



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2017 – 04:05 AM EDT

PDB ID : 2C4C  
Title : Crystal structure of the NADPH-treated monooxygenase domain of MICAL  
Authors : Siebold, C.; Berrow, N.; Walter, T.S.; Harlos, K.; Owens, R.J.; Terman, J.R.;  
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Deposited on : 2005-10-18  
Resolution : 2.90 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 : rb-20029077  
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) : rb-20029077

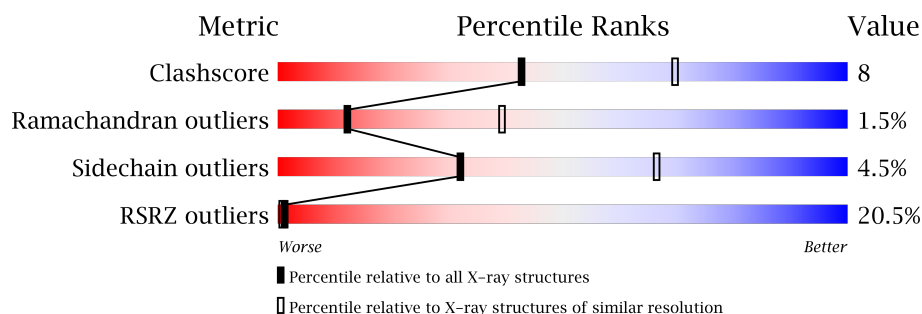
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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	497	<div> <div>19%</div> <div> <div></div> <div>77%</div> <div>16%</div> <div>• •</div> </div> </div>
1	B	497	<div> <div>20%</div> <div> <div></div> <div>78%</div> <div>16%</div> <div>• •</div> </div> </div>

## 2 Entry composition [i](#)

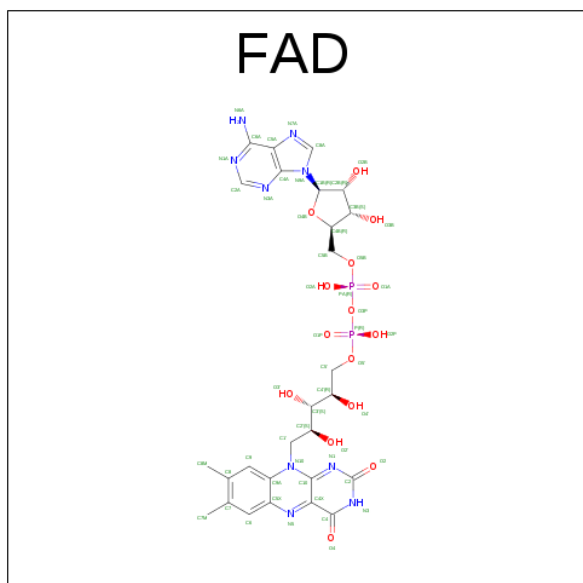
There are 4 unique types of molecules in this entry. The entry contains 7620 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NEDD9-INTERACTING PROTEIN WITH CALPONIN HO- MOLOGY AND LIM DOMAINS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3719	2374	665	664	16			
1	B	477	Total	C	N	O	S	0	0	0
			3723	2376	666	665	16			

- 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	1
			83	44	13	23	3		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Cl 1	0	0
3	A	1	Total 1	Cl 1	0	0

