



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 01:28 pm GMT

PDB ID : 2C67  
Title : MAO INHIBITION BY RASAGILINE ANALOGUES  
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Deposited on : 2005-11-07  
Resolution : 1.70 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

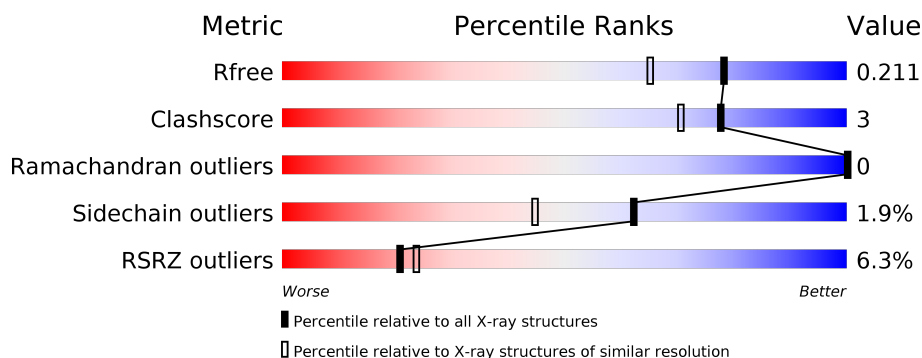
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	3453 (1.70-1.70)
Clashscore	112137	3876 (1.70-1.70)
Ramachandran outliers	110173	3815 (1.70-1.70)
Sidechain outliers	110143	3815 (1.70-1.70)
RSRZ outliers	101464	3491 (1.70-1.70)

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	520	<div> <div>6%</div> <div> <div></div> <div>91%</div> <div>5% • •</div> </div> </div>
1	B	520	<div> <div>6%</div> <div> <div></div> <div>87%</div> <div>7% • 5%</div> </div> </div>

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	RM1	A	1503	-	-	-	X
3	RM1	B	1498	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8666 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 AMINE OXIDASE (FLAVIN-CONTAINING) B.

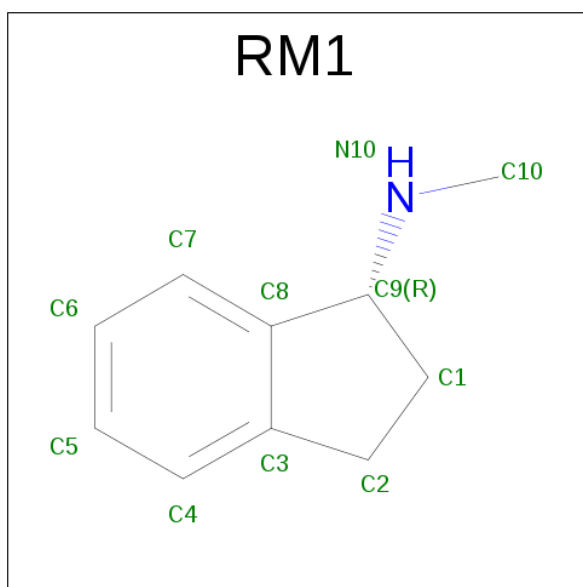
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total	C	N	O	S	0	0	0
			3971	2538	681	728	24			
1	B	494	Total	C	N	O	S	0	0	0
			3940	2519	676	721	24			

- 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		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is N-METHYL-1(R)-AMINOINDAN (three-letter code: RM1) (formula:  $C_{10}H_{13}N$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			11	10	1		
3	B	1	Total	C	N	0	0
			11	10	1		

