



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 02:01 pm GMT

PDB ID : 2YM2  
Title : SNAPSHOTS OF ENZYMATIC BAEYER-VILLIGER CATALYSIS: OXY-  
GEN ACTIVATION AND INTERMEDIATE STABILIZATION: ARG337LYS  
MUTANT REDUCED STATE WITH NADP  
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Deposited on : 2011-06-06  
Resolution : 2.70 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

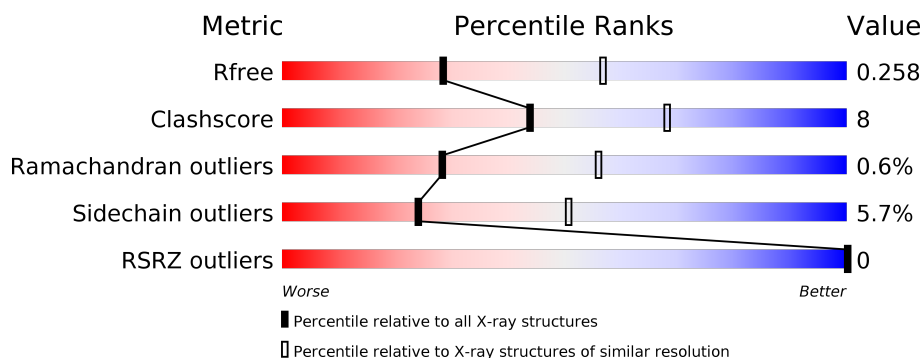
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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	542	 83% 13% . .

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4373 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 PHENYLACETONE MONOOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	531	Total	C	N	O	S	0	0	0
			4217	2690	725	793	9			

There is a discrepancy between the modelled and reference sequences:

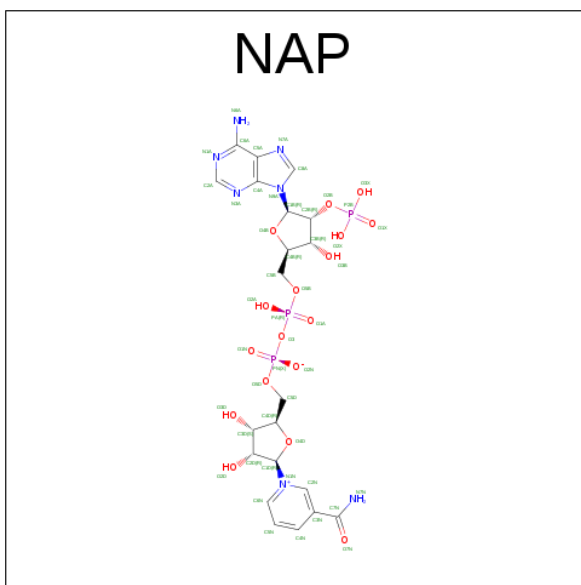
Chain	Residue	Modelled	Actual	Comment	Reference
A	337	LYS	ARG	ENGINEERED MUTATION	UNP ?

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



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

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula:  $C_{21}H_{28}N_7O_{17}P_3$ ).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	55	Total O 55 55	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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: PHENYLACETONE MONOOXYGENASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.45Å 108.45Å 108.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	70.90 – 2.70 54.23 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (70.90-2.70) 98.6 (54.23-2.70)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.77 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.202 , 0.259 0.203 , 0.258	Depositor DCC
$R_{free}$ test set	990 reflections (5.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	43.2	Xtriage
Anisotropy	0.190	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 35.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4373	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAP, 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	0.78	0/4328	0.83	7/5888 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	523	ARG	NE-CZ-NH1	8.75	124.68	120.30
1	A	89	ARG	NE-CZ-NH2	-8.07	116.26	120.30
1	A	523	ARG	NE-CZ-NH2	-7.73	116.43	120.30
1	A	279	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	A	89	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	279	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	A	390	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

### 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	4217	0	4060	63	0
2	A	53	0	31	2	0
3	A	48	0	25	3	0
4	A	55	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4373	0	4116	64	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 8.

