



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 12:30 PM UTC

PDB ID : 7AAU / pdb\_00007aau  
Title : Crystal structure of nitrosogluthione reductase from *Chlamydomonas reinhardtii* in complex with NAD<sup>+</sup>  
Authors : Fermani, S.; Zaffagnini, M.; Falini, G.; Lemaire, S.D.  
Deposited on : 2020-09-04  
Resolution : 2.30 Å (reported)

This is a wwPDB X-ray Structure Validation Summary 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

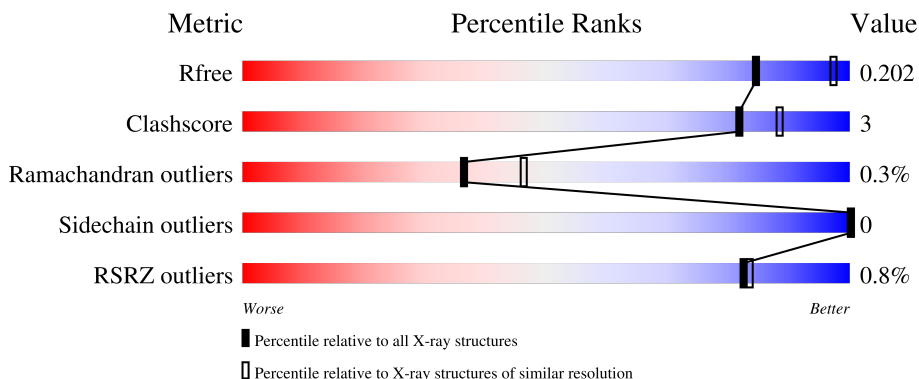
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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.



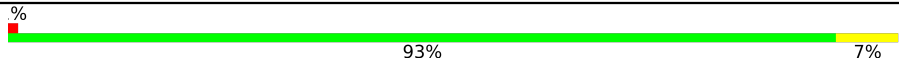
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 of 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	378	 96%
1	B	378	 94% 5%
1	C	378	 95% 5%
1	D	378	 95% 5%
1	E	378	 93% 6%

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Mol	Chain	Length	Quality of chain
1	F	378	 A horizontal bar chart representing the quality of chain. The bar is 93% green and 7% yellow. A small red square is at the beginning of the bar. The percentage values '93%' and '7%' are printed below the bar.

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
5	CL	F	407	-	-	X	-

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 18798 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 S-(hydroxymethyl)glutathione dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	377	2835	1796	482	534	23	0	2	0
1	B	377	2823	1788	482	530	23	0	0	0
1	C	378	2831	1793	483	531	24	0	0	0
1	D	378	2831	1793	483	531	24	0	0	0
1	E	376	2817	1785	481	528	23	0	0	0
1	F	377	2826	1790	482	530	24	0	1	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		
2	E	2	Total	Zn	0	0
			2	2		
2	F	2	Total	Zn	0	0
			2	2		

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>7</sub>O<sub>14</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 4 2	0	0
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0
4	B	1	Total C O 7 4 3	0	0
4	B	1	Total C O 6 4 2	0	0
4	C	1	Total C O 7 4 3	0	0
4	C	1	Total C O 7 4 3	0	0
4	D	1	Total C O 7 4 3	0	0
4	D	1	Total C O 6 4 2	0	0
4	D	1	Total C O 7 4 3	0	0
4	E	1	Total C O 7 4 3	0	0
4	E	1	Total C O 6 4 2	0	0
4	F	1	Total C O 7 4 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	1	Total	C O	0	0
			7	4 3		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total	Cl	0	0
			2	2		
5	F	2	Total	Cl	0	0
			2	2		

