



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:54 AM GMT

PDB ID : 3NHR
Title : X-ray Crystallographic Structure Activity Relationship (SAR) of Casimiroin and its Analogs Bound to Human Quinone Reductase 2
Authors : Sturdy, M.
Deposited on : 2010-06-14
Resolution : 1.80 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

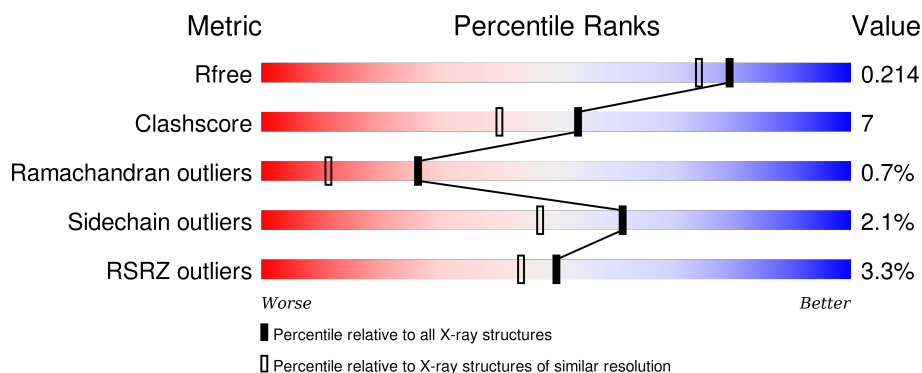
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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 ≥ 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	230	<div> <div>4%</div> <div>80%</div> <div>18%</div> <div>•</div> </div>
1	B	230	<div> <div>2%</div> <div>87%</div> <div>13%</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
4	RZW	A	234[A]	-	-	-	X
4	RZW	A	234[B]	-	-	-	X
4	RZW	B	233	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4214 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.

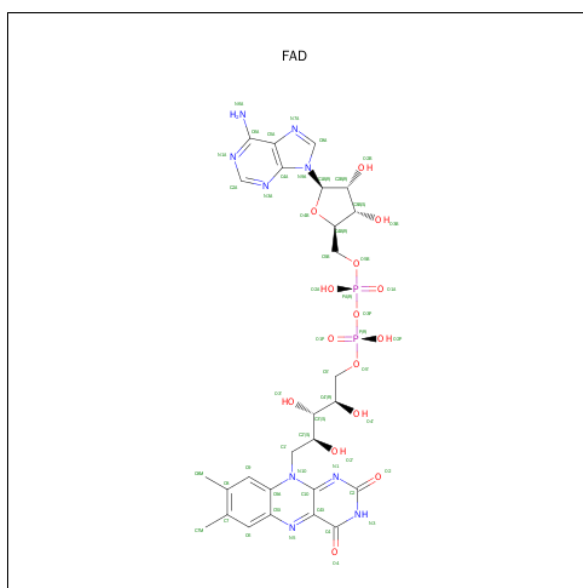
- Molecule 1 is a protein called Ribosyldihydronicotinamide dehydrogenase [quinone].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	229	Total	C	N	O	S	0	0	0
			1819	1171	303	337	8			
1	B	230	Total	C	N	O	S	0	1	0
			1833	1179	305	341	8			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

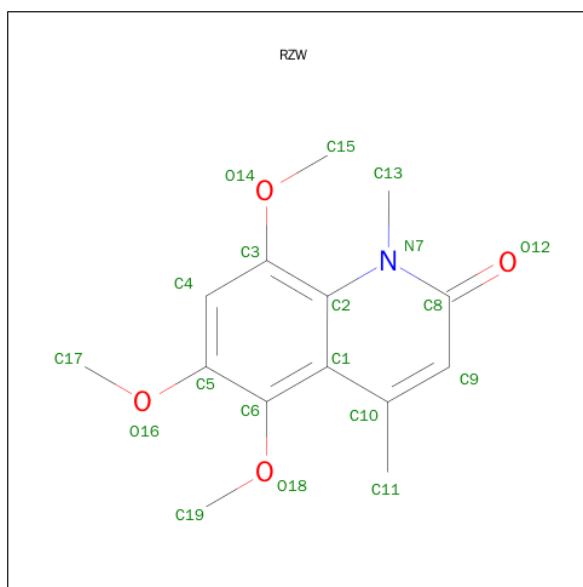
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- 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 5,6,8-TRIMETHOXY-1,4-DIMETHYLQUINOLIN-2(1H)-ONE (three-letter code: RZW) (formula: C₁₄H₁₇NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			19	14	1	4		
4	A	1	Total	C	N	O	0	1
			38	28	2	8		
4	B	1	Total	C	N	O	0	0
			19	14	1	4		