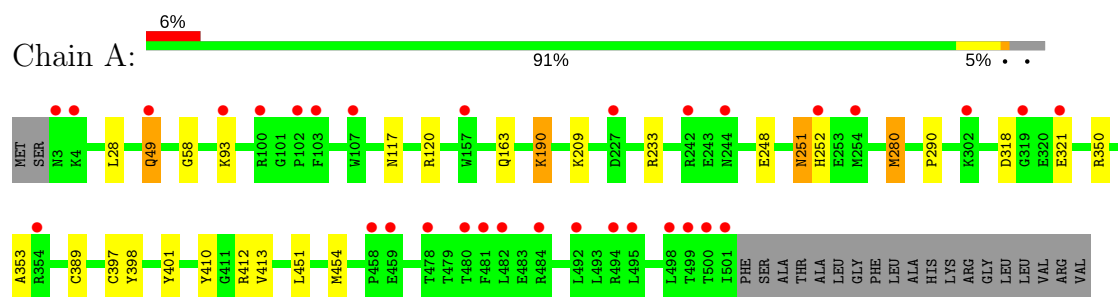
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	299	Total	O	0	0
			299	299		
4	B	328	Total	O	0	0
			328	328		

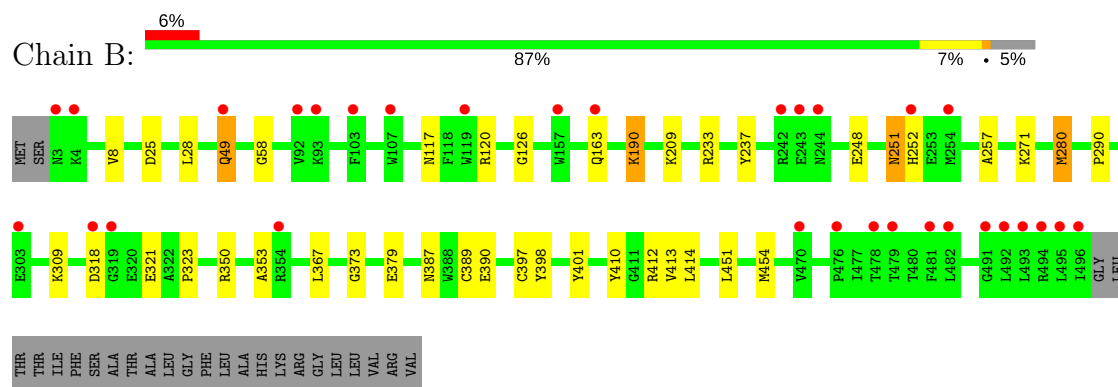
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ( $RSRZ > 2$ ). 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: AMINE OXIDASE (FLAVIN-CONTAINING) B



#### • Molecule 1: AMINE OXIDASE (FLAVIN-CONTAINING) B



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	131.27Å 222.45Å 86.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.70 27.86 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.7 (15.00-1.70) 97.7 (27.86-1.70)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.99 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.194 , 0.212 0.194 , 0.211	Depositor DCC
$R_{free}$ test set	3348 reflections (2.54%)	DCC
Wilson B-factor (Å <sup>2</sup> )	12.9	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 47.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.013 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8666	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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: RM1, 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	0.38	0/4068	0.53	1/5522 (0.0%)
1	B	0.39	0/4037	0.54	0/5479
All	All	0.38	0/8105	0.53	1/11001 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	190	LYS	CA-CB-CG	5.41	125.29	113.40

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	3971	0	3967	28	0
1	B	3940	0	3937	37	1
2	A	53	0	29	1	0
2	B	53	0	29	1	0
3	A	11	0	13	1	0
3	B	11	0	13	1	0
4	A	299	0	0	3	1
4	B	328	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8666	0	7988	54	2