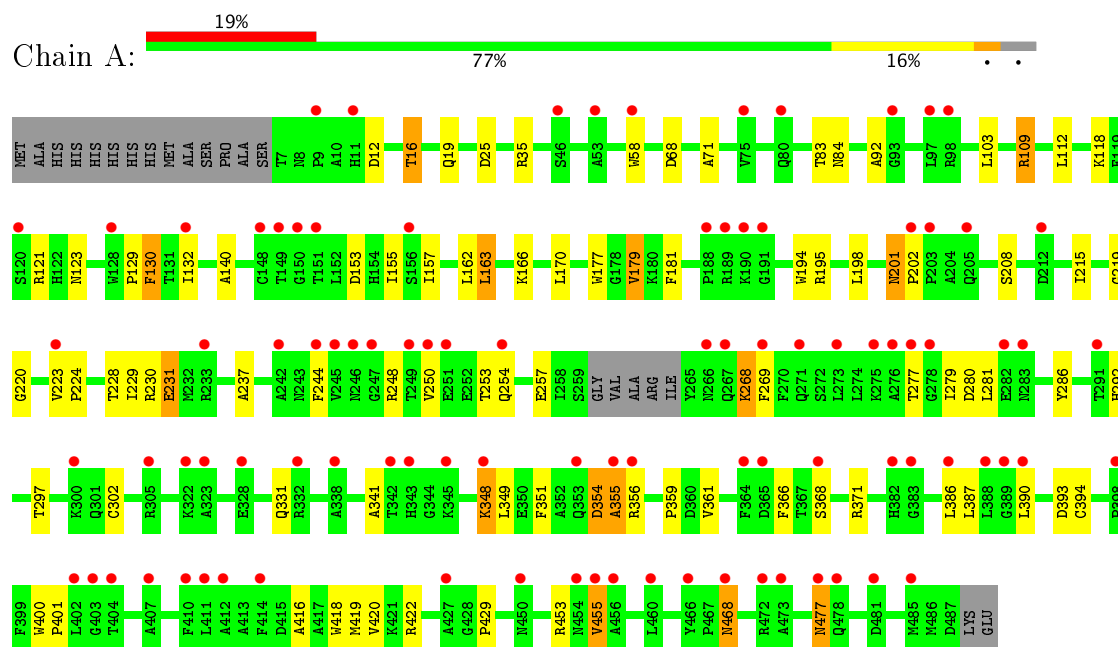
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	21	Total 21	O 21	0	0
4	B	19	Total 19	O 19	0	0

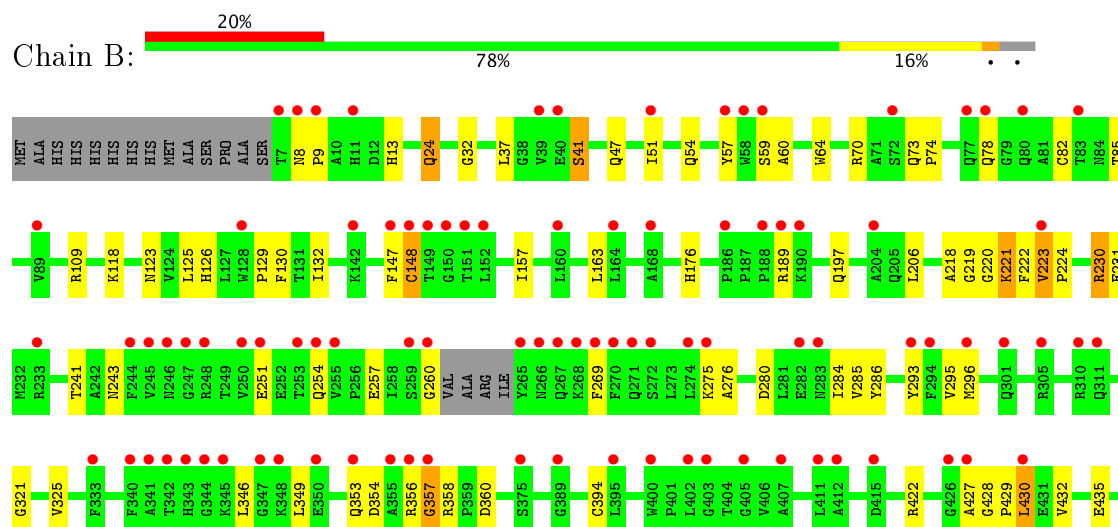
### 3 Residue-property plots

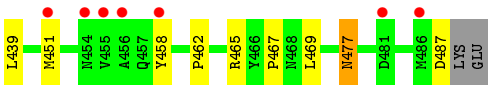
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 ( $RSRZ > 2$ ). 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: NEDD9-INTERACTING PROTEIN WITH CALPONIN HOMOLGY AND LIM DOMAINS



#### • Molecule 1: NEDD9-INTERACTING PROTEIN WITH CALPONIN HOMOLGY AND LIM DOMAINS





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.71Å 89.92Å 83.57Å 90.00° 113.82° 90.00°	Depositor
Resolution (Å)	30.00 – 2.90 25.48 – 2.68	Depositor EDS
% Data completeness (in resolution range)	99.3 (30.00-2.90) 98.5 (25.48-2.68)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.68Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.243 , 0.294 0.234 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	53.8	Xtriage
Anisotropy	0.340	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 78.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	7620	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.15% 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: FAD, CL

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	0.33	0/3801	0.52	0/5146
1	B	0.33	0/3805	0.51	0/5151
All	All	0.33	0/7606	0.51	0/10297

There are no bond length outliers.