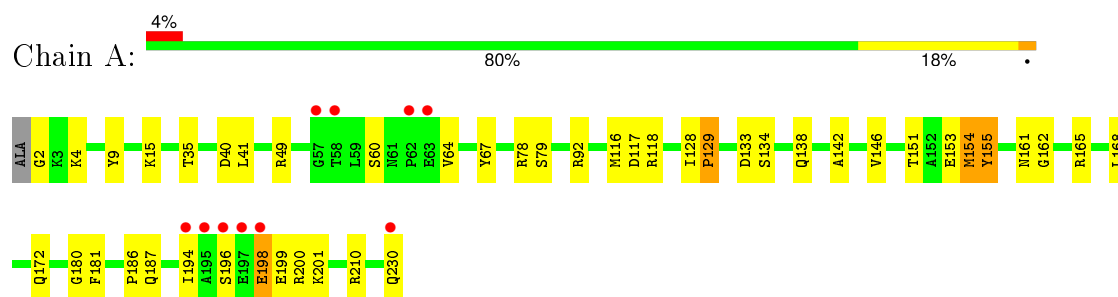
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	176	Total	O	0	0
			176	176		
5	B	202	Total	O	0	0
			202	202		

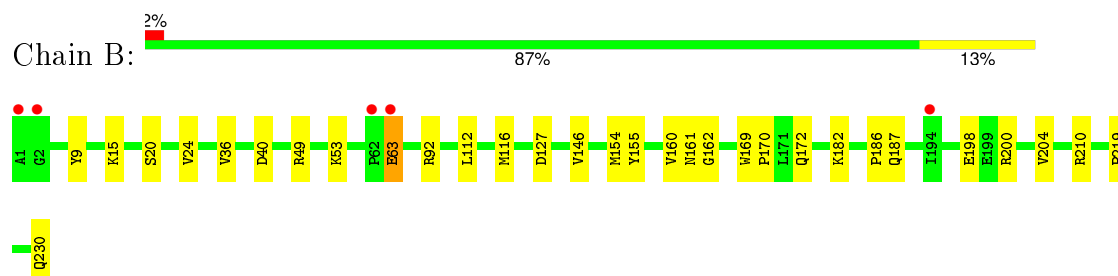
3 Residue-property plots

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: Ribosyldihyronicotinamide dehydrogenase [quinone]



- Molecule 1: Ribosyldihyronicotinamide dehydrogenase [quinone]



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.78 Å 83.61 Å 106.63 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.80 44.95 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.5 (50.00-1.80) 98.6 (44.95-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.65 (at 1.79 Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.179 , 0.215 0.178 , 0.214	Depositor DCC
R_{free} test set	2392 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	15.7	Xtriage
Anisotropy	0.701	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 47242 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4214	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: RZW, ZN, 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	1.35	4/1869 (0.2%)	1.12	13/2535 (0.5%)
1	B	1.32	4/1883 (0.2%)	1.12	8/2554 (0.3%)
All	All	1.34	8/3752 (0.2%)	1.12	21/5089 (0.4%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	146	VAL	CB-CG2	-6.35	1.39	1.52
1	A	155	TYR	CD1-CE1	5.95	1.48	1.39
1	B	63	GLU	CG-CD	5.41	1.60	1.51
1	A	153	GLU	CG-CD	5.40	1.60	1.51
1	A	67	TYR	CD1-CE1	5.23	1.47	1.39
1	B	36	VAL	CB-CG2	5.04	1.63	1.52
1	B	9	TYR	CE1-CZ	5.02	1.45	1.38
1	A	9	TYR	CG-CD2	5.01	1.45	1.39

