



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 11:57 PM GMT

PDB ID : 3AX7  
Title : Bovine Xanthine Oxidase, protease cleaved form  
Authors : Ishikita, H.; Eger, B.T.; Pai, E.F.; Okamoto, K.; Nishino, T.  
Deposited on : 2011-03-30  
Resolution : 2.34 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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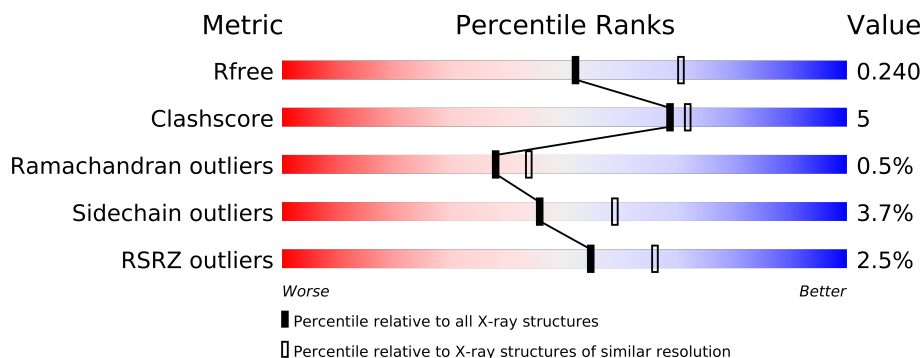
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.34 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))
$R_{free}$	66092	4049 (2.38-2.30)
Clashscore	79885	1094 (2.36-2.32)
Ramachandran outliers	78287	1080 (2.36-2.32)
Sidechain outliers	78261	1081 (2.36-2.32)
RSRZ outliers	66119	4050 (2.38-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	1332	
1	B	1332	

## 2 Entry composition i

There are 9 unique types of molecules in this entry. The entry contains 19746 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

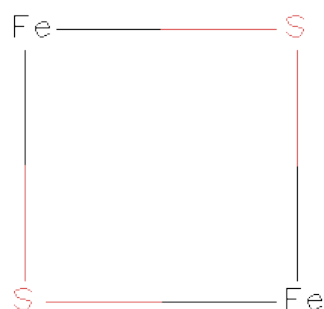
- Molecule 1 is a protein called Xanthine dehydrogenase/oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1225	Total	C	N	O	S	0	0	0
			9476	6013	1632	1771	60			
1	B	1218	Total	C	N	O	S	0	0	0
			9433	5988	1623	1763	59			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	552	HIS	ASP	CONFLICT	UNP P80457
B	552	HIS	ASP	CONFLICT	UNP P80457

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe<sub>2</sub>S<sub>2</sub>).



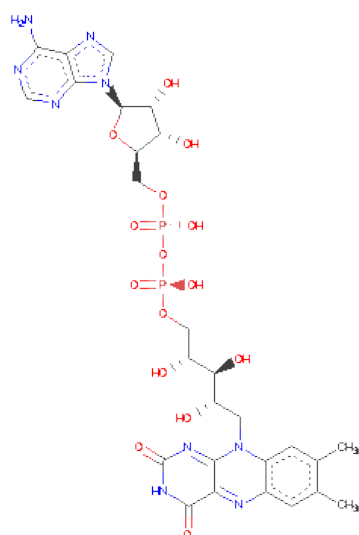
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			4	2	2		

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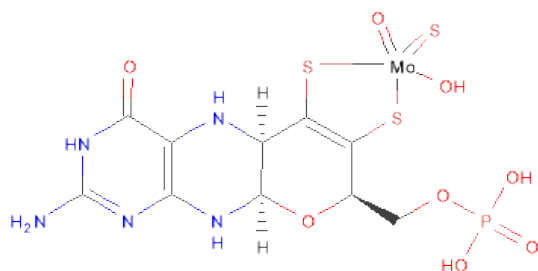
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			4	2	2		
2	B	1	Total	Fe	S	0	0
			4	2	2		
2	B	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



