



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:45 PM GMT

PDB ID : 4MOO  
Title : Pyranose 2-oxidase H450G mutant with 2-fluorinated galactose  
Authors : Tan, T.C.; Spadiut, O.; Gandini, R.; Haltrich, D.; Divne, C.  
Deposited on : 2013-09-12  
Resolution : 1.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<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

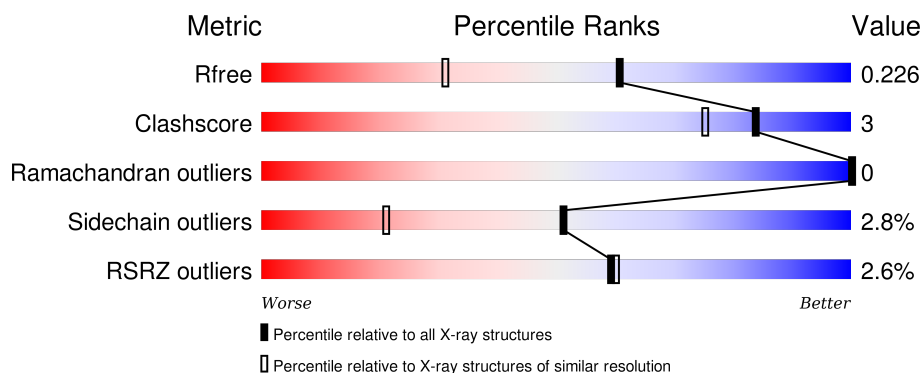
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 1.65 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	1226 (1.66-1.66)
Clashscore	102246	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)
RSRZ outliers	91569	1227 (1.66-1.66)

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	633	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5115 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.

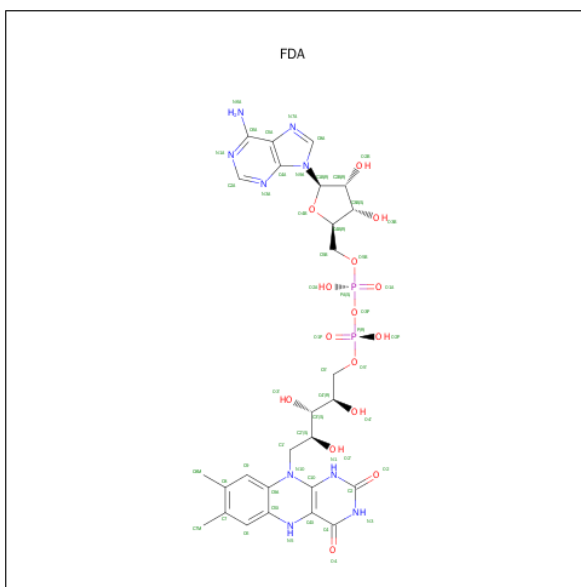
- Molecule 1 is a protein called Pyranose 2-oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	576	Total	C	N	O	S	0	0	0
			4536	2864	775	872	25			

There are 13 discrepancies between the modelled and reference sequences:

