5.7
1	C	62	PRO	5.7
1	C	63	ARG	5.6
1	D	69	PRO	5.6

### 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. 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	MN	B	803	1/1	0.98	0.10	1.97	38,38,38,38	0
3	G3F	A	802	12/12	0.83	0.16	0.37	27,30,33,34	0
4	MN	A	804	1/1	0.99	0.06	0.14	30,30,30,30	0
3	G3F	D	802	12/12	0.89	0.13	-0.11	23,31,33,35	0
3	G3F	B	802	12/12	0.81	0.13	-0.13	29,32,34,38	0
2	FDA	A	801	53/53	0.98	0.08	-0.47	8,11,15,16	0
2	FDA	B	801	53/53	0.98	0.08	-0.49	10,15,17,18	0
2	FDA	C	801	53/53	0.98	0.08	-0.49	10,14,17,18	0
2	FDA	D	801	53/53	0.98	0.08	-0.62	9,11,15,15	0
3	G3F	C	802	12/12	0.87	0.10	-0.65	26,30,32,36	0
4	MN	C	803	1/1	0.99	0.07	-0.67	35,35,35,35	0
4	MN	D	805	1/1	0.99	0.05	-1.88	33,33,33,33	0
4	MN	A	805	1/1	0.99	0.05	-2.18	34,34,34,34	0
4	MN	D	804	1/1	0.99	0.03	-2.39	32,32,32,32	0
4	MN	A	803	1/1	0.99	0.08	-	33,33,33,33	0
4	MN	D	803	1/1	0.99	0.05	-	13,13,13,13	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.