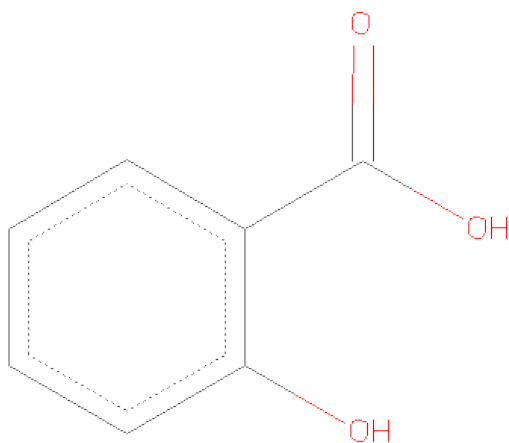
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is {[ (5AR,8R,9AR)-2-AMINO-4-OXO-6,7-DI(SULFANYL-KAPPAS)-3,5,5A,8,9A,10-HEXAHYDRO-4H-PYRANO[3,2-G]PTERIDIN-8-YL]METHYL DIHYDROGENATO(2-) PHOSPHATE}(HYDROXY)OXO(THIOXO)MOLYBDENUM (three-letter code: XAX) (formula:  $C_{10}H_{13}MoN_5O_8PS_3$ ).



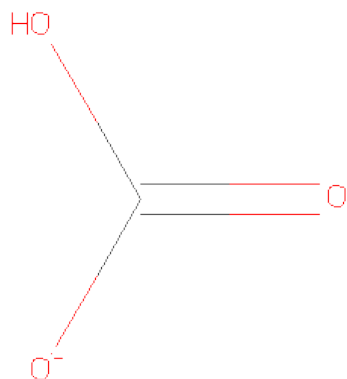
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
4	A	1	Total	C	Mo	N	O	P	S	0	0
			28	10	1	5	8	1	3		
4	B	1	Total	C	Mo	N	O	P	S	0	0
			28	10	1	5	8	1	3		

- Molecule 5 is 2-HYDROXYBENZOIC ACID (three-letter code: SAL) (formula: C<sub>7</sub>H<sub>6</sub>O<sub>3</sub>).



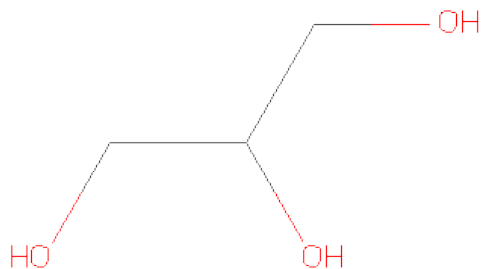
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	7	3		
5	B	1	Total	C	O	0	0
			10	7	3		

- Molecule 6 is BICARBONATE ION (three-letter code: BCT) (formula:  $\text{CHO}_3$ ).



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

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula:  $\text{C}_3\text{H}_8\text{O}_3$ ).



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

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

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Ca	0	0
			1	1		
8	A	1	Total	Ca	0	0
			1	1		

- Molecule 9 is water.

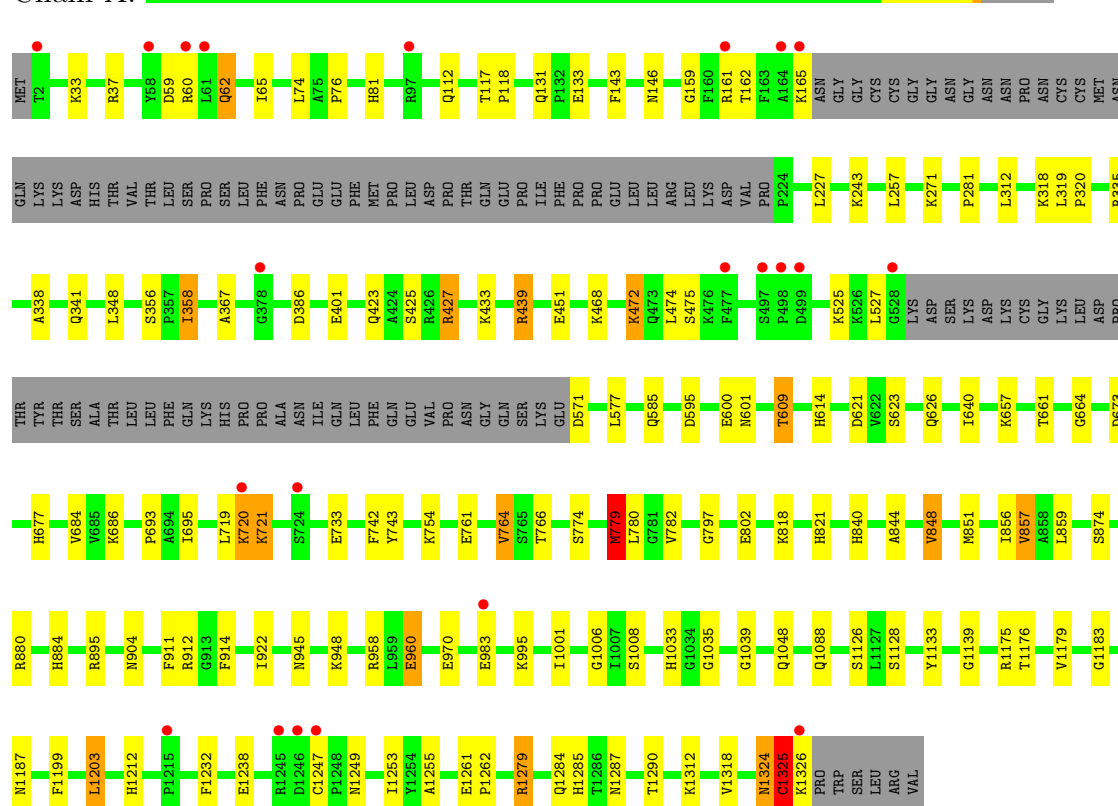
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	316	Total	O	0	0
			316	316		
9	B	283	Total	O	0	0
			283	283		