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	49	ARG	NE-CZ-NH1	10.95	125.77	120.30
1	B	116	MET	CG-SD-CE	-8.92	85.93	100.20
1	B	49	ARG	NE-CZ-NH2	-8.50	116.05	120.30
1	B	127	ASP	CB-CG-OD2	-8.36	110.77	118.30
1	A	117	ASP	CB-CG-OD1	7.11	124.70	118.30
1	A	78	ARG	NE-CZ-NH1	6.77	123.69	120.30
1	A	118	ARG	NE-CZ-NH2	-6.71	116.94	120.30
1	A	116	MET	CG-SD-CE	-6.61	89.63	100.20
1	B	40	ASP	CB-CG-OD1	6.46	124.12	118.30
1	A	146	VAL	CB-CA-C	-6.05	99.91	111.40
1	A	92	ARG	NE-CZ-NH2	-5.98	117.31	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	41	LEU	CB-CG-CD1	-5.81	101.12	111.00
1	A	40	ASP	CB-CG-OD2	-5.68	113.19	118.30
1	B	112	LEU	CB-CG-CD2	-5.66	101.38	111.00
1	A	78	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	A	92	ARG	NE-CZ-NH1	5.57	123.09	120.30
1	A	40	ASP	CB-CG-OD1	5.50	123.25	118.30
1	A	154	MET	CG-SD-CE	5.50	109.00	100.20
1	A	49	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	B	154	MET	CG-SD-CE	-5.21	91.87	100.20
1	B	40	ASP	CB-CG-OD2	-5.20	113.62	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	1819	0	1771	26	0
1	B	1833	0	1784	13	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	53	0	31	6	0
3	B	53	0	31	2	0
4	A	57	0	51	11	0
4	B	19	0	17	7	0
5	A	176	0	0	3	0
5	B	202	0	0	1	0
All	All	4214	0	3685	49	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 7.