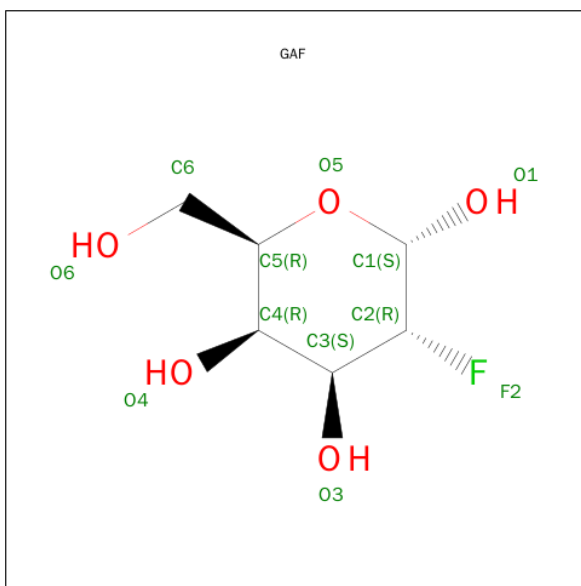
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	SER	SEE REMARK 999	UNP Q7ZA32
A	450	GLY	HIS	ENGINEERED MUTATION	UNP Q7ZA32
A	623	ALA	-	EXPRESSION TAG	UNP Q7ZA32
A	624	ALA	-	EXPRESSION TAG	UNP Q7ZA32
A	625	ALA	-	EXPRESSION TAG	UNP Q7ZA32
A	626	LEU	-	EXPRESSION TAG	UNP Q7ZA32
A	627	GLU	-	EXPRESSION TAG	UNP Q7ZA32
A	628	HIS	-	EXPRESSION TAG	UNP Q7ZA32
A	629	HIS	-	EXPRESSION TAG	UNP Q7ZA32
A	630	HIS	-	EXPRESSION TAG	UNP Q7ZA32
A	631	HIS	-	EXPRESSION TAG	UNP Q7ZA32
A	632	HIS	-	EXPRESSION TAG	UNP Q7ZA32
A	633	HIS	-	EXPRESSION TAG	UNP Q7ZA32

- Molecule 2 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (three-letter code: FDA) (formula: C<sub>27</sub>H<sub>35</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



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

- Molecule 3 is 2-DEOXY-2-FLUORO-ALPHA-D-GALACTOPYRANOSE (three-letter code: GAF) (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		

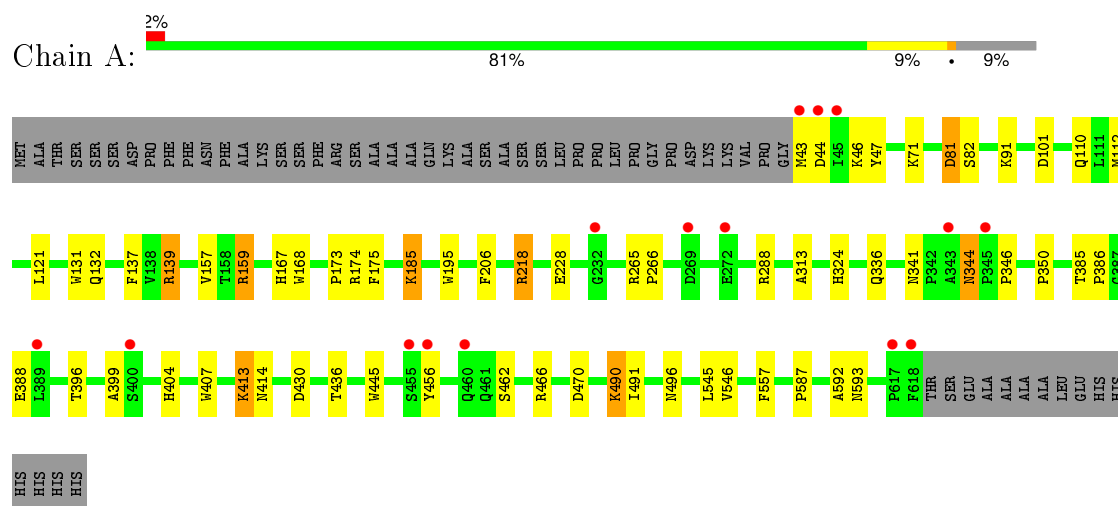
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	514	Total 514	O 514	0	0

### 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 ( $RSRZ > 2$ ). 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: Pyranose 2-oxidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 4 <sub>2</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.67Å 101.67Å 127.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.65 47.71 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-1.65) 99.8 (47.71-1.65)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.37 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.191 , 0.224 0.196 , 0.226	Depositor DCC
$R_{free}$ test set	1907 reflections (2.42%)	DCC
Wilson B-factor (Å <sup>2</sup> )	14.9	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 44.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 80572 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5115	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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, GAF

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	1.09	6/4651 (0.1%)	1.11	16/6323 (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

