



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:06 PM GMT

PDB ID : 1S3E  
Title : Crystal structure of MAOB in complex with 6-hydroxy-N-propargyl-1(R)-aminoindan  
Authors : Binda, C.; Hubalek, F.; Li, M.; Herzig, Y.; Sterling, J.; Edmondson, D.E.; Mattevi, A.  
Deposited on : 2004-01-13  
Resolution : 1.60 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

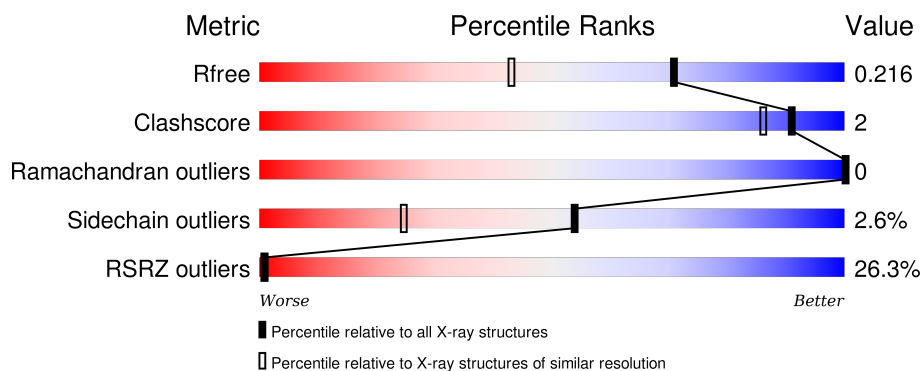
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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	
1	B	520	

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
2	RHP	A	601	-	-	-	X
2	RHP	B	601	-	-	-	X

## 2 Entry composition [i](#)

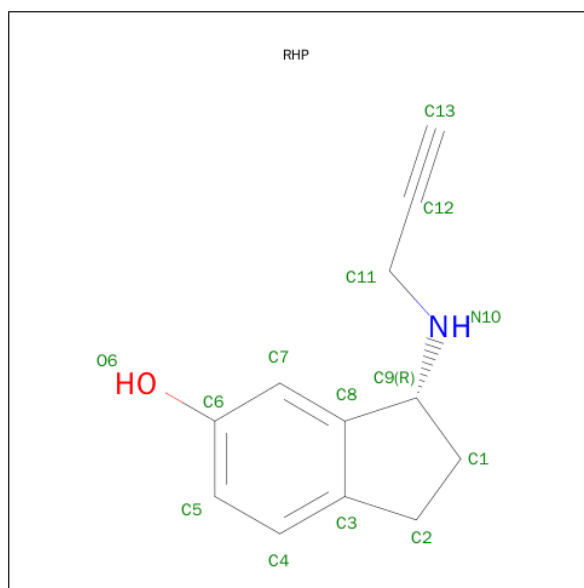
There are 3 unique types of molecules in this entry. The entry contains 8838 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	1	0
			3972	2538	681	728	25			
1	B	494	Total	C	N	O	S	0	1	0
			3941	2519	676	721	25			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: RHP, FAD) (formula:  $C_{12}H_{13}NO$ ,  $C_{27}H_{33}N_9O_{15}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	2	Total	C	N	O	P	0	0
			67	39	10	16	2		
2	B	2	Total	C	N	O	P	0	0
			67	39	10	16	2		