All (49) 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:24:VAL:HG11	1:B:204:VAL:CG1	2.24	0.68
1:A:196:SER:O	1:A:198:GLU:O	2.10	0.67
1:A:187:GLN:HE21	1:A:210:ARG:HH11	1.43	0.66
1:A:198:GLU:O	1:A:200:ARG:N	2.29	0.66
1:A:2:GLY:N	5:A:377:HOH:O	2.29	0.65
1:B:20:SER:O	1:B:24:VAL:HG13	1.97	0.64
1:A:172:GLN:HE22	1:A:186:PRO:HD3	1.67	0.60
1:A:187:GLN:NE2	1:A:210:ARG:HH11	2.00	0.59
1:A:128:ILE:HD11	4:A:234[A]:RZW:C2	2.34	0.57
4:A:234[B]:RZW:O14	4:A:234[B]:RZW:C13	2.54	0.55
4:B:233:RZW:C13	4:B:233:RZW:O14	2.55	0.55
1:A:161:ASN:HD21	4:A:233:RZW:H13	1.73	0.53
1:A:200:ARG:HB3	3:A:232:FAD:H2A	1.90	0.53
1:A:200:ARG:HD2	3:A:232:FAD:N3A	2.23	0.53
1:A:155:TYR:HA	1:A:162:GLY:O	2.08	0.53
4:A:233:RZW:O14	4:A:233:RZW:C13	2.56	0.53
1:A:15:LYS:O	3:A:232:FAD:H8A	2.09	0.53
1:B:155:TYR:HA	1:B:162:GLY:O	2.09	0.52
1:A:134:SER:O	5:A:375:HOH:O	2.18	0.52
1:B:169:TRP:HB3	1:B:170:PRO:HD3	1.92	0.52
1:B:161:ASN:ND2	4:B:233:RZW:H13	2.26	0.51
4:A:234[B]:RZW:H19B	4:A:234[B]:RZW:O16	2.12	0.50
4:A:234[A]:RZW:O14	4:A:234[A]:RZW:C13	2.58	0.50
1:B:161:ASN:HD21	4:B:233:RZW:H13	1.78	0.48
3:A:232:FAD:HM72	5:B:389:HOH:O	2.14	0.47
1:A:161:ASN:ND2	4:A:233:RZW:H13	2.28	0.47
1:B:187:GLN:HE21	1:B:210:ARG:HH11	1.62	0.47
4:A:234[A]:RZW:H17A	4:B:233:RZW:H9	1.96	0.47
1:A:64:VAL:HG22	1:B:15:LYS:HD3	1.97	0.47
1:A:165:ARG:HA	1:A:168:LEU:HD12	1.97	0.46
1:A:151:THR:OG1	1:A:154:MET:HG3	2.16	0.46
1:A:138:GLN:HA	1:A:180:GLY:O	2.16	0.46
1:A:187:GLN:HE21	1:A:210:ARG:NH1	2.13	0.45
1:B:24:VAL:HG11	1:B:204:VAL:HG13	1.97	0.45
3:A:232:FAD:O4	4:A:233:RZW:H15A	2.16	0.45
4:A:234[B]:RZW:H11B	4:B:233:RZW:H19A	2.00	0.43
1:A:128:ILE:HA	1:A:129:PRO:HA	1.65	0.43
4:B:233:RZW:C11	4:B:233:RZW:O18	2.66	0.43
1:A:142:ALA:HB2	1:A:181:PHE:CD1	2.53	0.43
1:B:182:LYS:HD2	1:B:219:PRO:HG3	1.99	0.43
1:B:172:GLN:HE22	1:B:186:PRO:HD3	1.84	0.42
1:A:133:ASP:HB2	5:A:296:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:LYS:HG2	1:A:35:THR:HB	2.02	0.42
1:A:200:ARG:HB3	3:A:232:FAD:C2A	2.49	0.41
1:A:151:THR:HG22	1:A:194:ILE:HD11	2.02	0.41
1:A:128:ILE:HG23	1:A:128:ILE:HD12	1.77	0.41
4:A:234[B]:RZW:H15A	4:B:233:RZW:H9	2.02	0.41
1:B:200:ARG:HD2	3:B:231:FAD:O4B	2.22	0.40
1:B:200:ARG:CD	3:B:231:FAD:O4B	2.69	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:92:ARG:NH1	1:B:230:GLN:OE1[3_554]	1.84	0.36

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	227/230 (99%)	217 (96%)	7 (3%)	3 (1%)	15	4
1	B	229/230 (100%)	219 (96%)	10 (4%)	0	100	100
All	All	456/460 (99%)	436 (96%)	17 (4%)	3 (1%)	26	11

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	198	GLU
1	A	199	GLU
1	A	129	PRO

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	194/194 (100%)	190 (98%)	4 (2%)	61	47
1	B	195/194 (100%)	191 (98%)	4 (2%)	61	47
All	All	389/388 (100%)	381 (98%)	8 (2%)	61	47

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	SER
1	A	79	SER
1	A	201	LYS
1	A	230	GLN
1	B	53	LYS
1	B	63	GLU
1	B	160	VAL
1	B	198	GLU

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	45	ASN
1	A	138	GLN
1	A	172	GLN
1	A	187	GLN
1	A	212	GLN
1	B	172	GLN
1	B	187	GLN

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 ⓘ

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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$
3	FAD	A	232	-	48,58,58	1.51	8 (16%)	54,89,89	2.60	12 (22%)
4	RZW	A	233	-	17,20,20	1.66	4 (23%)	21,29,29	2.14	8 (38%)
4	RZW	A	234[A]	-	17,20,20	2.13	5 (29%)	21,29,29	1.47	3 (14%)
4	RZW	A	234[B]	-	17,20,20	2.11	5 (29%)	21,29,29	1.29	3 (14%)
3	FAD	B	231	-	48,58,58	1.49	7 (14%)	54,89,89	2.44	14 (25%)
4	RZW	B	233	-	17,20,20	1.48	3 (17%)	21,29,29	1.92	4 (19%)

