



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2020 – 05:46 pm BST

PDB ID : 2RAB  
Title : Structure of glutathione amide reductase from *Chromatium gracile* in complex with NAD  
Authors : Van Petegem, F.; De Vos, D.; Savvides, S.; Vergauwen, B.; Van Beeumen, J.  
Deposited on : 2007-09-14  
Resolution : 2.50 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

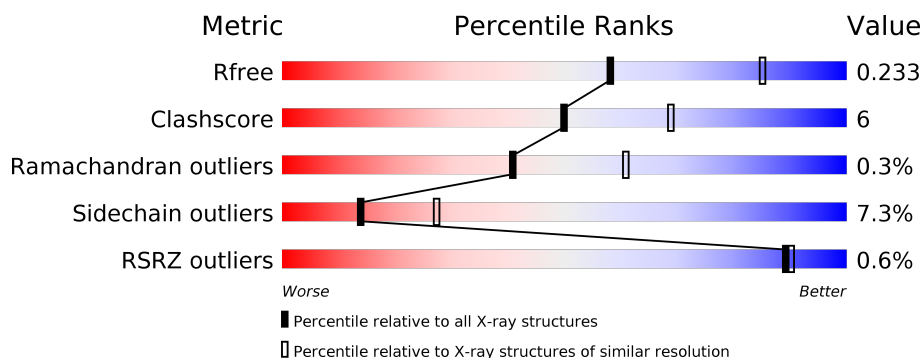
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 2.50 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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 respectively. 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	463	 81% 15% . .
1	B	463	 82% 14% . .

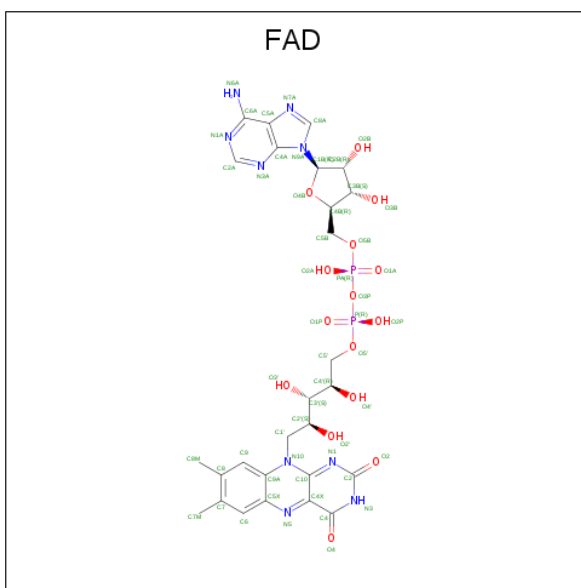


In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called glutathione amide reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	451	Total 3347	C 2113	N 594	O 630	S 10	0	1	0
1	B	452	Total 3346	C 2114	N 595	O 627	S 10	0	1	0

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$ ).



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

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula:  $\text{C}_{21}\text{H}_{27}\text{N}_7\text{O}_{14}\text{P}_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	4	Total	Cl	0	0
			4	4		
4	A	4	Total	Cl	0	0
			4	4		

- Molecule 5 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Ni	0	0
			2	2		
5	A	2	Total	Ni	0	0
			2	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	267	Total	O	0	0
			267	267		

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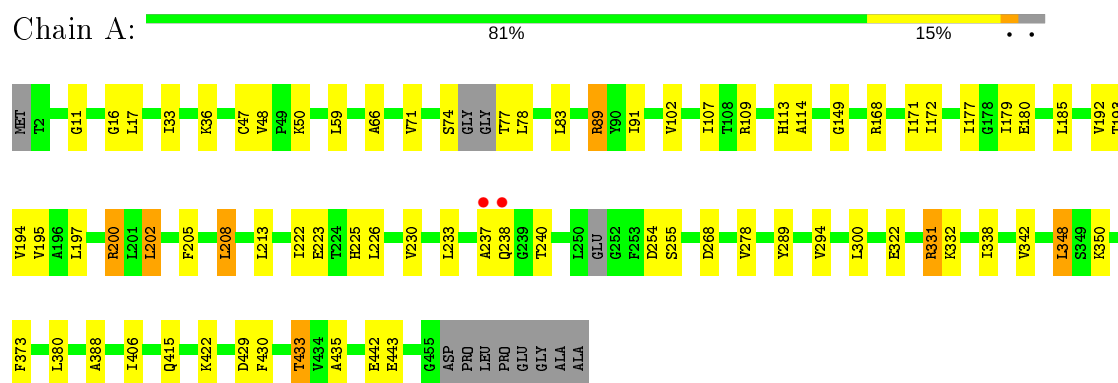
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	207	Total 207	O 207	0	0

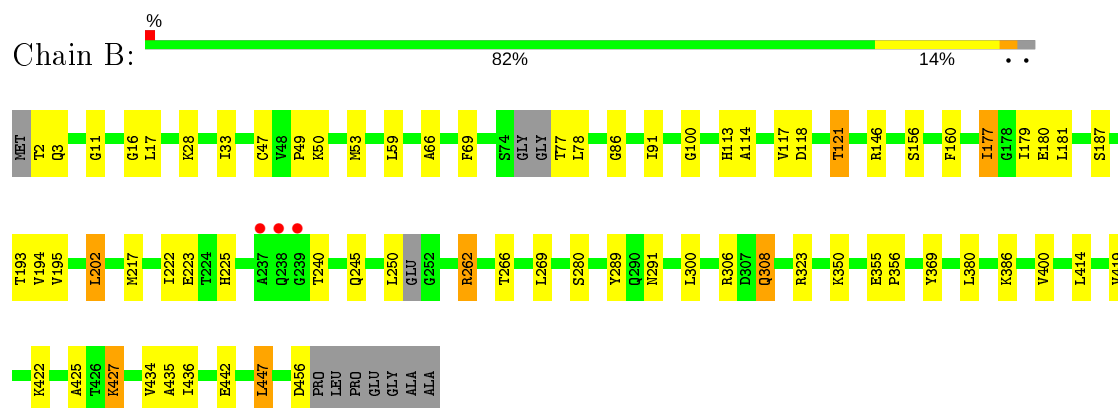
### 3 Residue-property plots

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: glutathione amide reductase