All (64) 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:246:ARG:CG	1:A:246:ARG:HH11	1.57	1.17
1:A:350:ARG:HH11	1:A:350:ARG:HG3	1.19	1.04
1:A:325:ARG:HG3	1:A:325:ARG:HH11	1.31	0.95
1:A:246:ARG:HH11	1:A:246:ARG:HG3	1.33	0.94
1:A:523:ARG:CZ	1:A:523:ARG:HB2	2.02	0.88
1:A:246:ARG:HH11	1:A:246:ARG:HG2	1.40	0.84
1:A:246:ARG:NH1	1:A:246:ARG:HG2	1.93	0.84
1:A:316:THR:HG21	1:A:345:TYR:HB3	1.61	0.81
1:A:325:ARG:HG3	1:A:325:ARG:NH1	1.95	0.79
1:A:246:ARG:CG	1:A:246:ARG:NH1	2.31	0.79
1:A:316:THR:HG21	1:A:345:TYR:CB	2.11	0.79
1:A:506:ASN:HD22	1:A:506:ASN:H	1.32	0.78
1:A:350:ARG:NH1	1:A:350:ARG:HG3	1.95	0.73
1:A:325:ARG:HD3	1:A:357:ASP:HB2	1.71	0.73
1:A:335:THR:OG1	1:A:498:THR:HG21	1.88	0.72
1:A:325:ARG:CG	1:A:325:ARG:HH11	2.03	0.69
1:A:279:ARG:HH11	1:A:279:ARG:CB	2.09	0.66
1:A:350:ARG:HH11	1:A:350:ARG:CG	2.02	0.65
1:A:310:ARG:HG2	1:A:327:VAL:HG13	1.81	0.62
1:A:366:ILE:HD12	1:A:371:VAL:HG22	1.82	0.62
1:A:279:ARG:CG	1:A:279:ARG:HH11	2.13	0.61
1:A:152:GLN:HE22	2:A:700:FAD:H5'2	1.66	0.61
1:A:523:ARG:HA	1:A:526:GLN:HE21	1.66	0.60
1:A:125:ASP:OD2	1:A:128:THR:OG1	2.16	0.60
1:A:316:THR:HG21	1:A:345:TYR:HB2	1.84	0.58
1:A:370:GLY:HA3	1:A:378:TYR:O	2.04	0.57
1:A:523:ARG:HB2	1:A:523:ARG:NH1	2.19	0.56
1:A:316:THR:CG2	1:A:345:TYR:HB3	2.35	0.56
1:A:177:TRP:CG	1:A:178:PRO:HD2	2.41	0.55
1:A:67:ILE:HG22	1:A:71:GLU:HB2	1.89	0.55
1:A:279:ARG:NH1	1:A:279:ARG:HG3	2.23	0.54
1:A:366:ILE:CD1	1:A:371:VAL:HG22	2.39	0.53
1:A:279:ARG:HH11	1:A:279:ARG:HG3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:ARG:NH1	1:A:279:ARG:CG	2.73	0.51
1:A:67:ILE:CG2	1:A:71:GLU:HB2	2.41	0.51
1:A:158:LEU:HD22	1:A:158:LEU:H	1.77	0.50
1:A:221:PHE:CE1	1:A:328:PRO:HG2	2.46	0.49
1:A:495:TYR:HB3	1:A:514:PHE:CE1	2.48	0.49
1:A:195:GLY:HA3	3:A:1543:NAP:O1N	2.13	0.49
2:A:700:FAD:HM73	3:A:1543:NAP:C5N	2.43	0.48
1:A:17:VAL:O	1:A:143:ALA:HA	2.13	0.48
1:A:202:SER:HB2	1:A:203:PRO:HD3	1.95	0.48
1:A:196:SER:HB3	1:A:339:ILE:HG12	1.96	0.47
1:A:23:GLY:O	1:A:28:GLY:HA3	2.14	0.47
1:A:504:GLY:HA2	4:A:2051:HOH:O	2.15	0.47
1:A:494:LEU:O	1:A:497:MET:HB2	2.15	0.46
1:A:158:LEU:HD22	1:A:158:LEU:N	2.30	0.46
1:A:58:ASN:ND2	1:A:175:GLY:HA2	2.31	0.46
1:A:506:ASN:HD22	1:A:506:ASN:N	2.03	0.46
1:A:75:SER:OG	1:A:250:ARG:NH2	2.44	0.45
1:A:210:ALA:O	1:A:352:ASN:HB2	2.17	0.44
1:A:222:ALA:HA	1:A:339:ILE:O	2.18	0.44
1:A:274:VAL:O	1:A:278:GLU:HB2	2.18	0.43
1:A:517:TYR:CE2	1:A:524:TYR:HB2	2.53	0.43
1:A:512:ARG:CG	1:A:512:ARG:HH11	2.32	0.43
1:A:188:ARG:HG3	1:A:381:ASP:OD2	2.19	0.42
1:A:297:ARG:NH2	4:A:2031:HOH:O	2.51	0.42
1:A:160:ASN:H	3:A:1543:NAP:H62A	1.67	0.42
1:A:163:GLY:HA3	1:A:366:ILE:O	2.20	0.42
1:A:494:LEU:HD22	1:A:497:MET:SD	2.59	0.42
1:A:520:GLY:HA3	1:A:523:ARG:HH12	1.85	0.42
1:A:128:THR:O	1:A:130:THR:HG23	2.20	0.41
1:A:471:ARG:O	1:A:541:LEU:HA	2.21	0.41
1:A:15:GLU:H	1:A:15:GLU:HG2	1.66	0.41