There are no bond angle outliers.

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	3719	0	3740	63	0
1	B	3723	0	3743	54	0
2	A	53	0	31	3	0
2	B	83	0	38	7	0
3	A	1	0	0	1	0
3	B	1	0	0	0	0
4	A	21	0	0	1	0
4	B	19	0	0	0	0
All	All	7620	0	7552	118	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 (118) 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:220:GLY:HA3	1:B:221:LYS:HB2	1.35	1.08
1:A:354:ASP:HB3	1:A:355:ALA:HB3	1.06	1.05
1:A:354:ASP:HB3	1:A:355:ALA:CB	1.86	1.05
1:B:222:PHE:HA	1:B:223:VAL:HB	1.48	0.93
1:A:354:ASP:CB	1:A:355:ALA:HB3	1.97	0.93
1:B:220:GLY:CA	1:B:221:LYS:HB2	2.11	0.80
1:A:354:ASP:HB2	1:A:356:ARG:N	2.04	0.72
1:B:220:GLY:HA3	1:B:221:LYS:CB	2.18	0.72
1:A:354:ASP:HB2	1:A:356:ARG:H	1.52	0.71
1:B:284:ILE:HG13	1:B:296:MET:HB3	1.74	0.68
1:B:123:ASN:HB3	2:B:600[B]:FAD:O4	1.94	0.68
1:A:230:ARG:HH12	1:A:371:ARG:HD2	1.61	0.64
1:A:269:PHE:HZ	1:A:341:ALA:HA	1.63	0.63
1:A:331:GLN:OE1	1:A:359:PRO:HG3	1.99	0.63
2:B:600[A]:FAD:H9	2:B:600[A]:FAD:O2'	1.98	0.63
1:A:250:VAL:O	1:A:254:GLN:HG2	2.00	0.60
1:A:400:TRP:N	1:A:401:PRO:HD2	2.15	0.60
1:B:222:PHE:HA	1:B:223:VAL:CB	2.25	0.60
1:A:123:ASN:O	1:A:157:ILE:HG13	2.02	0.59
1:A:132:ILE:HD11	1:A:153:ASP:HB2	1.84	0.59
1:A:166:LYS:O	1:A:170:LEU:HG	2.03	0.58
1:A:351:PHE:HE1	1:A:361:VAL:HB	1.69	0.58
1:A:195:ARG:HH11	1:A:208:SER:HA	1.68	0.58
1:B:435:GLU:O	1:B:439:LEU:HD12	2.04	0.57
1:A:103:LEU:HD11	1:A:215:ILE:HD12	1.86	0.56
1:A:268:LYS:HE3	1:A:268:LYS:H	1.71	0.56
1:B:47:GLN:O	1:B:51:ILE:HG12	2.05	0.56
1:B:241:THR:HG21	2:B:600[A]:FAD:HM73	1.86	0.56
1:A:477:ASN:N	1:A:477:ASN:HD22	2.05	0.55
1:A:354:ASP:HB3	1:A:355:ALA:CA	2.37	0.55
1:B:176:HIS:CD2	1:B:206:LEU:HD13	2.43	0.53
1:B:220:GLY:CA	1:B:221:LYS:CB	2.80	0.53
1:A:228:THR:HG21	1:B:230:ARG:NH1	2.23	0.53
1:A:219:GLY:O	1:A:394:CYS:HB3	2.08	0.53
1:B:430:LEU:HD23	1:B:430:LEU:H	1.74	0.53
1:B:70:ARG:O	1:B:73:GLN:HB2	2.09	0.52
1:A:68:ASP:HA	1:A:71:ALA:HB3	1.92	0.51
1:B:41:SER:HA	1:B:47:GLN:HE21	1.76	0.51
1:A:257:GLU:HA	1:A:286:TYR:HD2	1.76	0.51
2:A:600:FAD:O2'	2:A:600:FAD:C9	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:427:ALA:HB3	1:B:432:VAL:HG13	1.93	0.50
1:A:228:THR:HA	1:B:231:GLU:O	2.12	0.49
1:A:130:PHE:HA	1:A:455:VAL:CG2	2.42	0.49
1:A:16:THR:HA	1:A:19:GLN:HG2	1.95	0.49
1:A:130:PHE:HA	1:A:455:VAL:HG23	1.94	0.49
2:A:600:FAD:O2'	2:A:600:FAD:H9	2.13	0.49
1:A:387:LEU:HD21	1:A:419:MET:HG2	1.95	0.48
1:A:416:ALA:O	1:A:420:VAL:HG23	2.12	0.48
1:B:57:TYR:CE1	1:B:59:SER:HB3	2.48	0.48
1:B:243:ASN:HB2	1:B:360:ASP:HB3	1.95	0.48
1:B:257:GLU:HA	1:B:286:TYR:HD2	1.78	0.48
1:A:231:GLU:OE2	1:A:368:SER:HB3	2.14	0.48
1:A:92:ALA:HB2	1:A:112:LEU:HD21	1.96	0.47
1:A:280:ASP:HB3	1:A:302:CYS:SG	2.55	0.47