- Molecule 1: glutathione amide reductase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.99 Å 71.99 Å 224.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 15.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.8 (15.00-2.50) 96.2 (15.00-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.39 (at 2.51 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.185 , 0.233 0.184 , 0.233	Depositor DCC
$R_{free}$ test set	1888 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.7	Xtriage
Anisotropy	0.207	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 22.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.478 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7373	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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: NI, NAD, 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	0.43	0/3414	0.59	0/4641
1	B	0.43	0/3413	0.59	0/4641
All	All	0.43	0/6827	0.59	0/9282

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	3347	0	3302	42	0
1	B	3346	0	3300	42	0
2	A	53	0	31	0	0
2	B	53	0	31	1	0
3	A	44	0	26	1	0
3	B	44	0	26	3	0
4	A	4	0	0	2	0
4	B	4	0	0	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	267	0	0	7	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	207	0	0	6	1
All	All	7373	0	6716	79	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 6.

All (79) 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)
4:A:464:CL:CL	6:A:819:HOH:O	2.37	0.80
4:A:467:CL:CL	6:A:860:HOH:O	2.39	0.76
1:B:291:ASN:HD21	1:B:323:ARG:HH22	1.36	0.73
1:B:386:LYS:O	6:B:734:HOH:O	2.07	0.72
1:A:50:LYS:HD2	1:A:180:GLU:OE1	1.91	0.71
1:A:433:THR:HG21	1:B:419:VAL:HG22	1.73	0.70
1:A:89:ARG:HG3	1:A:89:ARG:HH21	1.56	0.69
1:B:33:ILE:HG21	1:B:114:ALA:HB2	1.75	0.68
1:A:429:ASP:O	1:A:433:THR:HG22	1.95	0.66
1:A:200:ARG:NH2	1:A:205:PHE:O	2.29	0.65
1:B:118:ASP:OD1	1:B:121:THR:HG23	1.97	0.65
1:B:113:HIS:HD2	6:B:776:HOH:O	1.82	0.63
1:A:255:SER:HB2	6:A:654:HOH:O	1.99	0.61
1:B:177:ILE:HG22	3:B:600:NAD:H5N	1.81	0.61
1:A:177:ILE:HG12	3:A:600:NAD:H5N	1.81	0.60
1:A:435:ALA:HB1	1:A:442:GLU:HB2	1.84	0.59
1:A:179:ILE:HG13	1:A:202:LEU:HD13	1.85	0.59
1:A:200:ARG:HD3	6:A:660:HOH:O	2.00	0.59
1:B:156:SER:HB3	1:B:177:ILE:HD13	1.85	0.58
1:A:195:VAL:HG12	1:A:225:HIS:HB2	1.85	0.58
1:B:195:VAL:HG12	1:B:225:HIS:HB2	1.85	0.58
1:A:193:THR:HG23	6:A:658:HOH:O	2.03	0.57
1:A:415:GLN:HE22	1:B:436:ILE:H	1.52	0.57
1:A:48:VAL:HG12	1:A:91:ILE:HD11	1.87	0.57
1:A:33:ILE:HG21	1:A:114:ALA:HB2	1.88	0.55
1:A:113:HIS:HE1	1:A:268:ASP:O	1.89	0.54
1:B:400:VAL:HG12	1:B:425:ALA:O	2.07	0.54
1:B:427:LYS:NZ	1:B:447:LEU:O	2.41	0.53
1:B:177:ILE:HG22	3:B:600:NAD:C5N	2.38	0.53
1:A:415:GLN:HE22	1:B:435:ALA:HA	1.73	0.52
1:A:192:VAL:HG23	1:A:222:ILE:HG23	1.90	0.52
1:B:100:GLY:HA3	6:B:646:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:THR:HA	1:A:223:GLU:O	2.09	0.52
1:A:415:GLN:NE2	1:B:436:ILE:H	2.08	0.52
1:A:89:ARG:HG3	1:A:89:ARG:NH2	2.26	0.51
1:A:342:VAL:HB	1:A:348:LEU:HG	1.93	0.50
1:A:322:GLU:OE1	1:A:331:ARG:HD2	2.12	0.49
1:A:380:LEU:HD13	1:B:86:GLY:HA3	1.93	0.49
1:B:262:ARG:HD3	6:B:752:HOH:O	2.13	0.48
1:A:406:ILE:HG12	6:A:836:HOH:O	2.14	0.48
1:A:66:ALA:HB1	1:A:71:VAL:HB	1.94	0.48
1:A:113:HIS:HD2	6:A:633:HOH:O	1.98	0.47
1:A:102:VAL:HG13	1:A:107:ILE:HB	1.97	0.47
1:B:179:ILE:HG13	1:B:202:LEU:HD13	1.97	0.47
1:B:69:PHE:HA	1:B:380:LEU:HD12	1.97	0.46
1:B:323:ARG:HD3	6:B:760:HOH:O	2.15	0.46
1:B:456:ASP:CB	6:B:770:HOH:O	2.64	0.46
1:A:430:PHE:O	1:A:433:THR:HG23	2.16	0.46
1:B:50:LYS:NZ	2:B:500:FAD:O4	2.47	0.46
1:A:59:LEU:HD13	1:B:66:ALA:HA	1.98	0.45
1:B:435:ALA:HB1	1:B:442:GLU:HB2	1.96	0.45
1:B:193:THR:HA	1:B:223:GLU:O	2.16	0.45
1:A:171:ILE:HB	1:A:194:VAL:HB	1.99	0.45
1:B:11:GLY:O	1:B:16:GLY:HA3	2.16	0.45
1:A:289:TYR:CE1	1:A:332:LYS:HD3	2.52	0.45
1:B:355:GLU:HB3	1:B:356:PRO:HD3	1.99	0.45
1:B:49:PRO:O	1:B:53:MET:HG3	2.17	0.45
1:B:289:TYR:O	1:B:323:ARG:NH1	2.50	0.44
1:A:172:ILE:HD13	1:A:230:VAL:HG11	2.00	0.44
1:A:48:VAL:HG12	1:A:91:ILE:CD1	2.46	0.44
1:A:50:LYS:CD	1:A:180:GLU:OE1	2.63	0.44
1:B:306:ARG:O	1:B:308:GLN:NE2	2.51	0.43
1:A:168:ARG:H	1:A:254:ASP:HB2	1.84	0.43
1:A:11:GLY:O	1:A:16:GLY:HA3	2.18	0.43
1:A:373:PHE:CE1	1:A:443:GLU:HG3	2.53	0.43
1:B:177:ILE:HG22	3:B:600:NAD:C6N	2.49	0.43
1:B:266:THR:HA	1:B:269:LEU:HD12	2.01	0.43
1:B:50:LYS:HD2	1:B:180:GLU:OE1	2.18	0.42
1:B:49:PRO:HB2	1:B:160:PHE:CD1	2.54	0.42
1:A:202:LEU:HD22	1:A:213:LEU:HD22	2.01	0.42
1:A:208:LEU:HD11	1:A:388:ALA:HB1	2.01	0.42
1:B:177:ILE:HD12	1:B:181:LEU:HG	2.00	0.42
1:B:291:ASN:ND2	1:B:323:ARG:HH22	2.12	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:369:TYR:HB3	1:B:447:LEU:HG	2.02	0.41
1:A:149:GLY:O	1:A:233:LEU:HB2	2.19	0.41
1:A:338:ILE:HD12	1:B:434:VAL:HG21	2.02	0.41
1:B:28:LYS:HA	1:B:28:LYS:HD3	1.90	0.41
1:B:49:PRO:HB3	1:B:91:ILE:HD11	2.01	0.41
1:B:217:MET:HG2	1:B:222:ILE:HD12	2.02	0.41