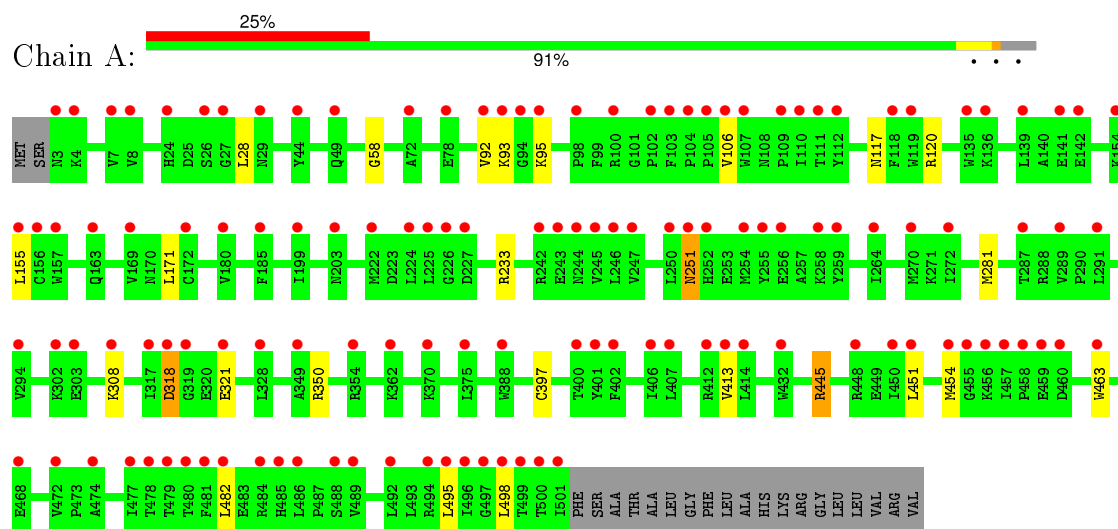
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	359	Total 359	O 359	0	0
3	B	432	Total 432	O 432	0	0

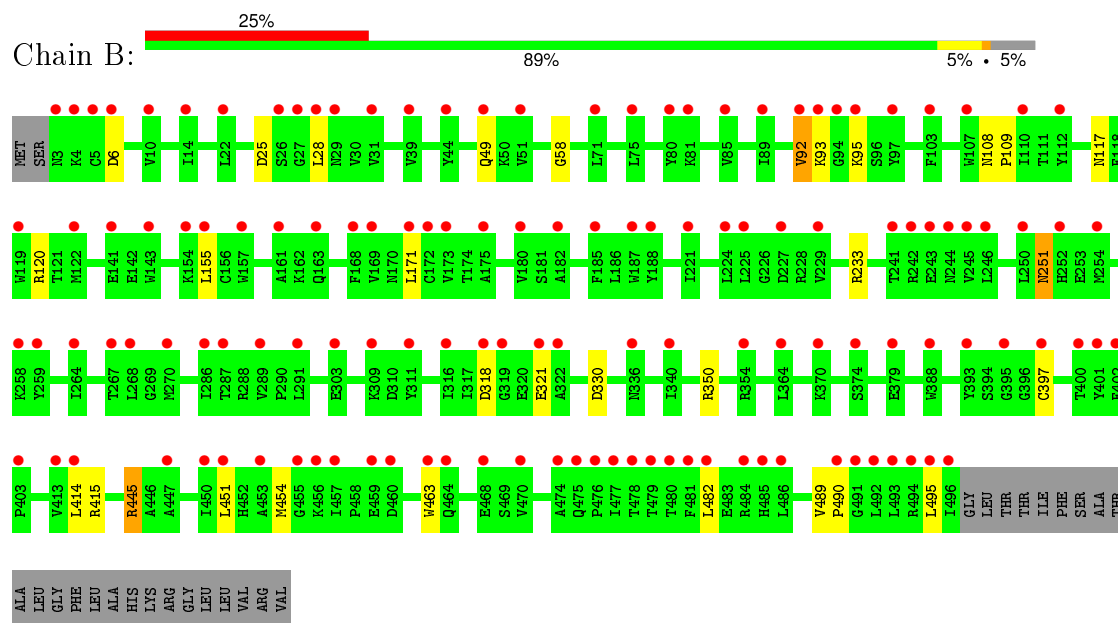
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: 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, $\alpha$ , $\beta$ , $\gamma$	131.96Å 224.06Å 86.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.60 47.04 – 1.60	Depositor EDS
% Data completeness (in resolution range)	88.6 (15.00-1.60) 88.6 (47.04-1.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.41 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.198 , 0.216 0.198 , 0.216	Depositor DCC
$R_{free}$ test set	3818 reflections (2.63%)	DCC
Wilson B-factor (Å <sup>2</sup> )	15.9	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 76.0	EDS
Estimated twinning fraction	0.009 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.011 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 149231 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8838	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: RHP, 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	0.36	0/4074	0.64	3/5530 (0.1%)
1	B	0.36	0/4043	0.64	4/5487 (0.1%)
All	All	0.36	0/8117	0.64	7/11017 (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	B	445	ARG	NE-CZ-NH2	-6.90	116.85	120.30
1	A	445	ARG	NE-CZ-NH2	-6.47	117.06	120.30
1	A	445	ARG	NE-CZ-NH1	5.83	123.22	120.30
1	B	445	ARG	NE-CZ-NH1	5.71	123.16	120.30
1	B	6	ASP	CB-CG-OD2	5.40	123.16	118.30
1	B	330	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	318	ASP	CB-CG-OD2	5.15	122.93	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	3972	0	3968	16	0
1	B	3941	0	3938	19	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	67	0	42	2	0
2	B	67	0	42	2	0
3	A	359	0	0	1	0
3	B	432	0	0	4	0
All	All	8838	0	7990	35	1