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	FAD	A	232	-	-	0/30/50/50	0/6/6/6
4	RZW	A	233	-	-	0/6/6/6	0/2/2/2
4	RZW	A	234[A]	-	-	0/6/6/6	0/2/2/2
4	RZW	A	234[B]	-	-	0/6/6/6	0/2/2/2
3	FAD	B	231	-	-	0/30/50/50	0/6/6/6
4	RZW	B	233	-	-	0/6/6/6	0/2/2/2

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	232	FAD	C9A-N10	2.00	1.41	1.38
4	A	234[A]	RZW	C8-N7	2.02	1.41	1.38
3	A	232	FAD	O4B-C1B	2.04	1.43	1.41
4	B	233	RZW	C6-C1	2.06	1.47	1.43
3	B	231	FAD	C9A-N10	2.07	1.41	1.38
4	A	233	RZW	C6-C1	2.11	1.47	1.43
3	B	231	FAD	C2A-N1A	2.27	1.38	1.33
3	A	232	FAD	C2A-N1A	2.29	1.38	1.33
4	B	233	RZW	C3-C2	2.37	1.46	1.42
4	A	234[B]	RZW	C10-C1	2.48	1.48	1.44
4	A	233	RZW	C10-C1	2.86	1.49	1.44
4	A	234[B]	RZW	C6-C1	2.91	1.49	1.43
3	B	231	FAD	C10-N1	2.92	1.40	1.35
3	B	231	FAD	C4X-N5	2.98	1.38	1.33
4	A	233	RZW	C5-C6	3.07	1.45	1.38
3	A	232	FAD	C10-N1	3.09	1.40	1.35
3	A	232	FAD	C4X-N5	3.12	1.38	1.33
4	A	234[A]	RZW	C10-C1	3.22	1.50	1.44
4	A	234[B]	RZW	C8-N7	3.25	1.43	1.38
3	B	231	FAD	C5'-C4'	3.30	1.56	1.51
4	A	234[A]	RZW	C6-C1	3.39	1.50	1.43
3	A	232	FAD	C4-N3	3.77	1.40	1.33
3	A	232	FAD	C1'-N10	3.82	1.52	1.48
3	A	232	FAD	C2A-N3A	3.96	1.39	1.32
3	B	231	FAD	C2A-N3A	4.06	1.39	1.32
4	B	233	RZW	C5-C6	4.16	1.47	1.38
4	A	233	RZW	C3-C2	4.27	1.48	1.42
4	A	234[B]	RZW	C3-C2	4.38	1.49	1.42
4	A	234[A]	RZW	C5-C6	4.71	1.48	1.38
4	A	234[B]	RZW	C5-C6	4.88	1.49	1.38
3	B	231	FAD	C4-N3	5.08	1.42	1.33
4	A	234[A]	RZW	C3-C2	5.13	1.50	1.42