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 (54) 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:353:ALA:HB1	1:B:280:MET:HE1	1.52	0.92
1:A:280:MET:HE1	1:B:353:ALA:HB1	1.56	0.86
1:A:251:ASN:H	1:A:251:ASN:HD22	1.32	0.76
1:B:117:ASN:HD22	1:B:120:ARG:HH21	1.34	0.75
1:B:251:ASN:H	1:B:251:ASN:HD22	1.33	0.74
1:A:117:ASN:HD22	1:A:120:ARG:HH21	1.37	0.72
1:B:49:GLN:NE2	4:B:2032:HOH:O	2.26	0.67
1:A:451:LEU:HA	1:A:454:MET:HE2	1.78	0.66
1:A:353:ALA:CB	1:B:280:MET:HE1	2.28	0.63
1:B:451:LEU:HA	1:B:454:MET:HE2	1.82	0.60
1:B:271:LYS:HE2	4:B:2264:HOH:O	2.02	0.58
1:B:309:LYS:HG3	4:B:2203:HOH:O	2.05	0.56
1:A:350:ARG:HD3	1:B:410:TYR:OH	2.08	0.54
1:B:451:LEU:HD23	1:B:454:MET:CE	2.38	0.54
1:A:28:LEU:HD11	1:A:454:MET:CE	2.39	0.52
1:A:451:LEU:HD23	1:A:454:MET:CE	2.40	0.52
1:B:28:LEU:HD11	1:B:454:MET:CE	2.40	0.52
1:A:248:GLU:OE2	1:B:252:HIS:NE2	2.43	0.51
1:A:251:ASN:ND2	1:A:251:ASN:H	2.07	0.51
1:A:321:GLU:CD	1:A:321:GLU:H	2.14	0.51
1:A:58:GLY:HA2	2:A:1502:FAD:C4X	2.42	0.50
1:A:49:GLN:HB3	4:A:2026:HOH:O	2.11	0.49
1:B:163:GLN:HB3	1:B:318:ASP:OD2	2.12	0.49
1:B:58:GLY:HA2	2:B:1497:FAD:C4X	2.44	0.48
1:A:233:ARG:HG3	1:A:251:ASN:HD21	1.79	0.48
1:B:309:LYS:NZ	1:B:373:GLY:O	2.47	0.47
1:A:280:MET:HE1	1:B:353:ALA:CB	2.35	0.47
1:B:233:ARG:HG3	1:B:251:ASN:HD21	1.80	0.47
1:B:251:ASN:H	1:B:251:ASN:ND2	2.08	0.47
1:A:280:MET:HG3	1:B:389:CYS:CB	2.45	0.47
1:B:412:ARG:HG2	4:B:2275:HOH:O	2.14	0.46
1:A:410:TYR:OH	1:B:350:ARG:HD3	2.15	0.46
1:B:387:ASN:O	1:B:390:GLU:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:321:GLU:CD	1:B:321:GLU:H	2.17	0.46
1:A:451:LEU:HA	1:A:454:MET:CE	2.45	0.46
1:A:252:HIS:NE2	1:B:248:GLU:OE2	2.45	0.45
1:A:389:CYS:CB	1:B:280:MET:HG3	2.47	0.45
1:B:126:GLY:O	1:B:190:LYS:HG3	2.17	0.45
1:A:163:GLN:HB3	1:A:318:ASP:OD2	2.17	0.44
1:B:117:ASN:HD22	1:B:120:ARG:NH2	2.10	0.44
1:B:451:LEU:HA	1:B:454:MET:CE	2.47	0.44
1:B:412:ARG:HD2	4:B:2274:HOH:O	2.17	0.43
1:A:117:ASN:HD22	1:A:120:ARG:NH2	2.10	0.43
1:B:398:TYR:CE2	3:B:1498:RM1:H9	2.54	0.43
1:A:398:TYR:CE2	3:A:1503:RM1:H9	2.55	0.42
1:A:93:LYS:HB2	4:A:2068:HOH:O	2.20	0.41
1:B:8:VAL:HG23	1:B:257:ALA:HB2	2.03	0.41
1:B:290:PRO:HG2	1:B:401:TYR:CZ	2.54	0.41
1:B:323:PRO:HD2	1:B:367:LEU:HD22	2.03	0.41
1:A:280:MET:HG3	1:B:389:CYS:HB3	2.03	0.40
1:A:412:ARG:HD2	4:A:2247:HOH:O	2.20	0.40
1:A:290:PRO:HG2	1:A:401:TYR:CZ	2.56	0.40
1:B:237:TYR:HB3	1:B:248:GLU:HB3	2.04	0.40
1:B:454:MET:HE2	1:B:454:MET:HB2	1.86	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2027:HOH:O	4:A:2027:HOH:O[3_655]	1.40	0.80
1:B:25:ASP:O	1:B:49:GLN:NE2[4_565]	1.96	0.24