1:A:244:PHE:CD1	1:A:349:LEU:HB3	2.50	0.47
1:B:126:HIS:H	2:B:600[A]:FAD:C4	2.28	0.47
1:B:356:ARG:HH11	1:B:358:ARG:HH22	1.63	0.46
1:A:140:ALA:HA	1:A:163:LEU:HD13	1.96	0.46
1:A:257:GLU:HA	1:A:286:TYR:CD2	2.50	0.46
1:A:223:VAL:HG13	1:A:229:ILE:HD13	1.97	0.46
1:A:121:ARG:HB3	1:A:157:ILE:HD12	1.98	0.46
1:B:37:LEU:HB3	1:B:54:GLN:NE2	2.31	0.46
1:B:147:PHE:O	1:B:148:CYS:C	2.54	0.46
1:B:353:GLN:HG3	1:B:357:GLY:HA2	1.98	0.45
1:B:439:LEU:HD21	1:B:462:PRO:HB3	1.98	0.45
1:B:125:LEU:HD21	1:B:157:ILE:HG12	1.98	0.45
1:B:477:ASN:N	1:B:477:ASN:OD1	2.48	0.45
1:A:83:THR:HG23	1:A:84:ASN:HD22	1.82	0.45
1:A:220:GLY:N	1:A:393:ASP:HB3	2.32	0.44
1:A:109:ARG:HD2	4:A:2015:HOH:O	2.17	0.44
1:B:285:VAL:HB	1:B:295:VAL:HG13	1.99	0.44
1:B:260:GLY:HA2	1:B:285:VAL:HG22	2.00	0.44
1:B:243:ASN:OD1	1:B:293:TYR:HD1	2.00	0.44
1:A:201:ASN:HA	1:A:202:PRO:HD2	1.91	0.44
1:B:223:VAL:N	1:B:224:PRO:HD3	2.33	0.43
1:A:348:LYS:H	1:A:348:LYS:HE2	1.84	0.43
1:A:354:ASP:CB	1:A:355:ALA:CA	2.96	0.43
1:A:224:PRO:HG2	1:A:390:LEU:HD21	1.98	0.43
1:A:468:ASN:HD22	1:A:468:ASN:HA	1.62	0.43
1:B:428:GLY:O	1:B:432:VAL:HG22	2.18	0.43
1:A:118:LYS:HB2	3:A:601:CL:CL	2.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:ASP:O	1:A:16:THR:HG23	2.19	0.43
1:A:162:LEU:O	1:A:166:LYS:HG3	2.19	0.43
1:B:219:GLY:O	1:B:394:CYS:HB3	2.19	0.42
1:A:279:ILE:HG22	1:A:281:LEU:HG	2.01	0.42
1:A:393:ASP:OD1	2:A:600:FAD:O3'	2.35	0.42
1:B:346:LEU:HB3	1:B:349:LEU:HD21	2.01	0.42
1:A:248:ARG:HA	1:A:253:THR:HG23	2.02	0.42
1:A:418:TRP:O	1:A:422:ARG:HG2	2.19	0.42
1:B:451:MET:HA	1:B:467:PRO:HD3	2.01	0.42
1:A:194:TRP:CD1	1:A:386:LEU:HB2	2.54	0.42
1:A:237:ALA:O	1:A:366:PHE:HB2	2.20	0.42
1:B:123:ASN:ND2	2:B:600[B]:FAD:H6	2.35	0.42
1:A:181:PHE:HA	1:A:198:LEU:HD23	2.01	0.42
1:B:123:ASN:O	1:B:157:ILE:HG13	2.20	0.42
1:A:244:PHE:HB2	1:A:292:HIS:HB2	2.02	0.41
1:B:13:HIS:CE1	1:B:32:GLY:HA3	2.55	0.41
1:A:277:THR:HB	1:A:279:ILE:HG12	2.02	0.41
1:B:125:LEU:HD22	2:B:600[A]:FAD:H2'	2.03	0.41
1:B:82:CYS:HB3	1:B:85:THR:OG1	2.20	0.41
1:B:321:GLY:O	1:B:325:VAL:HG22	2.21	0.41
1:A:177:TRP:O	1:A:179:VAL:HG22	2.20	0.41
1:B:60:ALA:HB1	1:B:64:TRP:NE1	2.36	0.41
1:B:8:ASN:HA	1:B:9:PRO:HD3	1.94	0.41
1:A:351:PHE:CE1	1:A:361:VAL:HB	2.52	0.41
1:B:60:ALA:HB1	1:B:64:TRP:CE2	2.56	0.41
1:B:24:GLN:OE1	1:B:24:GLN:HA	2.21	0.41
1:B:223:VAL:H	1:B:224:PRO:HD3	1.85	0.41
1:A:354:ASP:CB	1:A:355:ALA:CB	2.76	0.41
1:B:73:GLN:HA	1:B:74:PRO:HD3	1.93	0.41
1:B:125:LEU:HD11	1:B:157:ILE:HG23	2.04	0.40
1:A:123:ASN:HB2	1:A:157:ILE:HD11	2.04	0.40
1:B:129:PRO:HA	1:B:132:ILE:HD12	2.03	0.40
1:A:129:PRO:HA	1:A:132:ILE:HD12	2.03	0.40
1:B:353:GLN:CG	1:B:357:GLY:HA2	2.51	0.40
1:B:458:TYR:CD2	1:B:465:ARG:HG2	2.57	0.40
1:A:228:THR:HG21	1:B:230:ARG:HH11	1.84	0.40