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)
6:A:676:HOH:O	6:B:645:HOH:O[3_655]	2.05	0.15

## 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	446/463 (96%)	426 (96%)	18 (4%)	2 (0%)	34	54
1	B	447/463 (96%)	429 (96%)	17 (4%)	1 (0%)	47	68
All	All	893/926 (96%)	855 (96%)	35 (4%)	3 (0%)	41	61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	238	GLN
1	B	3	GLN
1	A	237	ALA

### 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	336/352 (96%)	312 (93%)	24 (7%)	14	28
1	B	335/352 (95%)	310 (92%)	25 (8%)	13	26
All	All	671/704 (95%)	622 (93%)	49 (7%)	14	27

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LEU
1	A	36	LYS
1	A	47	CYS
1	A	74	SER
1	A	77	THR
1	A	78	LEU
1	A	83	LEU
1	A	89	ARG
1	A	109	ARG
1	A	185	LEU
1	A	197	LEU
1	A	200	ARG
1	A	202	LEU
1	A	208	LEU
1	A	226	LEU
1	A	240	THR
1	A	278	VAL
1	A	294	VAL
1	A	300	LEU
1	A	331	ARG
1	A	348	LEU
1	A	350	LYS
1	A	422	LYS
1	A	433	THR
1	B	2	THR
1	B	17	LEU
1	B	47	CYS

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Mol	Chain	Res	Type
1	B	59	LEU
1	B	77	THR
1	B	78	LEU
1	B	117	VAL
1	B	121	THR
1	B	146	ARG
1	B	177	ILE
1	B	187	SER
1	B	194	VAL
1	B	202	LEU
1	B	240	THR
1	B	245	GLN
1	B	250	LEU
1	B	262	ARG
1	B	280	SER
1	B	300	LEU
1	B	308	GLN
1	B	350	LYS
1	B	414	LEU
1	B	422	LYS
1	B	427	LYS
1	B	447	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	HIS
1	A	163	GLN
1	A	165	GLN
1	A	415	GLN
1	B	113	HIS
1	B	165	GLN
1	B	291	ASN
1	B	308	GLN
1	B	383	HIS

### 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 16 ligands modelled in this entry, 12 are monoatomic - leaving 4 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	NAD	A	600	-	42,48,48	1.78	4 (9%)	50,73,73	1.27	4 (8%)
3	NAD	B	600	-	42,48,48	1.79	4 (9%)	50,73,73	1.29	3 (6%)
2	FAD	B	500	-	51,58,58	1.41	7 (13%)	60,89,89	1.63	9 (15%)
2	FAD	A	500	-	51,58,58	1.41	7 (13%)	60,89,89	1.70	10 (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
3	NAD	A	600	-	-	7/26/62/62	0/5/5/5
3	NAD	B	600	-	-	6/26/62/62	0/5/5/5
2	FAD	B	500	-	-	3/30/50/50	0/6/6/6
2	FAD	A	500	-	-	2/30/50/50	0/6/6/6

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	600	NAD	O7N-C7N	8.95	1.41	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	600	NAD	O7N-C7N	8.90	1.41	1.24
2	A	500	FAD	C10-N1	4.43	1.38	1.33
2	B	500	FAD	C10-N1	4.39	1.38	1.33
3	B	600	NAD	C2A-N3A	4.28	1.39	1.32
2	A	500	FAD	C4X-N5	4.21	1.39	1.33
3	A	600	NAD	C2A-N3A	4.21	1.38	1.32
2	B	500	FAD	C2A-N3A	4.00	1.38	1.32
2	B	500	FAD	C4X-N5	3.74	1.38	1.33
2	A	500	FAD	C2A-N3A	3.61	1.37	1.32
2	B	500	FAD	C4-N3	3.21	1.38	1.33
2	A	500	FAD	C4-N3	3.17	1.38	1.33
2	B	500	FAD	C1'-N10	3.01	1.51	1.48
3	B	600	NAD	C2N-N1N	2.89	1.38	1.35
2	A	500	FAD	C1'-N10	2.87	1.51	1.48
3	A	600	NAD	C2A-N1A	2.70	1.38	1.33
3	A	600	NAD	C2N-N1N	2.69	1.38	1.35
3	B	600	NAD	C2A-N1A	2.61	1.38	1.33
2	B	500	FAD	C2A-N1A	2.59	1.38	1.33
2	A	500	FAD	C2A-N1A	2.51	1.38	1.33
2	A	500	FAD	C5X-N5	2.48	1.39	1.35
2	B	500	FAD	C5X-N5	2.29	1.39	1.35