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	407	TRP	CD2-CE2	5.85	1.48	1.41
1	A	445	TRP	CG-CD2	5.57	1.53	1.43
1	A	81	ASP	CB-CG	-5.57	1.40	1.51
1	A	462	SER	CB-OG	-5.35	1.35	1.42
1	A	131	TRP	CD2-CE2	5.19	1.47	1.41
1	A	195	TRP	CD2-CE2	5.06	1.47	1.41

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	139	ARG	NE-CZ-NH2	-17.71	111.44	120.30
1	A	139	ARG	NE-CZ-NH1	16.09	128.34	120.30
1	A	81	ASP	CB-CG-OD1	-11.58	107.88	118.30
1	A	470	ASP	CB-CG-OD2	-9.78	109.50	118.30
1	A	159	ARG	NE-CZ-NH1	8.94	124.77	120.30
1	A	81	ASP	CB-CG-OD2	7.12	124.71	118.30
1	A	466	ARG	NE-CZ-NH2	-6.81	116.89	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	139	ARG	CD-NE-CZ	6.37	132.52	123.60
1	A	101	ASP	CB-CG-OD1	6.05	123.75	118.30
1	A	174	ARG	NE-CZ-NH2	-5.77	117.41	120.30
1	A	218	ARG	NE-CZ-NH1	5.73	123.17	120.30
1	A	121	LEU	CB-CG-CD1	-5.70	101.32	111.00
1	A	288	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	A	175	PHE	CB-CG-CD1	5.19	124.43	120.80
1	A	174	ARG	NE-CZ-NH1	5.06	122.83	120.30
1	A	91	LYS	CA-CB-CG	5.05	124.51	113.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	436	THR	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	4536	0	4384	26	0
2	A	53	0	31	2	0
3	A	12	0	11	3	0
4	A	514	0	0	6	0
All	All	5115	0	4426	27	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.

All (27) 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:228:GLU:HG3	4:A:1359:HOH:O	1.76	0.86
1:A:185:LYS:HE3	1:A:557:PHE:CD2	2.20	0.77
1:A:110:GLN:HE21	1:A:167:HIS:HD1	1.33	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:HIS:HE1	4:A:1284:HOH:O	1.72	0.70
1:A:81:ASP:C	1:A:81:ASP:OD1	2.36	0.63
1:A:396:THR:HB	1:A:399:ALA:HB2	1.87	0.55
1:A:456:TYR:OH	3:A:802:GAF:O6	2.23	0.54
1:A:157:VAL:HG21	1:A:324:HIS:HE1	1.73	0.53
2:A:801:FDA:N5	3:A:802:GAF:H3	2.26	0.49
1:A:545:LEU:HD12	4:A:1370:HOH:O	2.12	0.49
1:A:265:ARG:HA	1:A:266:PRO:C	2.34	0.48
1:A:44:ASP:OD2	1:A:71:LYS:NZ	2.36	0.47
1:A:132:GLN:CG	4:A:1375:HOH:O	2.62	0.47
1:A:173:PRO:HG2	1:A:592:ALA:HB1	1.97	0.46
1:A:490:LYS:HD3	1:A:491:ILE:HD13	1.97	0.46
1:A:546:VAL:HA	3:A:802:GAF:H6C1	1.97	0.45
1:A:218:ARG:HD2	4:A:1066:HOH:O	2.17	0.45
1:A:47:TYR:O	1:A:313:ALA:HA	2.18	0.44
1:A:385:THR:HG22	1:A:386:PRO:O	2.17	0.44
1:A:82:SER:HB2	4:A:1196:HOH:O	2.16	0.44
1:A:137:PHE:CE2	1:A:139:ARG:HG3	2.53	0.44
1:A:81:ASP:N	1:A:81:ASP:OD1	2.50	0.43
1:A:218:ARG:HG3	1:A:430:ASP:OD2	2.18	0.42
1:A:346:PRO:HG2	1:A:350:PRO:HA	2.02	0.42
1:A:336:GLN:NE2	1:A:344:ASN:O	2.54	0.41
1:A:413:LYS:NZ	1:A:414:ASN:OD1	2.53	0.41
1:A:159:ARG:HA	2:A:801:FDA:O2B	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	574/633 (91%)	555 (97%)	19 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	503/547 (92%)	489 (97%)	14 (3%)	51 21