There are no symmetry-related clashes.

## 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	472/497 (95%)	436 (92%)	31 (7%)	5 (1%)	17	48
1	B	473/497 (95%)	442 (93%)	22 (5%)	9 (2%)	9	33
All	All	945/994 (95%)	878 (93%)	53 (6%)	14 (2%)	12	39

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	354	ASP
1	B	276	ALA
1	B	148	CYS
1	B	221	LYS
1	B	275	LYS
1	A	58	TRP
1	A	355	ALA
1	A	429	PRO
1	B	41	SER
1	B	218	ALA
1	B	357	GLY
1	B	223	VAL
1	A	201	ASN
1	B	429	PRO

### 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	386/403 (96%)	370 (96%)	16 (4%)	35	70
1	B	386/403 (96%)	367 (95%)	19 (5%)	29	63
All	All	772/806 (96%)	737 (96%)	35 (4%)	32	66

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	THR
1	A	25	ASP
1	A	35	ARG
1	A	109	ARG
1	A	130	PHE
1	A	155	ILE
1	A	163	LEU
1	A	179	VAL
1	A	231	GLU
1	A	268	LYS
1	A	297	THR
1	A	348	LYS
1	A	453	ARG
1	A	455	VAL
1	A	468	ASN
1	A	477	ASN
1	B	24	GLN
1	B	78	GLN
1	B	109	ARG
1	B	118	LYS
1	B	130	PHE
1	B	163	LEU
1	B	189	ARG
1	B	197	GLN
1	B	230	ARG
1	B	251	GLU
1	B	254	GLN
1	B	269	PHE
1	B	280	ASP
1	B	354	ASP
1	B	422	ARG
1	B	430	LEU
1	B	469	LEU
1	B	477	ASN
1	B	487	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	84	ASN
1	A	205	GLN
1	A	353	GLN
1	A	468	ASN
1	A	477	ASN
1	B	13	HIS
1	B	19	GLN
1	B	47	GLN
1	B	49	HIS
1	B	176	HIS
1	B	254	GLN
1	B	301	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](#)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	FAD	A	600	-	51,58,58	1.39	6 (11%)	54,89,89	2.05	9 (16%)
2	FAD	B	600[A]	-	51,58,58	1.40	6 (11%)	54,89,89	2.00	9 (16%)
2	FAD	B	600[B]	-	51,58,58	1.47	7 (13%)	54,89,89	2.08	9 (16%)

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	-	-	0/28/50/50	0/6/6/6
2	FAD	B	600[A]	-	-	0/28/50/50	0/6/6/6
2	FAD	B	600[B]	-	-	0/28/50/50	0/6/6/6

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600[B]	FAD	C1'-N10	2.25	1.50	1.48
2	A	600	FAD	C2A-N1A	2.44	1.38	1.33
2	B	600[B]	FAD	C2A-N1A	2.58	1.38	1.33
2	B	600[A]	FAD	C2A-N1A	2.58	1.38	1.33