### 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 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.

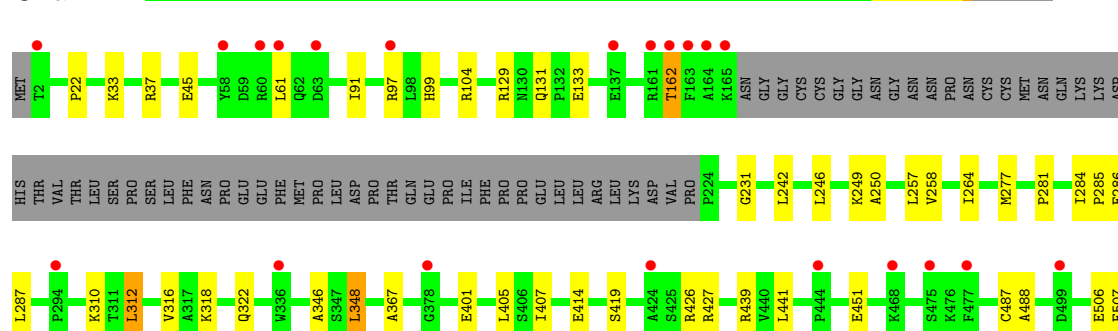
#### • Molecule 1: Xanthine dehydrogenase/oxidase