## 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	497/520 (96%)	486 (98%)	11 (2%)	0	100	100
1	B	492/520 (95%)	480 (98%)	12 (2%)	0	100	100
All	All	989/1040 (95%)	966 (98%)	23 (2%)	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	427/444 (96%)	420 (98%)	7 (2%)	68	53
1	B	424/444 (96%)	415 (98%)	9 (2%)	59	40
All	All	851/888 (96%)	835 (98%)	16 (2%)	62	45

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	GLN
1	A	190	LYS
1	A	209	LYS
1	A	251	ASN
1	A	280	MET
1	A	397	CYS
1	A	413	VAL
1	B	49	GLN
1	B	190	LYS
1	B	209	LYS
1	B	251	ASN
1	B	280	MET
1	B	379	GLU
1	B	397	CYS
1	B	413	VAL
1	B	414	LEU

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	117	ASN
1	A	251	ASN
1	B	117	ASN
1	B	251	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](#)

4 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	FAD	A	1502	1	51,58,58	1.31	7 (13%)	54,89,89	1.97	7 (12%)
3	RM1	A	1503	-	11,12,12	2.05	5 (45%)	14,16,16	1.82	3 (21%)
2	FAD	B	1497	1	51,58,58	1.33	6 (11%)	54,89,89	1.97	7 (12%)
3	RM1	B	1498	-	11,12,12	1.94	4 (36%)	14,16,16	1.71	3 (21%)

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	FAD	A	1502	1	-	0/28/50/50	0/6/6/6
3	RM1	A	1503	-	-	0/0/11/11	0/2/2/2
2	FAD	B	1497	1	-	0/28/50/50	0/6/6/6
3	RM1	B	1498	-	-	0/0/11/11	0/2/2/2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1503	RM1	C7-C8	-3.95	1.34	1.39
3	B	1498	RM1	C3-C8	-3.67	1.32	1.39
3	A	1503	RM1	C3-C8	-3.61	1.32	1.39
3	B	1498	RM1	C7-C8	-3.52	1.35	1.39
3	A	1503	RM1	C4-C3	-2.71	1.35	1.39
3	B	1498	RM1	C4-C3	-2.60	1.35	1.39
3	A	1503	RM1	C6-C7	-2.02	1.35	1.38
3	B	1498	RM1	C5-C4	-2.02	1.35	1.38
3	A	1503	RM1	C5-C4	-2.01	1.35	1.38
2	A	1502	FAD	C5X-N5	2.32	1.38	1.35
2	A	1502	FAD	C2A-N1A	2.36	1.38	1.33
2	B	1497	FAD	C2A-N1A	2.45	1.38	1.33
2	A	1502	FAD	C1'-N10	2.59	1.51	1.48
2	B	1497	FAD	C1'-N10	2.61	1.51	1.48
2	A	1502	FAD	C4-N3	3.09	1.38	1.33
2	A	1502	FAD	C2A-N3A	3.11	1.37	1.32
2	B	1497	FAD	C2A-N3A	3.42	1.37	1.32
2	B	1497	FAD	C4-N3	3.44	1.39	1.33
2	A	1502	FAD	C4X-N5	3.76	1.38	1.33
2	B	1497	FAD	C4X-N5	3.76	1.38	1.33
2	A	1502	FAD	C10-N1	4.06	1.39	1.33
2	B	1497	FAD	C10-N1	4.22	1.39	1.33