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 2.

All (35) 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:B:92:VAL:HB	3:B:1022:HOH:O	1.55	1.06
1:A:117:ASN:HD22	1:A:120:ARG:HH21	1.39	0.69
1:B:117:ASN:HD22	1:B:120:ARG:HH21	1.39	0.68
1:B:251:ASN:H	1:B:251:ASN:HD22	1.43	0.66
1:A:251:ASN:H	1:A:251:ASN:HD22	1.43	0.66
1:A:445:ARG:HD2	1:A:463:TRP:CH2	2.34	0.63
1:B:445:ARG:HD2	1:B:463:TRP:CH2	2.34	0.61
1:B:445:ARG:HD3	3:B:602:HOH:O	2.01	0.61
1:A:451:LEU:HD23	1:A:454:MET:HE1	1.83	0.58
1:B:451:LEU:HD23	1:B:454:MET:HE1	1.86	0.56
1:B:445:ARG:HD2	1:B:463:TRP:CZ2	2.42	0.54
1:B:233:ARG:HG3	1:B:251:ASN:HD21	1.73	0.53
1:A:445:ARG:HD3	3:A:628:HOH:O	2.09	0.52
1:A:445:ARG:HD2	1:A:463:TRP:CZ2	2.44	0.51
1:A:233:ARG:HG3	1:A:251:ASN:HD21	1.76	0.51
1:B:414:LEU:HD12	3:B:859:HOH:O	2.12	0.49
1:A:321:GLU:H	1:A:321:GLU:CD	2.20	0.46
1:B:321:GLU:CD	1:B:321:GLU:H	2.19	0.45
1:B:454:MET:HB2	1:B:454:MET:HE2	1.56	0.45
1:A:58:GLY:HA2	2:A:600:FAD:C4X	2.47	0.44
1:B:108:ASN:HA	1:B:109:PRO:HD3	1.88	0.44
1:A:171:LEU:HD21	2:A:601:RHP:H21	1.99	0.44
1:A:28:LEU:HD11	1:A:454:MET:HE1	2.00	0.43
1:A:308:LYS:HB2	1:A:308:LYS:HE2	1.78	0.43
1:A:251:ASN:H	1:A:251:ASN:ND2	2.15	0.43
1:B:171:LEU:HD21	2:B:601:RHP:H21	2.00	0.42
1:B:28:LEU:HD11	1:B:454:MET:HE1	2.02	0.42
1:A:117:ASN:HD22	1:A:120:ARG:NH2	2.11	0.42
1:B:58:GLY:HA2	2:B:600:FAD:C4X	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:ASN:HD22	1:B:120:ARG:NH2	2.13	0.41
1:B:415:ARG:NH1	3:B:897:HOH:O	2.52	0.41
1:B:251:ASN:H	1:B:251:ASN:ND2	2.15	0.41
1:A:454:MET:HB2	1:A:454:MET:HE2	1.57	0.41
1:B:489:VAL:N	1:B:490:PRO:HD2	2.36	0.41
1:A:281:MET:HB3	1:A:413:VAL:HG21	2.04	0.40