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	527/542 (97%)	497 (94%)	27 (5%)	3 (1%)	28	56

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	ARG
1	A	374	SER
1	A	12	GLN

### 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	439/453 (97%)	414 (94%)	25 (6%)	24	51

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	GLU
1	A	144	ARG
1	A	150	SER
1	A	158	LEU
1	A	217	ARG
1	A	218	THR
1	A	237	ASP
1	A	242	TYR
1	A	246	ARG
1	A	279	ARG
1	A	283	GLU
1	A	297	ARG
1	A	321	GLU
1	A	325	ARG
1	A	350	ARG
1	A	374	SER

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Mol	Chain	Res	Type
1	A	377	GLU
1	A	424	SER
1	A	484	GLU
1	A	498	THR
1	A	506	ASN
1	A	512	ARG
1	A	523	ARG
1	A	534	LYS
1	A	540	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	ASN
1	A	129	ASN
1	A	152	GLN
1	A	157	GLN
1	A	315	ASN
1	A	506	ASN
1	A	526	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](#)

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
3	NAP	A	1543	-	44,52,52	1.56	7 (15%)	51,80,80	2.14	8 (15%)
2	FAD	A	700	-	51,58,58	1.43	6 (11%)	54,89,89	2.15	7 (12%)

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
3	NAP	A	1543	-	-	0/27/67/67	0/5/5/5
2	FAD	A	700	-	-	0/28/50/50	0/6/6/6

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1543	NAP	C3D-C4D	2.00	1.58	1.53
2	A	700	FAD	C2A-N1A	2.36	1.38	1.33
2	A	700	FAD	C4-N3	2.53	1.37	1.33
3	A	1543	NAP	P2B-O2B	2.58	1.64	1.59
2	A	700	FAD	C5X-N5	2.77	1.39	1.35
3	A	1543	NAP	C7N-N7N	3.01	1.38	1.33
3	A	1543	NAP	C4N-C3N	3.24	1.44	1.39
3	A	1543	NAP	P2B-O1X	3.39	1.62	1.50
2	A	700	FAD	C2A-N3A	3.39	1.37	1.32
3	A	1543	NAP	O4B-C1B	3.88	1.46	1.41
3	A	1543	NAP	O4D-C1D	4.08	1.46	1.41
2	A	700	FAD	C4X-N5	4.27	1.39	1.33
2	A	700	FAD	C10-N1	4.98	1.40	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	700	FAD	N3A-C2A-N1A	-12.14	118.29	128.86
3	A	1543	NAP	N3A-C2A-N1A	-10.14	120.03	128.86
3	A	1543	NAP	O7N-C7N-C3N	-4.01	114.94	119.62
3	A	1543	NAP	O3B-C3B-C4B	-3.38	101.22	111.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	700	FAD	O2'-C2'-C1'	-2.86	103.17	109.79
3	A	1543	NAP	O2D-C2D-C1D	-2.51	103.75	111.61
2	A	700	FAD	C4-C4X-C10	-2.38	118.04	119.96
3	A	1543	NAP	C3B-C2B-C1B	-2.33	98.20	102.75
2	A	700	FAD	C4X-C4-N3	-2.25	120.28	123.48
2	A	700	FAD	C5X-C9A-N10	2.09	119.21	117.66
2	A	700	FAD	C2A-N1A-C6A	2.11	122.47	118.77
3	A	1543	NAP	N6A-C6A-N1A	2.24	123.21	118.77
3	A	1543	NAP	O2X-P2B-O1X	2.25	119.29	110.50
3	A	1543	NAP	C3N-C7N-N7N	5.94	124.56	117.77
2	A	700	FAD	C4-N3-C2	6.23	120.61	115.16

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
3	A	1543	NAP	3	0
2	A	700	FAD	2	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	531/542 (97%)	-0.34	0 100 100	19, 34, 53, 64	0

There are no RSRZ outliers to report.

### 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
2	FAD	A	700	53/53	0.98	0.13	-0.03	15,22,37,39	0
3	NAP	A	1543	48/48	0.97	0.12	-0.52	19,28,38,39	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.