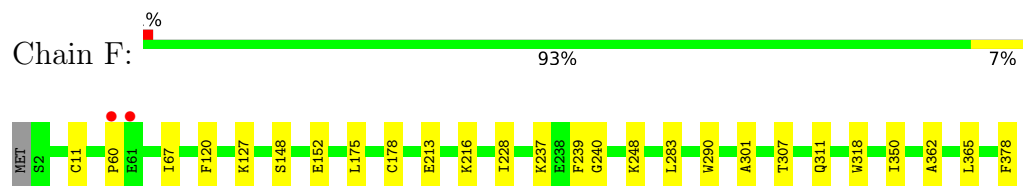
- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	265	Total	O	0	0
			265	265		
7	B	283	Total	O	0	0
			283	283		
7	C	260	Total	O	0	0
			260	260		
7	D	258	Total	O	0	0
			258	258		
7	E	169	Total	O	0	0
			169	169		
7	F	218	Total	O	0	0
			218	218		





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.75Å 142.72Å 206.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.56 – 2.30 48.56 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.56-2.30) 99.6 (48.56-2.30)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.52 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, $R_{free}$	0.178 , 0.226 (Not available) , 0.202	Depositor DCC
$R_{free}$ test set	5029 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.6	Xtrriage
Anisotropy	0.287	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 37.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	18798	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.05% 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 [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, CL, NAD, PEG

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	0.18	0/2903	0.38	0/3940
1	B	0.17	0/2885	0.37	0/3916
1	C	0.20	0/2893	0.41	0/3926
1	D	0.16	0/2893	0.37	0/3926
1	E	0.16	0/2879	0.39	1/3908 (0.0%)
1	F	0.18	0/2891	0.39	0/3924
All	All	0.18	0/17344	0.39	1/23540 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	369	GLY	N-CA-C	5.04	119.68	113.79

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	2835	0	2812	11	0
1	B	2823	0	2800	10	0
1	C	2831	0	2812	16	0
1	D	2831	0	2812	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2817	0	2795	13	0
1	F	2826	0	2805	15	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
3	A	44	0	26	0	0
3	B	44	0	26	1	0
3	C	44	0	26	2	0
3	D	44	0	26	1	0
3	E	44	0	26	2	0
3	F	44	0	26	1	0
4	A	27	0	36	3	0
4	B	13	0	16	0	0
4	C	14	0	20	0	0
4	D	20	0	26	2	0
4	E	13	0	16	0	0
4	F	14	0	20	0	0
5	C	2	0	0	0	0
5	F	2	0	0	2	0
6	F	1	0	0	0	0
7	A	265	0	0	2	0
7	B	283	0	0	0	0
7	C	260	0	0	5	0
7	D	258	0	0	4	0
7	E	169	0	0	1	1
7	F	218	0	0	6	0
All	All	18798	0	17126	87	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 3.

The worst 5 of 87 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)
5:F:407:CL:CL	7:F:559:HOH:O	2.26	0.89
1:C:289:GLY:O	7:C:501:HOH:O	1.93	0.86
5:F:407:CL:CL	7:F:643:HOH:O	2.29	0.86
1:F:307:THR:OG1	7:F:501:HOH:O	1.98	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:TYR:HD2	4:A:405:PEG:H41	1.46	0.80

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)
7:E:559:HOH:O	7:E:644:HOH:O[4_445]	2.18	0.02

## 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	377/378 (100%)	366 (97%)	11 (3%)	0	100	100
1	B	375/378 (99%)	364 (97%)	10 (3%)	1 (0%)	36	46
1	C	376/378 (100%)	362 (96%)	13 (4%)	1 (0%)	36	46
1	D	376/378 (100%)	364 (97%)	12 (3%)	0	100	100
1	E	374/378 (99%)	360 (96%)	12 (3%)	2 (0%)	24	31
1	F	376/378 (100%)	363 (96%)	11 (3%)	2 (0%)	24	31
All	All	2254/2268 (99%)	2179 (97%)	69 (3%)	6 (0%)	36	46

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	3	GLU
1	E	251	GLU
1	E	178	CYS
1	C	178	CYS
1	F	178	CYS

### 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	301/300 (100%)	301 (100%)	0	100	100
1	B	299/300 (100%)	299 (100%)	0	100	100
1	C	300/300 (100%)	300 (100%)	0	100	100
1	D	300/300 (100%)	300 (100%)	0	100	100
1	E	298/300 (99%)	298 (100%)	0	100	100
1	F	300/300 (100%)	300 (100%)	0	100	100
All	All	1798/1800 (100%)	1798 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	352	HIS
1	D	353	ASN
1	F	311	GLN
1	F	49	GLN
1	F	303	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 oligosaccharides in this entry.