All (1) 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)
1:B:25:ASP:O	1:B:49:GLN:NE2[4_565]	1.59	0.61

## 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	498/520 (96%)	487 (98%)	11 (2%)	0	100	100
1	B	493/520 (95%)	481 (98%)	12 (2%)	0	100	100
All	All	991/1040 (95%)	968 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	428/444 (96%)	416 (97%)	12 (3%)	51	22
1	B	425/444 (96%)	415 (98%)	10 (2%)	57	27
All	All	853/888 (96%)	831 (97%)	22 (3%)	54	25

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	VAL
1	A	93	LYS
1	A	95	LYS
1	A	106	VAL
1	A	155	LEU
1	A	251	ASN
1	A	318	ASP
1	A	350	ARG
1	A	397	CYS
1	A	482	LEU
1	A	495	LEU
1	A	498	LEU
1	B	92	VAL
1	B	93	LYS
1	B	95	LYS
1	B	155	LEU
1	B	251	ASN
1	B	318	ASP
1	B	350	ARG
1	B	397	CYS
1	B	482	LEU
1	B	495	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 ⓘ

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 ⓘ

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	600	1,2	48,58,58	1.19	6 (12%)	54,89,89	2.03	5 (9%)
2	RHP	A	601	2	13,15,15	5.19	3 (23%)	18,20,20	12.47	4 (22%)
2	FAD	B	600	1,2	48,58,58	1.22	6 (12%)	54,89,89	2.06	9 (16%)
2	RHP	B	601	2	13,15,15	5.13	3 (23%)	18,20,20	12.46	4 (22%)

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	600	1,2	-	0/30/50/50	0/6/6/6
2	RHP	A	601	2	-	0/3/13/13	0/2/2/2
2	FAD	B	600	1,2	-	0/30/50/50	0/6/6/6
2	RHP	B	601	2	-	0/3/13/13	0/2/2/2

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	RHP	C11-N10	-15.07	1.29	1.46
2	B	601	RHP	C11-N10	-14.84	1.29	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600	FAD	C10-N1	2.05	1.39	1.35
2	A	600	FAD	C5X-N5	2.16	1.38	1.35
2	A	600	FAD	C2A-N1A	2.31	1.38	1.33
2	B	600	FAD	C2A-N1A	2.37	1.38	1.33
2	A	600	FAD	C1'-N10	2.43	1.51	1.48
2	B	600	FAD	C4-N3	2.57	1.37	1.33
2	A	600	FAD	C4-N3	2.63	1.38	1.33
2	B	600	FAD	C1'-N10	2.82	1.51	1.48
2	A	600	FAD	C2A-N3A	3.14	1.37	1.32
2	B	600	FAD	C2A-N3A	3.28	1.38	1.32
2	B	600	FAD	C4X-N5	3.97	1.39	1.33
2	A	600	FAD	C4X-N5	4.04	1.39	1.33
2	A	601	RHP	C12-C13	5.42	1.30	1.17
2	B	601	RHP	C12-C13	5.45	1.30	1.17
2	B	601	RHP	C11-C12	9.34	1.53	1.47
2	A	601	RHP	C11-C12	9.48	1.54	1.47