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	FAD	C4-N3-C2	6.74	120.83	115.14
2	B	500	FAD	C4-N3-C2	6.22	120.39	115.14
2	A	500	FAD	N3A-C2A-N1A	-5.55	120.00	128.68
3	B	600	NAD	N3A-C2A-N1A	-5.52	120.06	128.68
3	A	600	NAD	N3A-C2A-N1A	-5.42	120.21	128.68
2	B	500	FAD	N3A-C2A-N1A	-5.40	120.24	128.68
2	B	500	FAD	C4X-N5-C5X	4.18	120.95	116.77
2	A	500	FAD	C4X-N5-C5X	4.06	120.83	116.77
3	A	600	NAD	C3D-C2D-C1D	3.36	106.04	100.98
3	B	600	NAD	C3D-C2D-C1D	3.16	105.74	100.98
3	B	600	NAD	C6N-N1N-C2N	-3.11	119.14	121.97
2	A	500	FAD	C10-C4X-N5	-3.04	119.16	121.26
2	A	500	FAD	C1'-N10-C9A	3.00	120.65	118.29
3	A	600	NAD	C6N-N1N-C2N	-2.99	119.25	121.97
2	B	500	FAD	P-O3P-PA	-2.83	123.12	132.83
2	B	500	FAD	C1'-N10-C9A	2.81	120.51	118.29
2	A	500	FAD	C4-C4X-N5	2.71	121.70	118.60

*Continued on next page...*

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	FAD	C4X-C4-N3	-2.65	119.81	123.43
2	B	500	FAD	C4X-C4-N3	-2.44	120.10	123.43
2	B	500	FAD	C10-C4X-N5	-2.38	119.61	121.26
2	A	500	FAD	C5X-C9A-N10	2.26	119.35	117.72
2	B	500	FAD	C5X-C9A-N10	2.21	119.32	117.72
2	A	500	FAD	P-O3P-PA	-2.17	125.37	132.83
2	B	500	FAD	C5'-C4'-C3'	-2.15	108.05	112.20
2	A	500	FAD	O4B-C1B-C2B	-2.12	103.83	106.93
3	A	600	NAD	C3N-C7N-N7N	2.06	120.22	117.75

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	600	NAD	C5B-O5B-PA-O2A
3	A	600	NAD	C5B-O5B-PA-O3
3	A	600	NAD	C3B-C4B-C5B-O5B
3	B	600	NAD	PA-O3-PN-O5D
3	B	600	NAD	C5D-O5D-PN-O1N
3	B	600	NAD	O4B-C4B-C5B-O5B
3	B	600	NAD	C3B-C4B-C5B-O5B
2	B	500	FAD	O4B-C4B-C5B-O5B
2	A	500	FAD	O4B-C4B-C5B-O5B
3	A	600	NAD	O4B-C4B-C5B-O5B
2	B	500	FAD	C3B-C4B-C5B-O5B
2	A	500	FAD	C3B-C4B-C5B-O5B
2	B	500	FAD	PA-O3P-P-O5'
3	B	600	NAD	O4D-C4D-C5D-O5D
3	A	600	NAD	C5B-O5B-PA-O1A
3	A	600	NAD	PA-O3-PN-O1N
3	B	600	NAD	C5D-O5D-PN-O3
3	A	600	NAD	PA-O3-PN-O2N

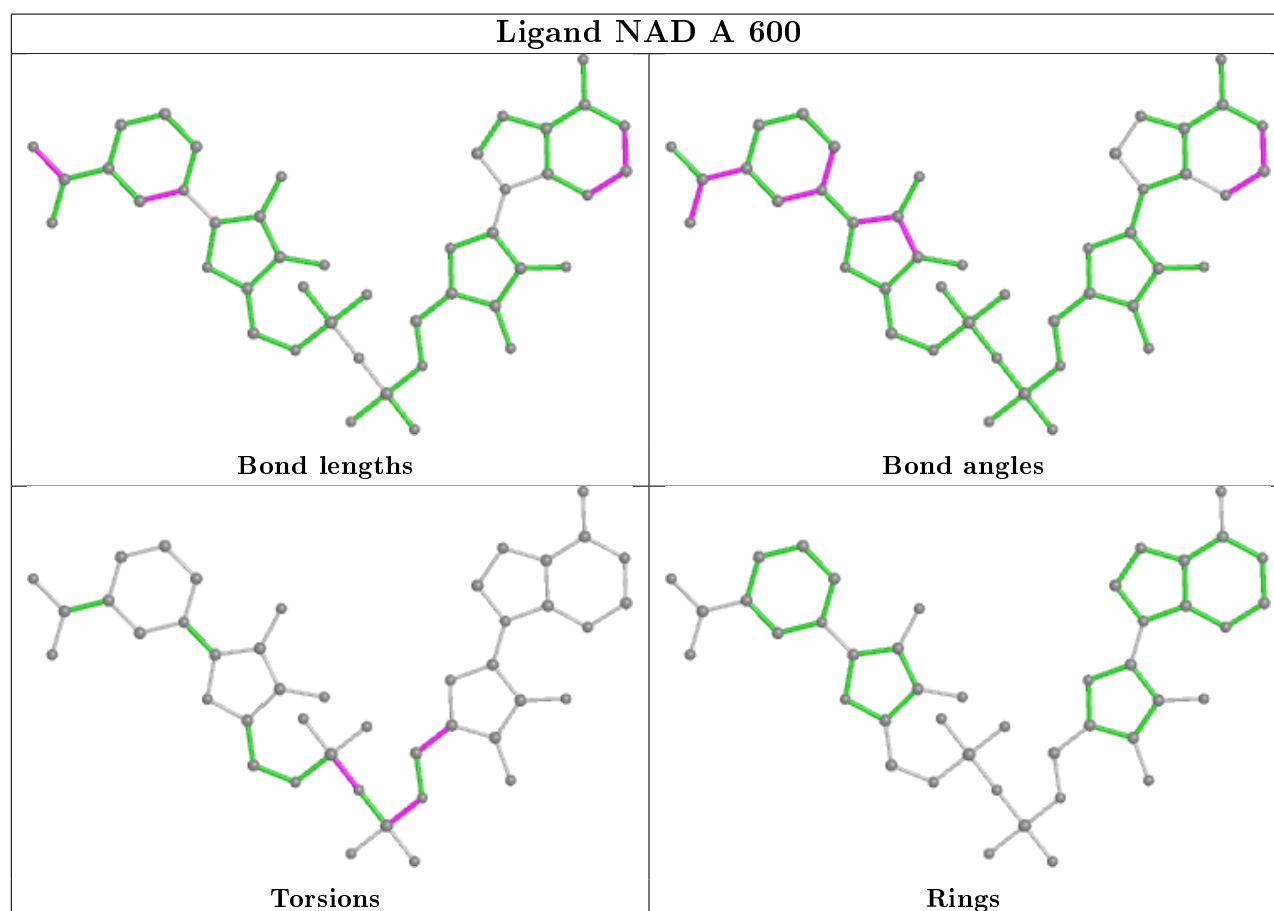
There are no ring outliers.