## 5.6 Ligand geometry i

Of 38 ligands modelled in this entry, 17 are monoatomic - leaving 21 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
4	PEG	A	404	4	5,5,6	0.49	0	4,4,5	0.30	0
4	PEG	C	405	-	6,6,6	0.51	0	5,5,5	0.27	0
4	PEG	C	404	-	6,6,6	0.53	0	5,5,5	0.26	0
4	PEG	D	404	4	6,6,6	0.50	0	5,5,5	0.37	0
3	NAD	D	403	-	46,48,48	4.09	17 (36%)	64,73,73	1.79	13 (20%)
4	PEG	F	405	-	6,6,6	0.47	0	5,5,5	0.26	0
4	PEG	F	404	-	6,6,6	0.49	0	5,5,5	0.30	0
4	PEG	A	406	-	6,6,6	0.48	0	5,5,5	0.35	0
4	PEG	A	405	4	6,6,6	0.54	0	5,5,5	1.59	2 (40%)
4	PEG	B	404	4	6,6,6	0.50	0	5,5,5	0.51	0
4	PEG	D	406	-	6,6,6	0.48	0	5,5,5	0.25	0
3	NAD	C	403	-	46,48,48	4.03	16 (34%)	64,73,73	1.80	13 (20%)
4	PEG	E	405	4	5,5,6	0.52	0	4,4,5	0.20	0
3	NAD	E	403	-	46,48,48	4.06	16 (34%)	64,73,73	1.78	14 (21%)
4	PEG	D	405	4	5,5,6	0.52	0	4,4,5	0.29	0
3	NAD	F	403	-	46,48,48	4.10	16 (34%)	64,73,73	1.73	14 (21%)
4	PEG	E	404	4	6,6,6	0.48	0	5,5,5	0.35	0
4	PEG	B	405	4	5,5,6	0.55	0	4,4,5	0.35	0
3	NAD	B	403	-	46,48,48	4.02	16 (34%)	64,73,73	1.77	12 (18%)
3	NAD	A	403	-	46,48,48	4.03	17 (36%)	64,73,73	1.69	12 (18%)
4	PEG	A	407	-	6,6,6	0.49	0	5,5,5	0.27	0

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
4	PEG	A	404	4	-	3/3/3/4	-
4	PEG	C	405	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PEG	C	404	-	-	1/4/4/4	-
4	PEG	D	404	4	-	2/4/4/4	-
3	NAD	D	403	-	-	6/30/62/62	0/5/5/5
4	PEG	F	405	-	-	2/4/4/4	-
4	PEG	F	404	-	-	1/4/4/4	-
4	PEG	A	406	-	-	1/4/4/4	-
4	PEG	A	405	4	-	2/4/4/4	-
4	PEG	B	404	4	-	3/4/4/4	-
4	PEG	D	406	-	-	3/4/4/4	-
3	NAD	C	403	-	-	5/30/62/62	0/5/5/5
4	PEG	E	405	4	-	2/3/3/4	-
3	NAD	E	403	-	-	6/30/62/62	0/5/5/5
4	PEG	D	405	4	-	2/3/3/4	-
3	NAD	F	403	-	-	4/30/62/62	0/5/5/5
4	PEG	E	404	4	-	1/4/4/4	-
4	PEG	B	405	4	-	2/3/3/4	-
3	NAD	B	403	-	-	6/30/62/62	0/5/5/5
3	NAD	A	403	-	-	6/30/62/62	0/5/5/5
4	PEG	A	407	-	-	2/4/4/4	-

The worst 5 of 98 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	403	NAD	O4D-C1D	15.88	1.61	1.40
3	F	403	NAD	O4D-C1D	15.83	1.61	1.40
3	C	403	NAD	O4D-C1D	15.67	1.61	1.40
3	B	403	NAD	O4D-C1D	15.57	1.61	1.40
3	E	403	NAD	O4D-C1D	15.55	1.61	1.40

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	403	NAD	N3A-C2A-N1A	-5.86	119.71	128.58
3	C	403	NAD	N3A-C2A-N1A	-5.81	119.78	128.58
3	D	403	NAD	N3A-C2A-N1A	-5.80	119.80	128.58
3	E	403	NAD	N3A-C2A-N1A	-5.60	120.10	128.58
3	F	403	NAD	N3A-C2A-N1A	-5.46	120.31	128.58

There are no chirality outliers.