2	B	600[B]	FAD	C5X-N5	2.67	1.39	1.35
2	A	600	FAD	C4-N3	3.04	1.38	1.33
2	B	600[A]	FAD	C4-N3	3.04	1.38	1.33
2	B	600[A]	FAD	C1'-N10	3.31	1.51	1.48
2	A	600	FAD	C1'-N10	3.44	1.51	1.48
2	B	600[A]	FAD	C4X-N5	3.60	1.38	1.33
2	B	600[B]	FAD	C4-N3	3.68	1.39	1.33
2	A	600	FAD	C4X-N5	3.89	1.38	1.33
2	A	600	FAD	C2A-N3A	3.93	1.38	1.32
2	A	600	FAD	C10-N1	3.97	1.38	1.33
2	B	600[B]	FAD	C4X-N5	4.17	1.39	1.33
2	B	600[A]	FAD	C10-N1	4.22	1.39	1.33
2	B	600[B]	FAD	C2A-N3A	4.31	1.39	1.32
2	B	600[A]	FAD	C2A-N3A	4.31	1.39	1.32
2	B	600[B]	FAD	C10-N1	4.88	1.40	1.33

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600	FAD	N3A-C2A-N1A	-10.73	119.51	128.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	600[B]	FAD	N3A-C2A-N1A	-10.30	119.89	128.86
2	B	600[A]	FAD	N3A-C2A-N1A	-10.30	119.89	128.86
2	A	600	FAD	C1B-N9A-C4A	-2.92	121.59	126.64
2	B	600[B]	FAD	O3B-C3B-C4B	-2.80	102.90	111.09
2	B	600[A]	FAD	O3B-C3B-C4B	-2.80	102.90	111.09
2	A	600	FAD	C4X-C4-N3	-2.69	119.65	123.48
2	B	600[A]	FAD	C4X-C4-N3	-2.68	119.67	123.48
2	B	600[A]	FAD	C4X-C10-N10	-2.48	118.80	120.52
2	B	600[A]	FAD	C9A-C5X-N5	-2.47	118.56	122.24
2	A	600	FAD	C9A-C5X-N5	-2.45	118.59	122.24
2	B	600[B]	FAD	C4X-C4-N3	-2.40	120.06	123.48
2	A	600	FAD	O3B-C3B-C4B	-2.20	104.67	111.09
2	B	600[B]	FAD	C2B-C3B-C4B	2.10	106.71	102.62
2	B	600[A]	FAD	C2B-C3B-C4B	2.10	106.71	102.62
2	A	600	FAD	C2B-C3B-C4B	2.20	106.91	102.62
2	A	600	FAD	C4-C4X-N5	2.36	121.27	118.68
2	A	600	FAD	C5X-C9A-N10	2.47	119.49	117.66
2	B	600[A]	FAD	C5X-C9A-N10	2.53	119.54	117.66
2	B	600[B]	FAD	C4B-O4B-C1B	2.57	112.50	109.77
2	B	600[A]	FAD	C4B-O4B-C1B	2.57	112.50	109.77
2	B	600[B]	FAD	C5X-C9A-N10	3.03	119.91	117.66
2	B	600[B]	FAD	C4-C4X-N5	3.13	122.12	118.68
2	B	600[B]	FAD	C4X-N5-C5X	4.08	121.07	116.76
2	A	600	FAD	C4-N3-C2	5.76	120.20	115.16
2	B	600[A]	FAD	C4-N3-C2	5.80	120.23	115.16
2	B	600[B]	FAD	C4-N3-C2	5.86	120.28	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	FAD	3	0
2	B	600[A]	FAD	5	0
2	B	600[B]	FAD	2	0