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	RHP	C11-C12-C13	-52.32	125.76	178.33
2	B	601	RHP	C11-C12-C13	-52.28	125.81	178.33
2	B	600	FAD	N3A-C2A-N1A	-11.31	120.23	128.89
2	A	600	FAD	N3A-C2A-N1A	-11.13	120.37	128.89
2	B	601	RHP	C5-C4-C3	-2.75	117.59	121.41
2	B	600	FAD	C4X-C4-N3	-2.67	119.93	123.59
2	A	600	FAD	C1B-N9A-C4A	-2.65	122.94	126.94
2	A	600	FAD	C4X-C4-N3	-2.58	120.06	123.59
2	B	600	FAD	C9A-C5X-N5	-2.56	118.58	122.36
2	A	601	RHP	C5-C4-C3	-2.55	117.86	121.41
2	B	600	FAD	C4A-C5A-N7A	-2.39	107.28	109.48
2	A	600	FAD	C9A-C5X-N5	-2.31	118.94	122.36
2	B	600	FAD	C1B-N9A-C4A	-2.29	123.49	126.94
2	B	600	FAD	C4X-C10-N10	-2.12	119.27	120.52
2	B	601	RHP	C3-C8-C9	2.26	112.50	110.47
2	A	601	RHP	C3-C8-C9	2.34	112.57	110.47
2	B	600	FAD	C4-C4X-N5	2.35	121.58	118.72
2	B	600	FAD	C4X-N5-C5X	2.42	119.55	116.76
2	B	601	RHP	C12-C11-N10	5.92	120.18	112.19
2	A	601	RHP	C12-C11-N10	6.15	120.50	112.19
2	A	600	FAD	C4-N3-C2	6.22	120.62	115.25
2	B	600	FAD	C4-N3-C2	6.45	120.83	115.25

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	600	FAD	1	0
2	A	601	RHP	1	0
2	B	600	FAD	1	0
2	B	601	RHP	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%)	1.57	129 (25%)	<b>1</b> <b>1</b>	28, 34, 51, 77	1 (0%)
1	B	494/520 (95%)	1.60	132 (26%)	<b>1</b> <b>1</b>	26, 34, 48, 69	1 (0%)
All	All	993/1040 (95%)	1.59	261 (26%)	<b>1</b> <b>1</b>	26, 34, 49, 77	2 (0%)

All (261) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	495	LEU	10.1
1	A	500	THR	9.7
1	A	499	THR	9.6
1	B	496	ILE	8.7
1	A	107	TRP	7.6
1	A	252	HIS	7.5
1	A	501	ILE	7.4
1	B	494	ARG	7.1
1	B	107	TRP	6.4
1	A	103	PHE	6.3
1	B	244	ASN	5.9
1	A	496	ILE	5.9
1	A	498	LEU	5.9
1	B	481	PHE	5.8
1	B	492	LEU	5.8
1	A	354	ARG	5.7
1	A	478	THR	5.6
1	A	246	LEU	5.6
1	A	479	THR	5.5
1	B	243	GLU	5.5
1	B	482	LEU	5.4
1	B	252	HIS	5.4
1	B	242	ARG	5.4
1	A	482	LEU	5.3