5 of 62 torsion outliers are listed below:

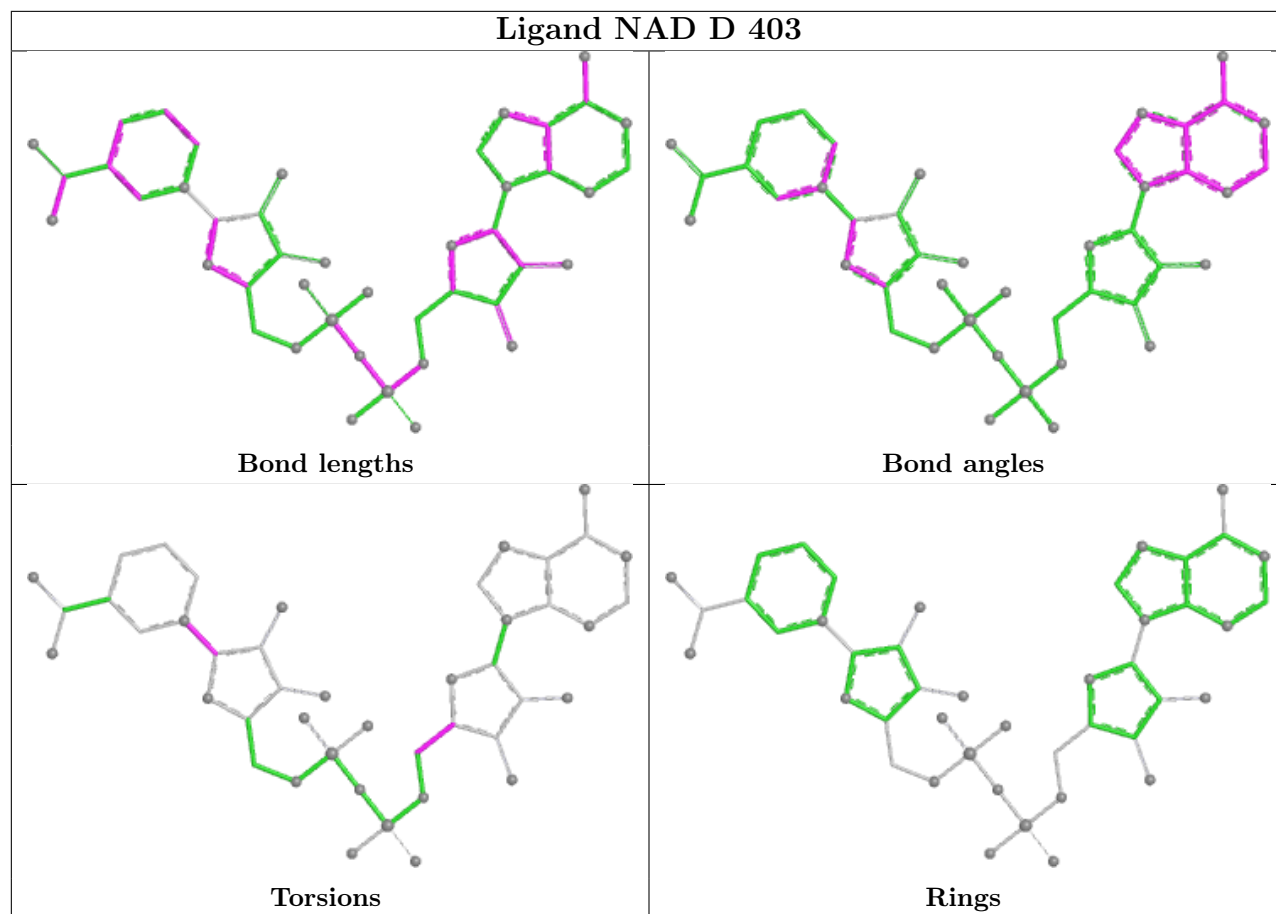
Mol	Chain	Res	Type	Atoms
3	A	403	NAD	O4D-C1D-N1N-C2N
3	A	403	NAD	O4D-C1D-N1N-C6N
3	A	403	NAD	C2D-C1D-N1N-C2N
3	A	403	NAD	C2D-C1D-N1N-C6N
3	B	403	NAD	O4D-C1D-N1N-C2N