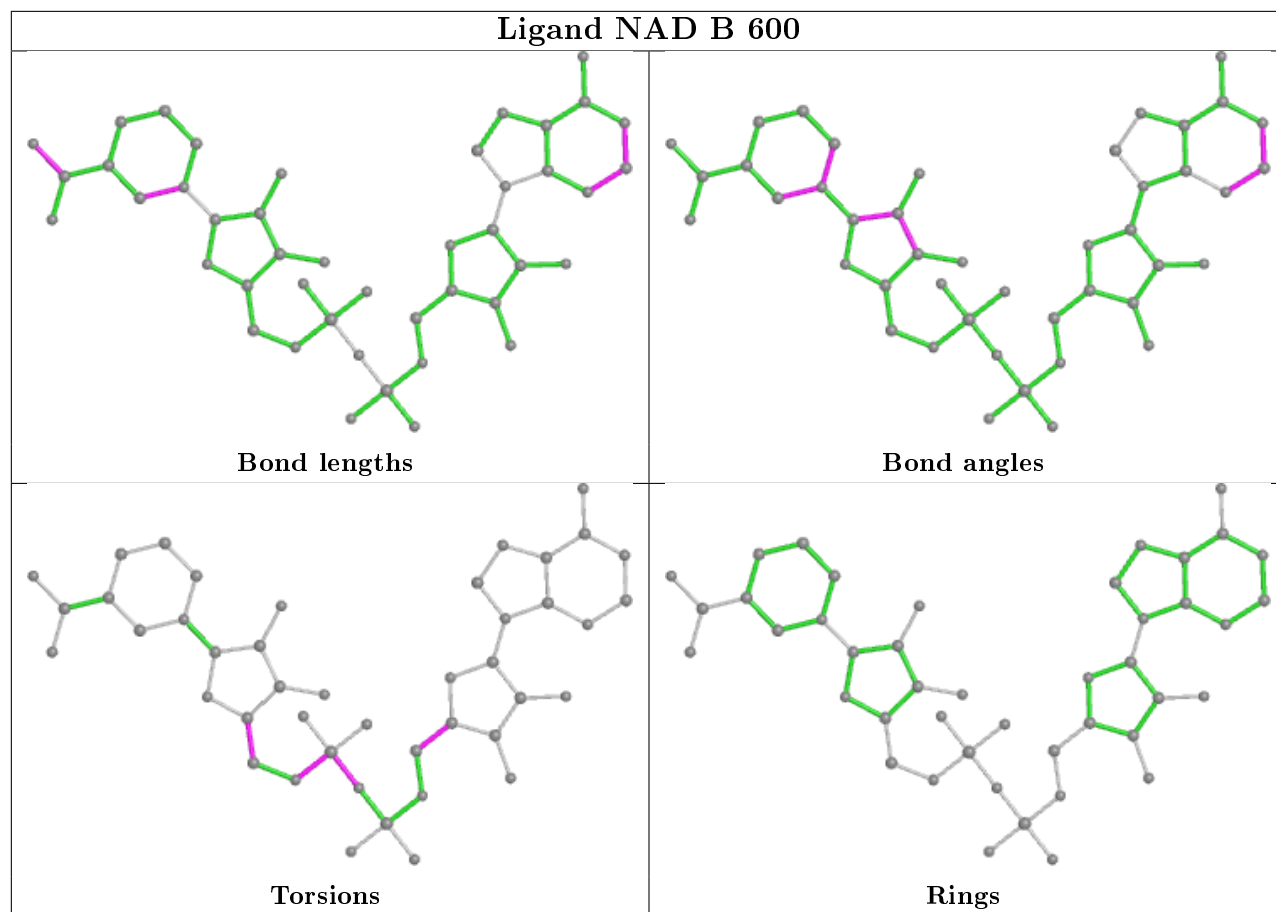
3 monomers are involved in 5 short contacts:

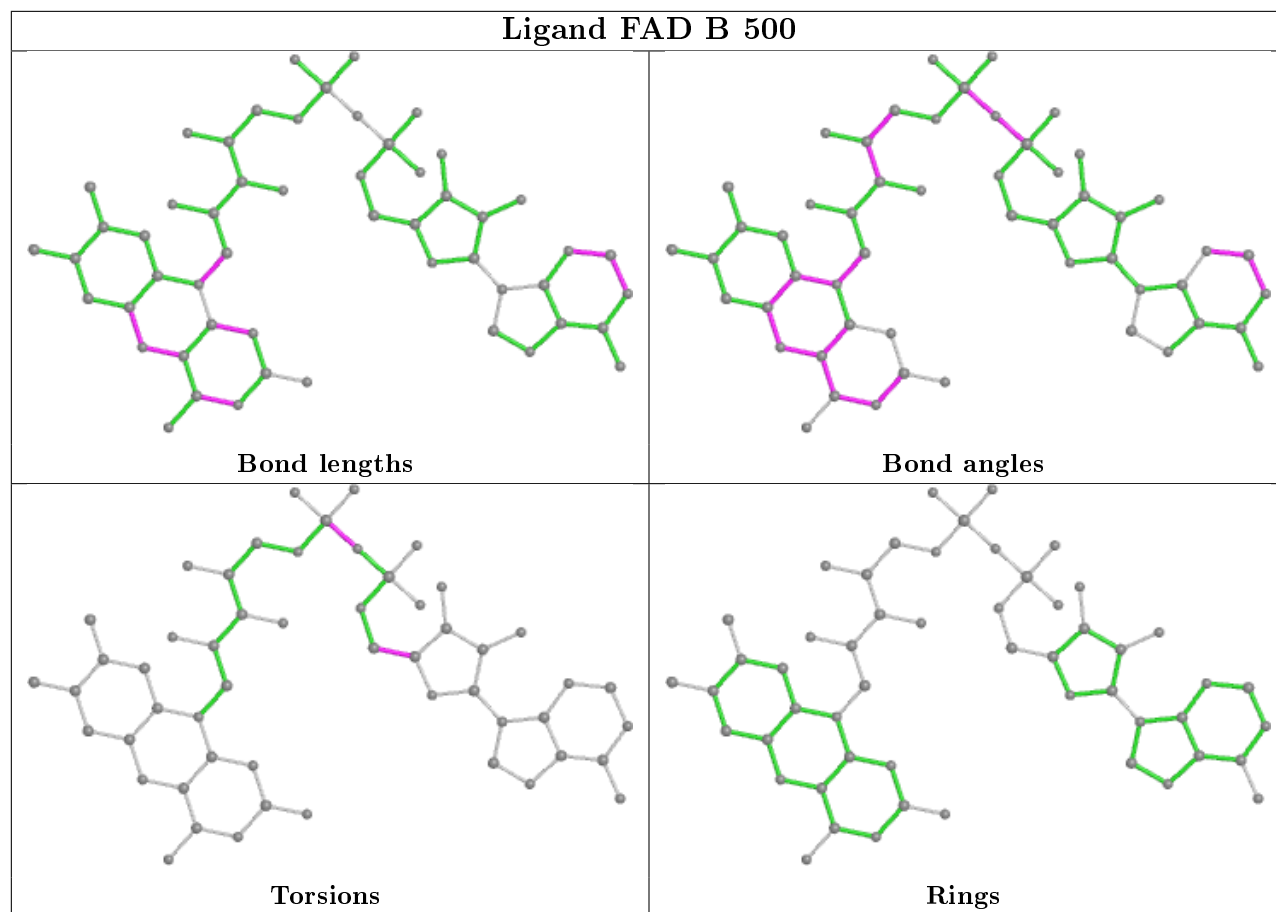
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	600	NAD	1	0
3	B	600	NAD	3	0
2	B	500	FAD	1	0

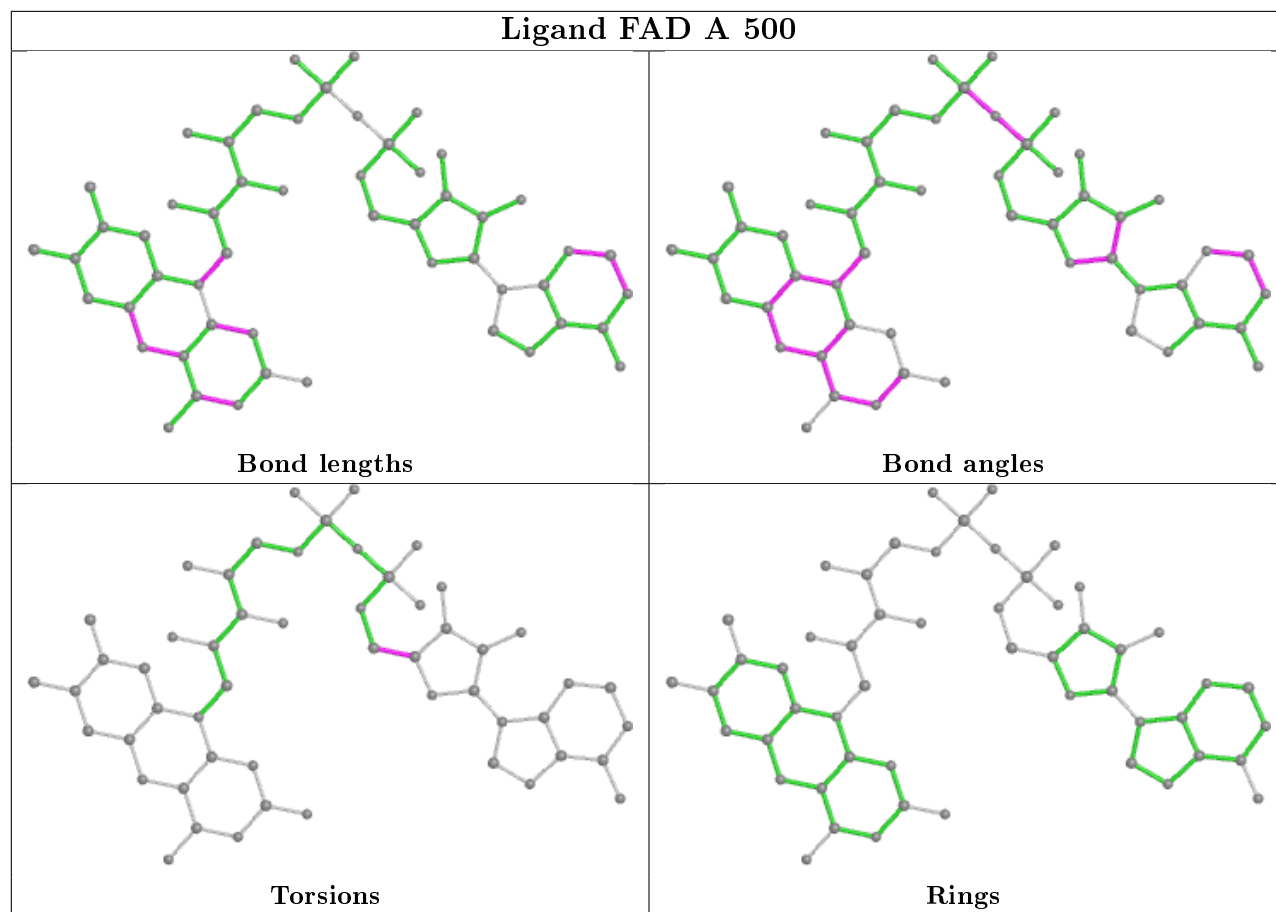


The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	451/463 (97%)	-0.37	2 (0%) 92 93	27, 34, 43, 48	0
1	B	452/463 (97%)	-0.33	3 (0%) 87 89	26, 34, 43, 48	0
All	All	903/926 (97%)	-0.35	5 (0%) 89 90	26, 34, 43, 48	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	238	GLN	4.1
1	B	237	ALA	3.7
1	A	238	GLN	3.4
1	B	239	GLY	3.4
1	A	237	ALA	2.4