## 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	476/497 (95%)	1.26	95 (19%) <b>1</b> <b>1</b>	72, 81, 89, 97	0
1	B	477/497 (95%)	1.29	100 (20%) <b>1</b> <b>1</b>	72, 81, 88, 98	0
All	All	953/994 (95%)	1.28	195 (20%) <b>1</b> <b>1</b>	72, 81, 89, 98	0

All (195) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	276	ALA	12.1
1	B	148	CYS	10.1
1	B	150	GLY	9.6
1	B	254	GLN	7.2
1	A	191	GLY	7.2
1	B	151	THR	7.0
1	A	250	VAL	7.0
1	B	265	TYR	6.9
1	A	323	ALA	6.7
1	B	250	VAL	6.4
1	B	267	GLN	6.1
1	A	485	MET	5.5
1	A	266	ASN	5.5
1	A	271	GLN	5.5
1	B	251	GLU	5.4
1	A	148	CYS	5.3
1	A	267	GLN	5.3
1	A	454	ASN	5.2
1	B	149	THR	5.2
1	B	269	PHE	5.2
1	A	345	LYS	5.0
1	B	274	LEU	5.0
1	A	151	THR	4.9
1	B	344	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	149	THR	4.9
1	B	402	LEU	4.8
1	B	59	SER	4.8
1	B	426	GLY	4.8
1	B	266	ASN	4.7
1	B	58	TRP	4.7
1	B	271	GLN	4.6
1	B	348	LYS	4.5
1	B	301	GLN	4.3
1	B	486	MET	4.3
1	B	83	THR	4.3
1	A	223	VAL	4.2
1	B	8	ASN	4.2
1	B	343	HIS	4.2
1	B	456	ALA	4.1
1	B	353	GLN	4.0
1	A	190	LYS	4.0
1	B	255	VAL	4.0
1	B	270	PHE	4.0
1	A	277	THR	3.9
1	A	481	ASP	3.9
1	A	407	ALA	3.8
1	B	40	GLU	3.8
1	A	282	GLU	3.7
1	B	7	THR	3.6
1	B	80	GLN	3.6
1	A	189	ARG	3.6
1	A	427	ALA	3.6
1	A	456	ALA	3.5
1	B	189	ARG	3.5
1	A	188	PRO	3.4
1	B	345	LYS	3.4
1	B	403	GLY	3.4
1	B	186	PRO	3.4
1	A	120	SER	3.4
1	A	404	THR	3.4
1	A	251	GLU	3.4
1	B	342	THR	3.4
1	A	468	ASN	3.3
1	B	245	VAL	3.3
1	A	245	VAL	3.3
1	B	454	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	382	HIS	3.2
1	B	11	HIS	3.2
1	B	340	PHE	3.2
1	B	458	TYR	3.2
1	A	455	VAL	3.1
1	B	356	ARG	3.1
1	B	305	ARG	3.1
1	A	246	ASN	3.1
1	A	342	THR	3.1
1	A	412	ALA	3.0
1	A	300	LYS	3.0
1	A	269	PHE	3.0
1	A	273	LEU	3.0
1	A	247	GLY	3.0
1	B	268	LYS	3.0
1	B	9	PRO	3.0
1	A	128	TRP	3.0
1	B	389	GLY	3.0
1	B	78	GLN	3.0
1	B	333	PHE	3.0
1	A	212	ASP	3.0
1	A	203	PRO	2.9
1	A	278	GLY	2.9
1	B	481	ASP	2.9
1	B	455	VAL	2.9
1	A	473	ALA	2.9
1	A	80	GLN	2.8
1	B	341	ALA	2.8
1	A	410	PHE	2.8
1	B	164	LEU	2.8
1	A	478	GLN	2.8
1	A	249	THR	2.8
1	A	53	ALA	2.8