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	MET
1	A	46	LYS
1	A	112	MET
1	A	168	TRP
1	A	185	LYS
1	A	206	PHE
1	A	341	ASN
1	A	344	ASN
1	A	388	GLU
1	A	413	LYS
1	A	490	LYS
1	A	496	ASN
1	A	587	PRO
1	A	593	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	132	GLN
1	A	263	GLN
1	A	331	ASN
1	A	341	ASN
1	A	365	GLN
1	A	404	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

2 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	FDA	A	801	1	48,58,58	1.57	9 (18%)	54,89,89	2.95	13 (24%)
3	GAF	A	802	-	11,12,12	0.71	0	15,17,17	2.35	4 (26%)

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	GAF	A	802	-	-	0/2/22/22	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	FDA	C1'-N10	-4.24	1.44	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	FDA	O4B-C4B	-4.05	1.35	1.45
2	A	801	FDA	O3B-C3B	-2.64	1.36	1.43
2	A	801	FDA	P-O1P	-2.52	1.42	1.51
2	A	801	FDA	C4X-C10	-2.42	1.36	1.41
2	A	801	FDA	C4-C4X	2.26	1.45	1.41
2	A	801	FDA	C5X-N5	2.26	1.38	1.35
2	A	801	FDA	C4-N3	2.30	1.37	1.33
2	A	801	FDA	C2A-N3A	2.40	1.36	1.32

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	FDA	N3A-C2A-N1A	-8.78	122.17	128.89
2	A	801	FDA	C4X-C4-N3	-7.95	112.72	123.59
3	A	802	GAF	F2-C2-C3	-4.86	105.08	108.52
3	A	802	GAF	O3-C3-C2	-3.74	102.37	109.05
2	A	801	FDA	C4-C4X-C10	-3.68	117.59	119.94
2	A	801	FDA	C4X-C10-N10	-3.57	118.42	120.52
2	A	801	FDA	C4B-O4B-C1B	-2.09	107.42	109.72
2	A	801	FDA	C6-C5X-C9A	2.23	121.91	118.98
2	A	801	FDA	O2'-C2'-C3'	2.36	114.95	109.02
2	A	801	FDA	C2A-N1A-C6A	2.76	123.69	118.77
3	A	802	GAF	O3-C3-C4	3.27	117.71	110.34
2	A	801	FDA	O3B-C3B-C4B	3.40	121.27	111.05
2	A	801	FDA	O4B-C4B-C3B	3.74	112.69	105.15
2	A	801	FDA	C2B-C1B-N9A	5.12	122.12	114.29
3	A	802	GAF	F2-C2-C1	5.35	116.14	108.59
2	A	801	FDA	C1'-N10-C9A	5.94	125.53	118.86
2	A	801	FDA	C4-N3-C2	12.10	125.70	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	FDA	2	0
3	A	802	GAF	3	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	576/633 (90%)	-0.09	15 (2%) 59 60	10, 15, 34, 60	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	45	ILE	5.8
1	A	618	PHE	5.7
1	A	43	MET	3.6
1	A	232	GLY	3.5
1	A	389	LEU	3.3
1	A	44	ASP	2.8
1	A	400	SER	2.7
1	A	456	TYR	2.6
1	A	455	SER	2.4
1	A	272	GLU	2.4
1	A	345	PRO	2.3
1	A	617	PRO	2.3
1	A	269	ASP	2.3
1	A	343	ALA	2.2
1	A	460	GLN	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no 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( $\text{\AA}^2$ )	Q<0.9
3	GAF	A	802	12/12	0.91	0.13	0.89	22,29,33,34	0
2	FDA	A	801	53/53	0.98	0.07	-0.57	8,10,12,15	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.