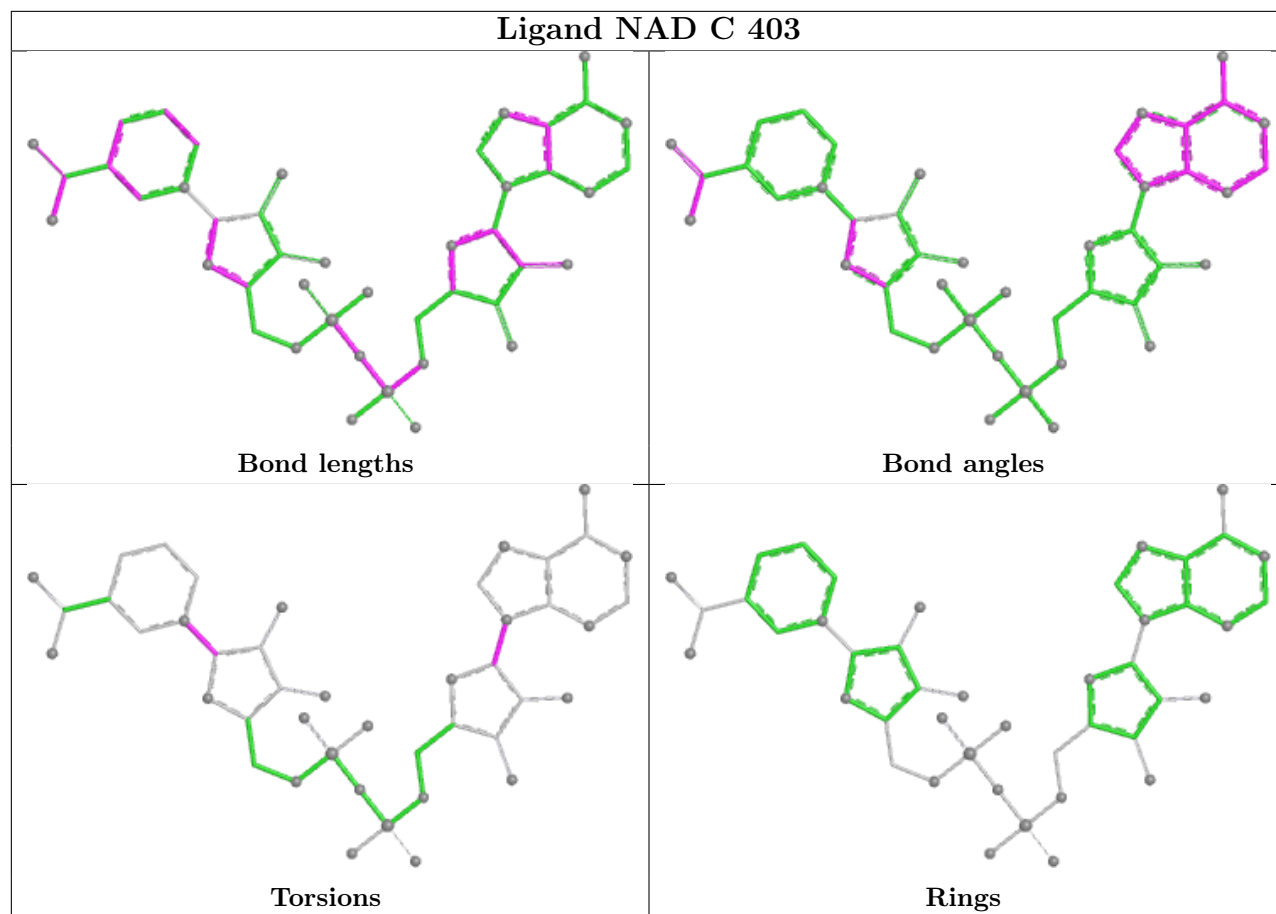
There are no ring outliers.