### 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](#)

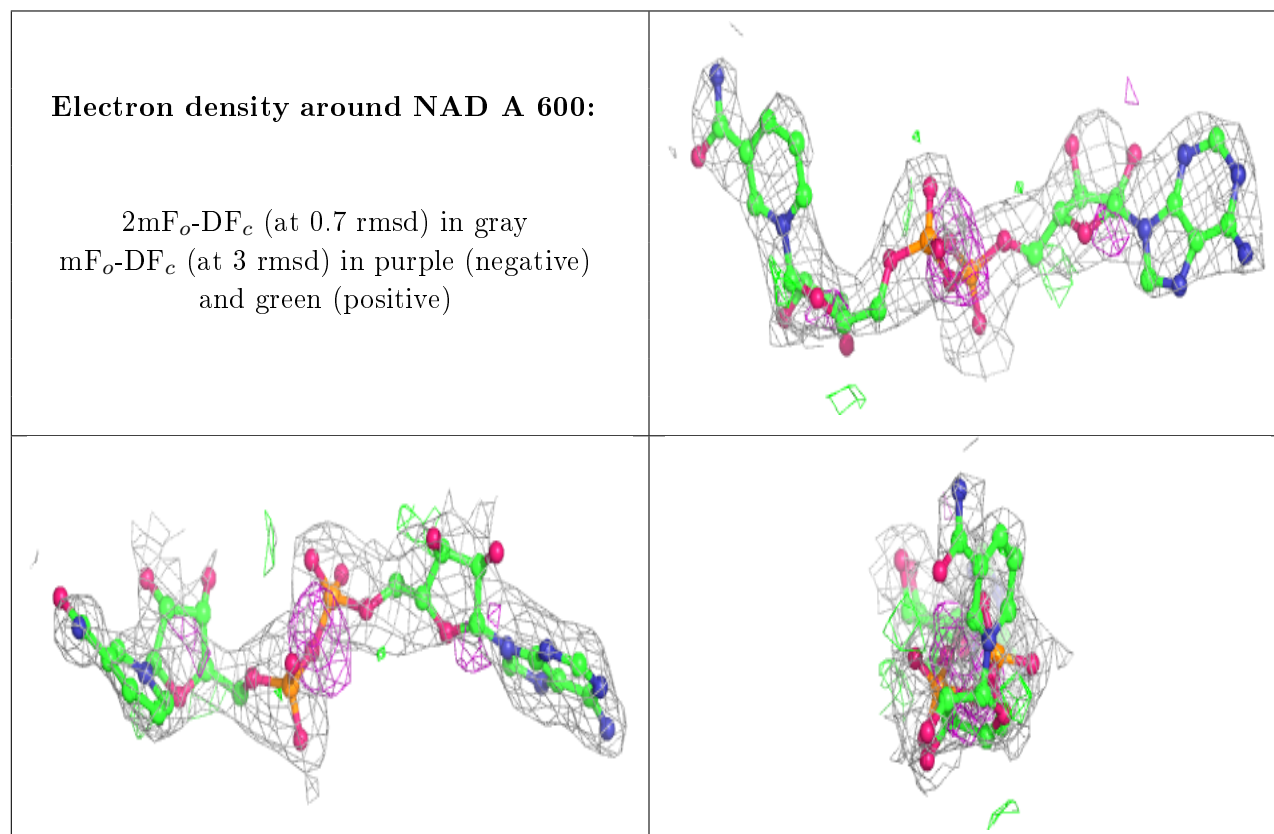
There are no carbohydrates in this entry.

### 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. 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.

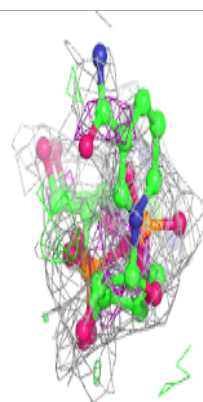
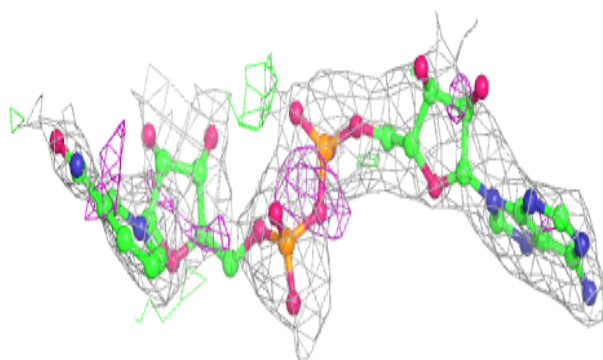
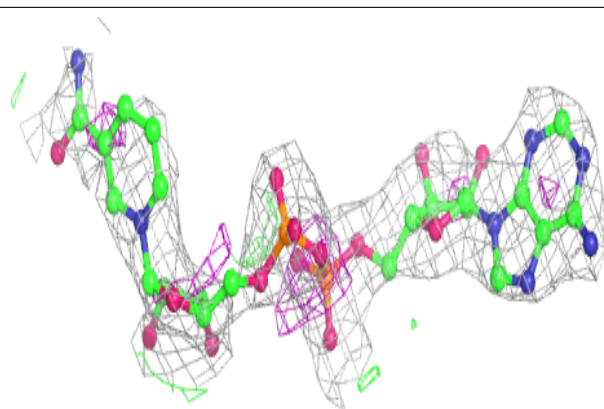
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAD	A	600	44/44	0.84	0.25	83,85,89,89	0
3	NAD	B	600	44/44	0.85	0.27	86,89,92,92	0
4	CL	B	469	1/1	0.93	0.07	65,65,65,65	0
4	CL	A	469	1/1	0.93	0.08	66,66,66,66	0
4	CL	B	464	1/1	0.95	0.16	47,47,47,47	0
4	CL	A	464	1/1	0.95	0.14	50,50,50,50	0
4	CL	A	467	1/1	0.95	0.07	64,64,64,64	0
4	CL	A	465	1/1	0.97	0.07	49,49,49,49	0
4	CL	B	467	1/1	0.97	0.06	59,59,59,59	0
2	FAD	B	500	53/53	0.98	0.10	31,34,35,36	0
4	CL	B	465	1/1	0.98	0.14	48,48,48,48	0
5	NI	A	468	1/1	0.98	0.07	42,42,42,42	0
2	FAD	A	500	53/53	0.98	0.11	30,34,35,36	0
5	NI	A	466	1/1	0.99	0.10	42,42,42,42	0
5	NI	B	466	1/1	0.99	0.09	46,46,46,46	0
5	NI	B	468	1/1	0.99	0.08	42,42,42,42	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