##### Chain A:

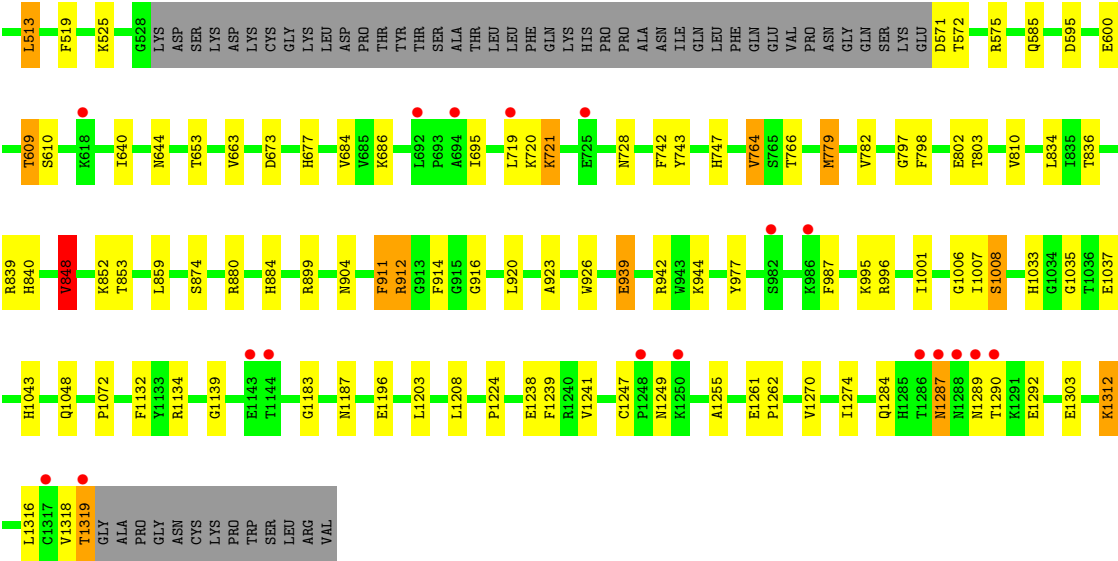


#### • Molecule 1: Xanthine dehydrogenase/oxidase

##### Chain B:







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.48Å 73.15Å 146.27Å 90.00° 98.18° 90.00°	Depositor
Resolution (Å)	36.37 – 2.34 36.37 – 2.34	Depositor EDS
% Data completeness (in resolution range)	93.8 (36.37-2.34) 93.8 (36.37-2.34)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.40 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, $R_{free}$	0.194 , 0.240 0.195 , 0.240	Depositor DCC
$R_{free}$ test set	5554 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.4	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 23.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 110452 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	19746	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: XAX, GOL, SAL, CA, FES, BCT, 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	0.64	0/9675	0.69	6/13085 (0.0%)
1	B	0.62	0/9631	0.68	6/13026 (0.0%)
All	All	0.63	0/19306	0.68	12/26111 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	839	ARG	NE-CZ-NH2	-7.26	116.67	120.30
1	B	942	ARG	NE-CZ-NH2	-6.35	117.12	120.30
1	A	779	MET	CG-SD-CE	-5.94	90.69	100.20
1	A	1325	CYS	N-CA-C	5.65	126.26	111.00
1	A	439	ARG	NE-CZ-NH2	-5.51	117.54	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9476	0	9483	91	0
1	B	9433	0	9439	97	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	8	0	0	0	0
2	B	8	0	0	0	0
3	A	53	0	31	1	0
3	B	53	0	31	3	0
4	A	28	0	10	0	0
4	B	28	0	10	1	0
5	A	10	0	5	1	0
5	B	10	0	4	1	0
6	A	4	0	0	0	0
6	B	4	0	0	0	0
7	A	18	0	24	0	0
7	B	12	0	16	0	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
9	A	316	0	0	3	0
9	B	283	0	0	9	0
All	All	19746	0	19053	185	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

The worst 5 of 185 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:779:MET:SD	9:B:1452:HOH:O	2.09	1.10
1:A:884:HIS:HE1	1:A:1006:GLY:H	1.17	0.92
1:A:720:LYS:O	1:A:721:LYS:HB2	1.70	0.90
1:A:131:GLN:HE21	1:A:133:GLU:H	1.14	0.88
1:A:995:LYS:NZ	1:A:1284:GLN:HE21	1.72	0.86

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	1219/1332 (92%)	1172 (96%)	39 (3%)	8 (1%)	30	33
1	B	1212/1332 (91%)	1162 (96%)	45 (4%)	5 (0%)	43	50
All	All	2431/2664 (91%)	2334 (96%)	84 (4%)	13 (0%)	38	44

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	721	LYS
1	A	1008	SER
1	A	1325	CYS
1	B	1008	SER
1	B	721	LYS

### 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	1030/1128 (91%)	990 (96%)	40 (4%)	43	57
1	B	1026/1128 (91%)	990 (96%)	36 (4%)	48	62
All	All	2056/2256 (91%)	1980 (96%)	76 (4%)	45	59

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1001	ILE
1	B	129	ARG
1	B	1238	GLU
1	A	1203	LEU
1	A	1287	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1284	GLN
1	B	131	GLN
1	B	1048	GLN

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Mol	Chain	Res	Type
1	A	1324	ASN
1	B	146	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

Of 19 ligands modelled in this entry, 2 are monoatomic - leaving 17 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	FES	A	1333	1	0,4,4	0.00	-	0,4,4	0.00	-
2	FES	A	1334	1	0,4,4	0.00	-	0,4,4	0.00	-
3	FAD	A	1335	-	58,58,58	0.98	2 (3%)	85,89,89	1.88	11 (12%)
5	SAL	A	1336	-	10,10,10	1.86	1 (10%)	13,13,13	1.22	2 (15%)
6	BCT	A	1337	-	0,3,3	0.00	-	0,3,3	0.00	-
7	GOL	A	1338	-	5,5,5	0.59	0	5,5,5	0.53	0
7	GOL	A	1339	-	5,5,5	0.32	0	5,5,5	0.31	0
7	GOL	A	1340	-	5,5,5	0.33	0	5,5,5	0.49	0
4	XAX	A	3003	-	29,31,31	7.46	10 (34%)	37,52,52	1.71	9 (24%)
2	FES	B	1333	1	0,4,4	0.00	-	0,4,4	0.00	-
2	FES	B	1334	1	0,4,4	0.00	-	0,4,4	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	FAD	B	1335	-	58,58,58	1.07	4 (6%)	85,89,89	1.83	13 (15%)
5	SAL	B	1336	-	10,10,10	1.96	1 (10%)	13,13,13	1.13	2 (15%)
6	BCT	B	1337	-	0,3,3	0.00	-	0,3,3	0.00	-
7	GOL	B	1338	-	5,5,5	0.32	0	5,5,5	0.44	0
7	GOL	B	1339	-	5,5,5	0.32	0	5,5,5	0.34	0
4	XAX	B	3003	-	29,31,31	7.75	8 (27%)	37,52,52	2.14	13 (35%)