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1497	FAD	N3A-C2A-N1A	-10.49	119.73	128.86
2	A	1502	FAD	N3A-C2A-N1A	-10.45	119.75	128.86
3	A	1503	RM1	C1-C9-N10	-4.48	106.50	115.56
3	B	1498	RM1	C1-C9-N10	-3.95	107.59	115.56
2	A	1502	FAD	C4X-C4-N3	-2.77	119.54	123.48
2	B	1497	FAD	C4X-C4-N3	-2.72	119.61	123.48
2	A	1502	FAD	C1B-N9A-C4A	-2.41	122.47	126.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1497	FAD	C9A-C5X-N5	-2.22	118.93	122.24
3	B	1498	RM1	C6-C7-C8	-2.09	118.33	121.01
2	A	1502	FAD	C9A-C5X-N5	-2.06	119.17	122.24
2	B	1497	FAD	C1B-N9A-C4A	-2.04	123.10	126.64
3	A	1503	RM1	C10-N10-C9	2.00	120.13	113.60
2	B	1497	FAD	C1'-N10-C9A	2.39	120.54	118.35
2	A	1502	FAD	C4X-N5-C5X	2.40	119.30	116.76
2	A	1502	FAD	C1'-N10-C9A	2.56	120.70	118.35
3	A	1503	RM1	C3-C8-C9	2.74	112.80	110.27
3	B	1498	RM1	C3-C8-C9	2.85	112.90	110.27
2	B	1497	FAD	C4X-N5-C5X	3.15	120.09	116.76
2	A	1502	FAD	C4-N3-C2	6.10	120.50	115.16
2	B	1497	FAD	C4-N3-C2	6.13	120.52	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1502	FAD	1	0
3	A	1503	RM1	1	0
2	B	1497	FAD	1	0
3	B	1498	RM1	1	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

### 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	499/520 (95%)	0.23	32 (6%) 20 23	6, 12, 29, 52	0
1	B	494/520 (95%)	0.27	31 (6%) 21 24	6, 12, 27, 46	0
All	All	993/1040 (95%)	0.25	63 (6%) 21 24	6, 12, 29, 52	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	495	LEU	9.0
1	A	107	TRP	6.3
1	B	494	ARG	5.7
1	B	496	ILE	5.6
1	B	493	LEU	5.1
1	B	107	TRP	4.9
1	A	103	PHE	4.7
1	A	252	HIS	4.6
1	B	243	GLU	4.6
1	B	242	ARG	4.5
1	B	103	PHE	4.4
1	B	252	HIS	4.3
1	A	354	ARG	4.0
1	B	3	ASN	3.9
1	B	93	LYS	3.9
1	A	500	THR	3.9
1	B	481	PHE	3.9
1	A	242	ARG	3.8
1	A	501	ILE	3.7
1	B	492	LEU	3.6
1	A	495	LEU	3.6
1	B	479	THR	3.5
1	A	482	LEU	3.5
1	A	481	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	92	VAL	3.3
1	B	49	GLN	3.2
1	B	354	ARG	3.2
1	A	494	ARG	3.2
1	B	244	ASN	3.1
1	A	3	ASN	3.0
1	A	480	THR	2.9
1	B	476	PRO	2.9
1	A	100	ARG	2.8
1	A	102	PRO	2.8
1	A	492	LEU	2.7
1	B	470	VAL	2.7
1	A	4	LYS	2.7
1	B	318	ASP	2.6
1	A	498	LEU	2.6
1	B	4	LYS	2.6
1	A	319	GLY	2.6
1	A	459	GLU	2.6
1	A	478	THR	2.5
1	A	302	LYS	2.5
1	B	163	GLN	2.5
1	B	482	LEU	2.4
1	B	254	MET	2.4
1	B	157	TRP	2.4
1	A	49	GLN	2.4
1	A	254	MET	2.3
1	B	491	GLY	2.3
1	A	499	THR	2.3
1	A	227	ASP	2.2
1	B	319	GLY	2.2
1	B	478	THR	2.2
1	B	119	TRP	2.2
1	A	93	LYS	2.1
1	A	157	TRP	2.1
1	A	484	ARG	2.1
1	A	458	PRO	2.1
1	A	321	GLU	2.1
1	B	303	GLU	2.0
1	A	244	ASN	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	RM1	B	1498	11/11	0.89	0.15	3.02	12,13,13,14	0
3	RM1	A	1503	11/11	0.93	0.13	2.09	12,13,14,14	0
2	FAD	A	1502	53/53	0.98	0.08	-0.52	6,7,8,9	0
2	FAD	B	1497	53/53	0.98	0.08	-0.72	6,7,8,9	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.