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Mol	Chain	Res	Type	RSRZ
1	A	480	THR	4.8
1	B	93	LYS	4.8
1	B	493	LEU	4.8
1	A	495	LEU	4.7
1	A	243	GLU	4.7
1	A	242	ARG	4.6
1	B	3	ASN	4.5
1	B	119	TRP	4.4
1	B	157	TRP	4.4
1	A	494	ARG	4.3
1	A	484	ARG	4.3
1	A	3	ASN	4.3
1	A	106	VAL	4.1
1	A	92	VAL	4.1
1	A	251	ASN	4.0
1	B	478	THR	3.9
1	A	49	GLN	3.9
1	B	459	GLU	3.8
1	B	303	GLU	3.8
1	B	95	LYS	3.8
1	A	105	PRO	3.8
1	B	491	GLY	3.8
1	B	457	ILE	3.7
1	A	451	LEU	3.7
1	A	110	ILE	3.7
1	B	103	PHE	3.7
1	B	354	ARG	3.7
1	A	93	LYS	3.6
1	B	490	PRO	3.6
1	A	226	GLY	3.6
1	B	414	LEU	3.6
1	A	4	LYS	3.6
1	B	5	CYS	3.6
1	B	453	ALA	3.5
1	A	227	ASP	3.5
1	A	112	TYR	3.5
1	B	27	GLY	3.4
1	A	302	LYS	3.3
1	B	110	ILE	3.3
1	A	459	GLU	3.3
1	B	49	GLN	3.3
1	B	254	MET	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	318	ASP	3.3
1	A	259	TYR	3.3
1	B	475	GLN	3.3
1	B	155	LEU	3.2
1	A	497	GLY	3.2
1	A	78	GLU	3.2
1	A	308	LYS	3.2
1	A	481	PHE	3.2
1	B	92	VAL	3.2
1	B	289	VAL	3.2
1	B	450	ILE	3.2
1	A	102	PRO	3.1
1	B	485	HIS	3.1
1	A	458	PRO	3.1
1	A	163	GLN	3.1
1	A	245	VAL	3.1
1	A	100	ARG	3.1
1	A	321	GLU	3.1
1	A	457	ILE	3.0
1	A	486	LEU	3.0
1	A	454	MET	3.0
1	A	119	TRP	3.0
1	A	460	ASP	3.0
1	B	477	ILE	3.0
1	A	224	LEU	3.0
1	A	406	ILE	3.0
1	B	479	THR	3.0
1	B	224	LEU	3.0
1	B	270	MET	3.0
1	B	267	THR	3.0
1	B	229	VAL	3.0
1	A	26	SER	3.0
1	B	112	TYR	2.9
1	B	393	TYR	2.9
1	B	318	ASP	2.9
1	A	169	VAL	2.9
1	B	245	VAL	2.9
1	B	246	LEU	2.8
1	B	264	ILE	2.8
1	A	142	GLU	2.8
1	B	28	LEU	2.8
1	B	319	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	256	GLU	2.8
1	A	468	GLU	2.8
1	A	104	PRO	2.8
1	A	157	TRP	2.8
1	B	4	LYS	2.8
1	B	268	LEU	2.8
1	A	319	GLY	2.7
1	A	29	ASN	2.7
1	A	264	ILE	2.7
1	B	241	THR	2.7
1	B	476	PRO	2.7
1	B	225	LEU	2.7
1	A	118	PHE	2.7
1	A	349	ALA	2.7
1	B	29	ASN	2.7
1	B	468	GLU	2.7
1	A	270	MET	2.7
1	B	97	TYR	2.7
1	A	244	ASN	2.7
1	B	480	THR	2.6
1	A	456	LYS	2.6
1	A	94	GLY	2.6
1	A	72	ALA	2.6
1	B	484	ARG	2.6
1	B	321	GLU	2.6
1	A	489	VAL	2.6
1	B	85	VAL	2.6
1	A	272	ILE	2.6
1	B	221	ILE	2.6
1	B	175	ALA	2.5
1	B	470	VAL	2.5
1	A	250	LEU	2.5
1	A	414	LEU	2.5
1	B	259	TYR	2.5
1	B	397	CYS	2.5
1	A	413	VAL	2.5
1	B	31	VAL	2.5
1	A	463	TRP	2.5
1	A	141	GLU	2.5
1	B	89	ILE	2.5
1	B	168	PHE	2.5
1	B	122	MET	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	474	ALA	2.5