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	FES	A	1333	1	-	0/0/4/4	0/0/1/1
2	FES	A	1334	1	-	0/0/4/4	0/0/1/1
3	FAD	A	1335	-	-	0/34/50/50	0/1/6/6
5	SAL	A	1336	-	-	0/4/4/4	0/1/1/1
6	BCT	A	1337	-	-	0/0/0/0	0/0/0/0
7	GOL	A	1338	-	-	0/4/4/4	0/0/0/0
7	GOL	A	1339	-	-	0/4/4/4	0/0/0/0
7	GOL	A	1340	-	-	0/4/4/4	0/0/0/0
4	XAX	A	3003	-	-	0/6/46/46	0/0/4/4
2	FES	B	1333	1	-	0/0/4/4	0/0/1/1
2	FES	B	1334	1	-	0/0/4/4	0/0/1/1
3	FAD	B	1335	-	-	0/34/50/50	0/1/6/6
5	SAL	B	1336	-	-	0/4/4/4	0/1/1/1
6	BCT	B	1337	-	-	0/0/0/0	0/0/0/0
7	GOL	B	1338	-	-	0/4/4/4	0/0/0/0
7	GOL	B	1339	-	-	0/4/4/4	0/0/0/0
4	XAX	B	3003	-	-	0/6/46/46	0/0/4/4

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	3003	XAX	O1-MO	39.97	2.08	1.70
4	A	3003	XAX	O1-MO	37.95	2.06	1.70
4	A	3003	XAX	C9-C10	6.34	1.50	1.41
5	B	1336	SAL	C1-C2	5.82	1.50	1.40
4	A	3003	XAX	O4-C4	5.80	1.35	1.24

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1335	FAD	N3A-C2A-N1A	-11.85	118.80	128.71
3	B	1335	FAD	N3A-C2A-N1A	-9.65	120.64	128.71
4	B	3003	XAX	C6-C1'-S1'	-6.78	118.38	124.27
3	B	1335	FAD	C2-N1-C10	5.77	120.79	114.98
3	B	1335	FAD	C1'-N10-C9A	4.96	123.70	118.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	1225/1332 (91%)	-0.03	22 (1%) 65 75	17, 27, 43, 62	0
1	B	1218/1332 (91%)	0.02	39 (3%) 45 57	17, 28, 44, 64	0
All	All	2443/2664 (91%)	-0.00	61 (2%) 54 66	17, 28, 43, 64	0

The worst 5 of 61 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1287	ASN	6.2
1	B	165	LYS	5.4
1	A	58	TYR	5.3
1	B	1290	THR	5.2
1	B	2	THR	5.1

### 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	SAL	B	1336	10/10	0.17	1.84	35,37,38,40	0
5	SAL	A	1336	10/10	0.17	1.70	27,30,31,31	0
7	GOL	B	1338	6/6	0.15	1.24	29,30,30,31	0
7	GOL	B	1339	6/6	0.12	0.80	19,25,27,27	0
8	CA	B	1340	1/1	0.11	0.50	24,24,24,24	0
7	GOL	A	1339	6/6	0.11	0.34	26,27,28,29	0
7	GOL	A	1340	6/6	0.12	0.13	40,40,40,41	0
4	XAX	B	3003	28/28	0.14	0.04	14,23,29,34	0
3	FAD	B	1335	53/53	0.13	-0.01	23,28,30,31	0
4	XAX	A	3003	28/28	0.15	-0.06	15,20,25,33	0
2	FES	B	1333	4/4	0.12	-0.16	20,20,21,23	0
7	GOL	A	1338	6/6	0.11	-0.23	27,28,30,30	0
6	BCT	A	1337	4/4	0.17	-0.43	20,21,22,22	0
3	FAD	A	1335	53/53	0.13	-0.53	20,24,27,30	0
2	FES	A	1333	4/4	0.10	-1.02	20,20,21,24	0
2	FES	B	1334	4/4	0.10	-1.08	20,21,22,23	0
6	BCT	B	1337	4/4	0.12	-1.19	17,17,18,20	0
2	FES	A	1334	4/4	0.10	-1.40	19,21,21,22	0
8	CA	A	1341	1/1	0.09	-1.48	22,22,22,22	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.