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	232	FAD	N3A-C2A-N1A	-13.21	118.78	128.89
3	B	231	FAD	N3A-C2A-N1A	-11.79	119.87	128.89
3	A	232	FAD	C4X-C4-N3	-4.41	117.56	123.59
4	B	233	RZW	C8-N7-C2	-4.41	117.66	121.75
3	B	231	FAD	C4A-C5A-N7A	-3.60	106.17	109.48
4	A	233	RZW	C8-N7-C2	-3.14	118.83	121.75
3	A	232	FAD	O3'-C3'-C2'	-2.90	101.45	108.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	231	FAD	C4X-C4-N3	-2.86	119.68	123.59
3	B	231	FAD	C7-C6-C5X	-2.84	116.29	120.92
3	B	231	FAD	O4'-C4'-C3'	-2.71	102.21	109.02
3	B	231	FAD	O3P-P-O5'	-2.58	96.08	102.94
3	B	231	FAD	C2B-C1B-N9A	-2.53	110.43	114.29
4	A	234[A]	RZW	O16-C5-C4	-2.50	119.93	124.21
4	A	234[A]	RZW	O14-C3-C4	-2.41	119.79	123.60
4	A	233	RZW	O16-C5-C4	-2.37	120.16	124.21
3	A	232	FAD	C4A-C5A-N7A	-2.29	107.37	109.48
3	A	232	FAD	C4-C4X-C10	-2.22	118.52	119.94
3	A	232	FAD	C1B-N9A-C4A	-2.21	123.60	126.94
4	A	234[B]	RZW	C11-C10-C1	-2.15	119.54	124.25
3	B	231	FAD	C1'-C2'-C3'	-2.12	103.75	109.82
4	A	233	RZW	C4-C3-C2	-2.12	117.42	120.16
3	A	232	FAD	O3P-PA-O5B	-2.05	97.51	102.94
3	B	231	FAD	C1'-N10-C9A	2.04	121.15	118.86
3	B	231	FAD	C6-C5X-C9A	2.16	121.82	118.98
4	A	233	RZW	C4-C5-C6	2.21	123.88	120.55
4	A	233	RZW	C3-C2-C1	2.21	122.26	118.38
4	A	234[B]	RZW	O14-C3-C2	2.22	119.01	115.46
3	A	232	FAD	C4-C4X-N5	2.56	121.82	118.72
3	A	232	FAD	C4X-N5-C5X	2.84	120.03	116.76
3	A	232	FAD	O2A-PA-O3P	2.84	118.00	105.09
3	B	231	FAD	C4X-C10-N10	2.86	122.20	120.52
4	A	234[B]	RZW	C17-O16-C5	2.89	121.93	117.54
4	A	234[A]	RZW	O14-C3-C2	2.97	120.22	115.46
3	A	232	FAD	C2B-C1B-N9A	3.11	119.05	114.29
4	B	233	RZW	C9-C8-N7	3.17	124.77	119.75
3	B	231	FAD	C5X-C9A-N10	3.33	120.15	117.62
4	A	233	RZW	C13-N7-C2	3.50	122.89	118.11
4	A	233	RZW	C9-C8-N7	3.54	125.35	119.75
4	B	233	RZW	C13-N7-C2	3.96	123.52	118.11
4	B	233	RZW	C15-O14-C3	4.06	123.72	117.77
3	B	231	FAD	C4-N3-C2	5.27	119.80	115.25
4	A	233	RZW	C15-O14-C3	5.52	125.85	117.77
3	B	231	FAD	O4B-C1B-N9A	5.69	120.00	108.10
3	A	232	FAD	C4-N3-C2	8.64	122.72	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	232	FAD	6	0
4	A	233	RZW	4	0
4	A	234[A]	RZW	3	0
4	A	234[B]	RZW	4	0
3	B	231	FAD	2	0
4	B	233	RZW	7	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, 95th 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 ²)	Q < 0.9
1	A	229/230 (99%)	0.13	10 (4%) 38 32	5, 18, 39, 58	0
1	B	230/230 (100%)	-0.16	5 (2%) 65 60	5, 14, 36, 51	0
All	All	459/460 (99%)	-0.02	15 (3%) 50 44	5, 16, 38, 58	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	ALA	6.5
1	A	57	GLY	5.0
1	A	230	GLN	3.7
1	A	63	GLU	3.6
1	B	63	GLU	3.2
1	A	196	SER	3.1
1	A	197	GLU	3.0
1	B	2	GLY	3.0
1	A	194	ILE	2.9
1	A	198	GLU	2.9
1	A	62	PRO	2.5
1	A	58	THR	2.5
1	A	195	ALA	2.4
1	B	62	PRO	2.2
1	B	194	ILE	2.1

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

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, 95th 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 ²)	Q<0.9
4	RZW	A	234[B]	19/19	0.89	0.21	2.72	22,27,30,33	19
4	RZW	A	234[A]	19/19	0.89	0.21	2.61	61,63,64,65	19
3	FAD	B	231	53/53	0.92	0.14	0.60	8,15,49,52	0
3	FAD	A	232	53/53	0.91	0.15	0.47	7,19,64,65	0
4	RZW	A	233	19/19	0.94	0.10	-0.24	12,22,26,31	0
4	RZW	B	233	19/19	0.97	0.08	-0.56	11,16,21,23	0
2	ZN	B	232	1/1	0.99	0.06	-7.70	15,15,15,15	0
2	ZN	A	231	1/1	0.97	0.06	-	21,21,21,21	0

6.5 Other polymers

There are no such residues in this entry.