1	B	75	LEU	2.5
1	B	340	ILE	2.5
1	B	44	TYR	2.5
1	A	474	ALA	2.5
1	B	39	VAL	2.5
1	A	136	LYS	2.5
1	A	407	LEU	2.5
1	B	370	LYS	2.5
1	B	163	GLN	2.5
1	A	154	LYS	2.4
1	A	24	HIS	2.4
1	B	182	ALA	2.4
1	B	291	LEU	2.4
1	B	464	GLN	2.4
1	A	109	PRO	2.4
1	B	169	VAL	2.4
1	A	155	LEU	2.4
1	B	171	LEU	2.4
1	B	486	LEU	2.4
1	A	402	PHE	2.4
1	B	188	TYR	2.4
1	B	402	PHE	2.4
1	B	141	GLU	2.4
1	B	463	TRP	2.4
1	A	27	GLY	2.4
1	A	488	SER	2.4
1	A	492	LEU	2.4
1	A	258	LYS	2.4
1	B	364	LEU	2.3
1	A	254	MET	2.3
1	A	317	ILE	2.3
1	B	286	ILE	2.3
1	A	455	GLY	2.3
1	A	472	VAL	2.3
1	B	173	VAL	2.3
1	B	403	PRO	2.3
1	A	370	LYS	2.3
1	A	450	ILE	2.3
1	B	311	TYR	2.3
1	B	447	ALA	2.3
1	A	135	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	227	ASP	2.3
1	B	185	PHE	2.3
1	A	8	VAL	2.3
1	A	95	LYS	2.3
1	B	51	VAL	2.3
1	B	180	VAL	2.3
1	B	451	LEU	2.2
1	B	14	ILE	2.2
1	B	143	TRP	2.2
1	B	258	LYS	2.2
1	B	374	SER	2.2
1	B	71	LEU	2.2
1	A	412	ARG	2.2
1	A	485	HIS	2.2
1	A	247	VAL	2.2
1	A	111	THR	2.2
1	A	185	PHE	2.2
1	B	287	THR	2.2
1	A	225	LEU	2.2
1	A	401	TYR	2.2
1	A	432	TRP	2.2
1	A	180	VAL	2.2
1	B	413	VAL	2.2
1	B	455	GLY	2.2
1	A	303	GLU	2.2
1	A	98	PRO	2.2
1	A	255	TYR	2.2
1	A	388	TRP	2.1
1	A	291	LEU	2.1
1	A	287	THR	2.1
1	A	289	VAL	2.1
1	B	81	LYS	2.1
1	B	309	LYS	2.1
1	A	400	THR	2.1
1	A	362	LYS	2.1
1	A	7	VAL	2.1
1	B	10	VAL	2.1
1	A	44	TYR	2.1
1	B	94	GLY	2.1
1	B	395	GLY	2.1
1	B	400	THR	2.1
1	B	187	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	22	LEU	2.1
1	B	26	SER	2.1
1	B	316	ILE	2.1
1	A	156	CYS	2.1
1	B	172[A]	CYS	2.1
1	B	6	ASP	2.1
1	A	203	ASN	2.1
1	A	139	LEU	2.1
1	A	328	LEU	2.1
1	B	379	GLU	2.1
1	A	172[A]	CYS	2.0
1	A	294	VAL	2.0
1	B	80	TYR	2.0
1	B	401	TYR	2.0
1	B	161	ALA	2.0
1	B	322	ALA	2.0
1	A	375	LEU	2.0
1	B	154	LYS	2.0
1	B	250	LEU	2.0
1	B	388	TRP	2.0
1	A	199	ILE	2.0
1	A	477	ILE	2.0
1	B	456	LYS	2.0
1	A	448	ARG	2.0
1	B	336	ASN	2.0
1	A	222	MET	2.0
1	B	460	ASP	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(Å <sup>2</sup> )	Q<0.9
2	RHP	B	601	14/14	0.68	0.24	5.07	38,44,45,46	0
2	RHP	A	601	14/14	0.78	0.20	3.66	38,44,45,46	0
2	FAD	A	600	53/53	0.91	0.14	-0.37	27,29,31,31	0
2	FAD	B	600	53/53	0.94	0.14	-1.00	27,29,31,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.