1	A	205	GLN	2.8
1	B	244	PHE	2.7
1	B	188	PRO	2.7
1	B	233	ARG	2.7
1	B	259	SER	2.7
1	A	348	LYS	2.7
1	A	338	ALA	2.7
1	B	253	THR	2.7
1	B	275	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	72	SER	2.6
1	A	58	TRP	2.6
1	B	147	PHE	2.6
1	B	128	TRP	2.6
1	B	411	LEU	2.6
1	B	246	ASN	2.6
1	B	51	ILE	2.6
1	A	390	LEU	2.6
1	B	272	SER	2.6
1	A	305	ARG	2.6
1	B	247	GLY	2.5
1	B	310	ARG	2.5
1	B	152	LEU	2.5
1	A	75	VAL	2.5
1	A	275	LYS	2.5
1	A	11	HIS	2.5
1	A	411	LEU	2.5
1	A	322	LYS	2.5
1	A	343	HIS	2.5
1	B	77	GLN	2.5
1	A	9	PRO	2.4
1	A	356	ARG	2.4
1	B	190	LYS	2.4
1	A	254	GLN	2.4
1	B	412	ALA	2.4
1	A	355	ALA	2.4
1	B	160	LEU	2.4
1	A	365	ASP	2.4
1	B	168	ALA	2.4
1	A	460	LEU	2.4
1	A	364	PHE	2.3
1	B	57	TYR	2.3
1	A	368	SER	2.3
1	A	450	ASN	2.3
1	B	400	TRP	2.3
1	B	294	PHE	2.3
1	A	150	GLY	2.3
1	B	357	GLY	2.3
1	B	347	GLY	2.3
1	A	156	SER	2.3
1	A	472	ARG	2.2
1	B	204	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	355	ALA	2.2
1	B	142	LYS	2.2
1	B	39	VAL	2.2
1	A	202	PRO	2.2
1	A	328	GLU	2.2
1	A	466	TYR	2.2
1	A	98	ARG	2.2
1	B	248	ARG	2.2
1	A	414	PHE	2.2
1	B	296	MET	2.2
1	B	415	ASP	2.2
1	A	388	LEU	2.2
1	A	332	ARG	2.2
1	B	375	SER	2.2
1	B	451	MET	2.2
1	B	260	GLY	2.1
1	A	242	ALA	2.1
1	A	403	GLY	2.1
1	A	93	GLY	2.1
1	A	291	THR	2.1
1	A	389	GLY	2.1
1	B	395	LEU	2.1
1	A	353	GLN	2.1
1	A	97	LEU	2.1
1	B	427	ALA	2.1
1	B	223	VAL	2.1
1	A	386	LEU	2.1
1	A	402	LEU	2.1
1	A	244	PHE	2.1
1	B	293	TYR	2.1
1	A	477	ASN	2.1
1	B	283	ASN	2.1
1	A	46	SER	2.1
1	B	282	GLU	2.1
1	A	233	ARG	2.1
1	A	398	PRO	2.1
1	A	132	ILE	2.0
1	B	407	ALA	2.0
1	A	383	GLY	2.0
1	B	89	VAL	2.0
1	B	405	GLY	2.0
1	B	430	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	350	GLU	2.0
1	B	311	GLN	2.0
1	A	283	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	CL	A	601	1/1	0.98	0.31	1.27	64,64,64,64	0
2	FAD	B	600[B]	53/53	0.89	0.24	-0.09	37,41,47,48	30
2	FAD	B	600[A]	53/53	0.89	0.24	-0.81	45,49,60,60	30
2	FAD	A	600	53/53	0.91	0.21	-0.94	48,54,69,69	0
3	CL	B	601	1/1	0.96	0.16	-3.25	65,65,65,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.