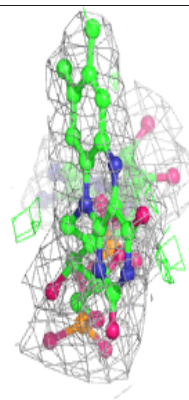
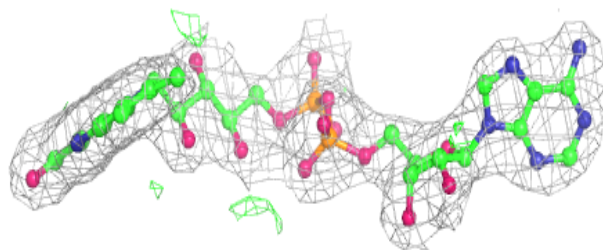
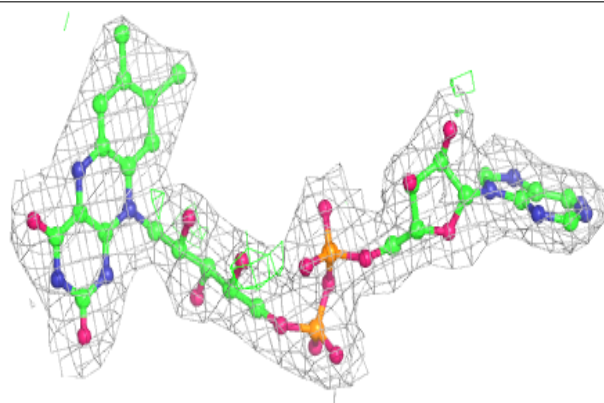


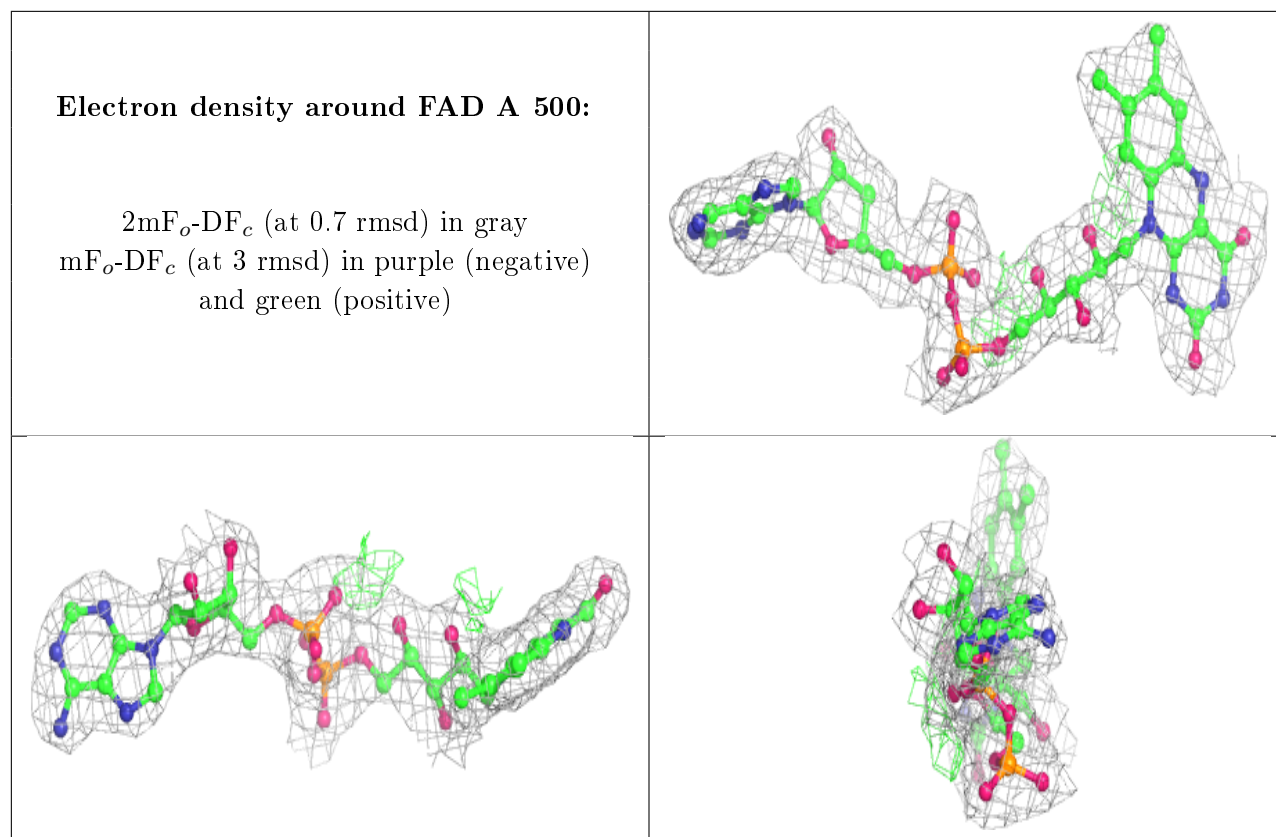
**Electron density around NAD B 600:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around FAD B 500:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.