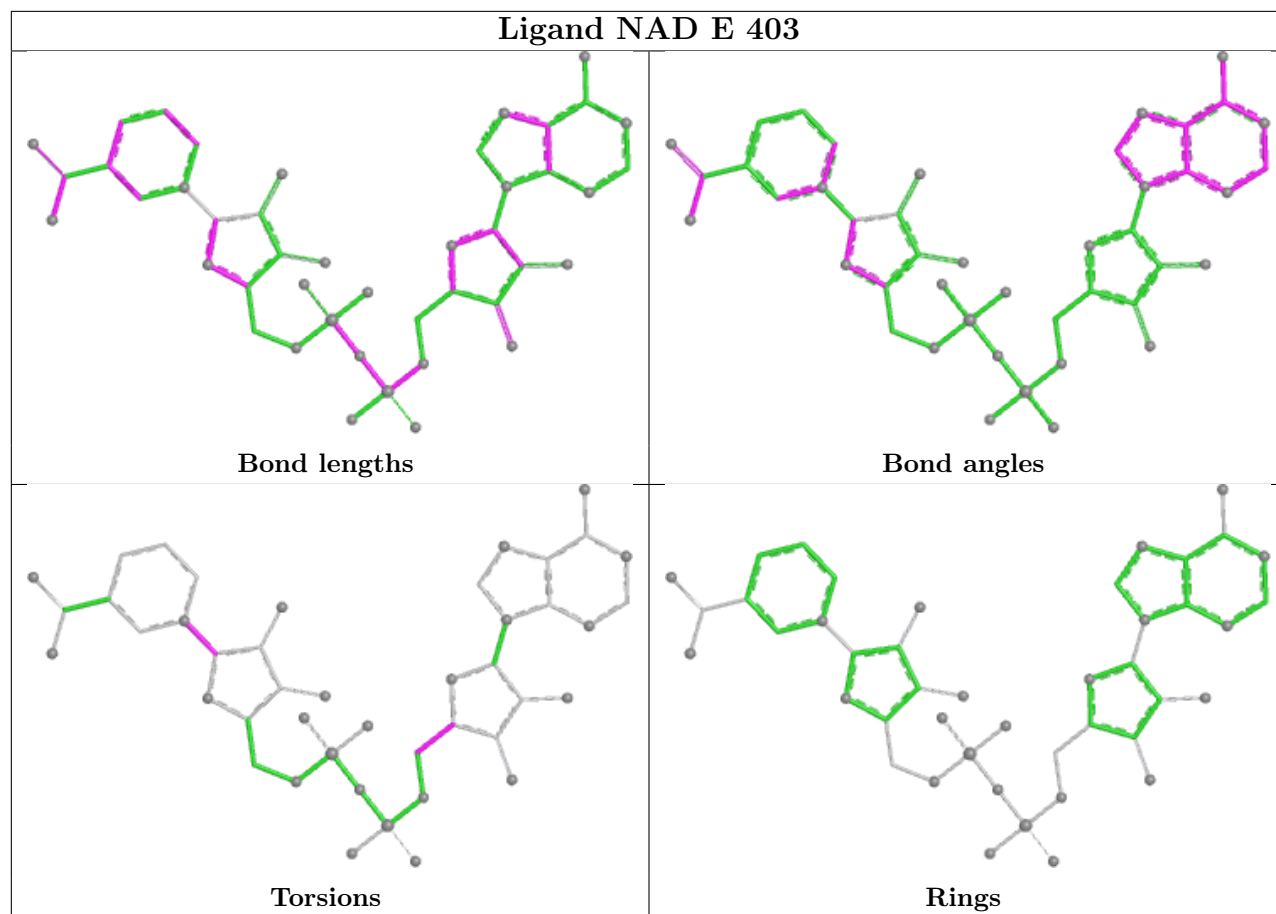
9 monomers are involved in 12 short contacts:

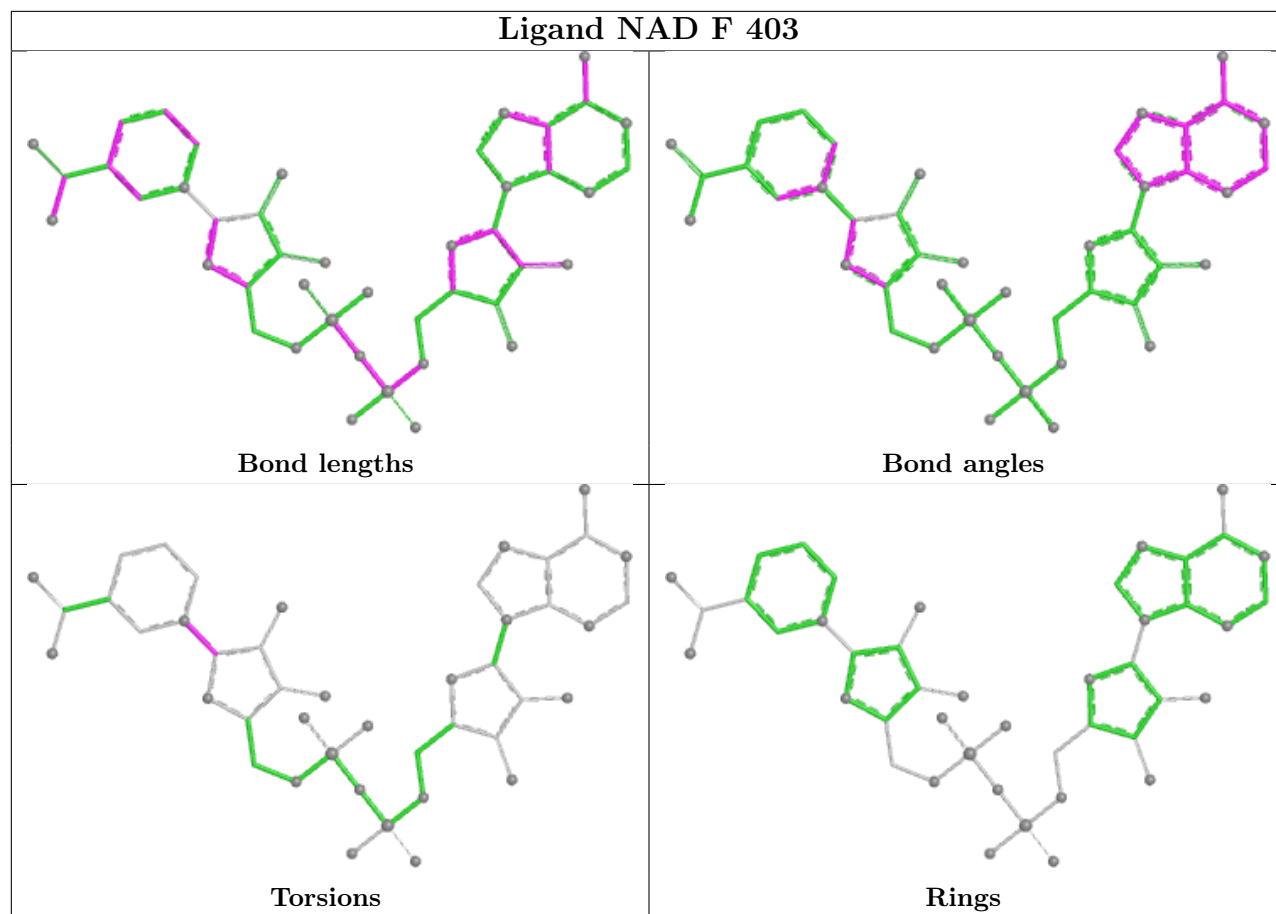
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	404	PEG	1	0
3	D	403	NAD	1	0
4	A	406	PEG	1	0
4	A	405	PEG	2	0
3	C	403	NAD	2	0
3	E	403	NAD	2	0
4	D	405	PEG	1	0
3	F	403	NAD	1	0
3	B	403	NAD	1	0

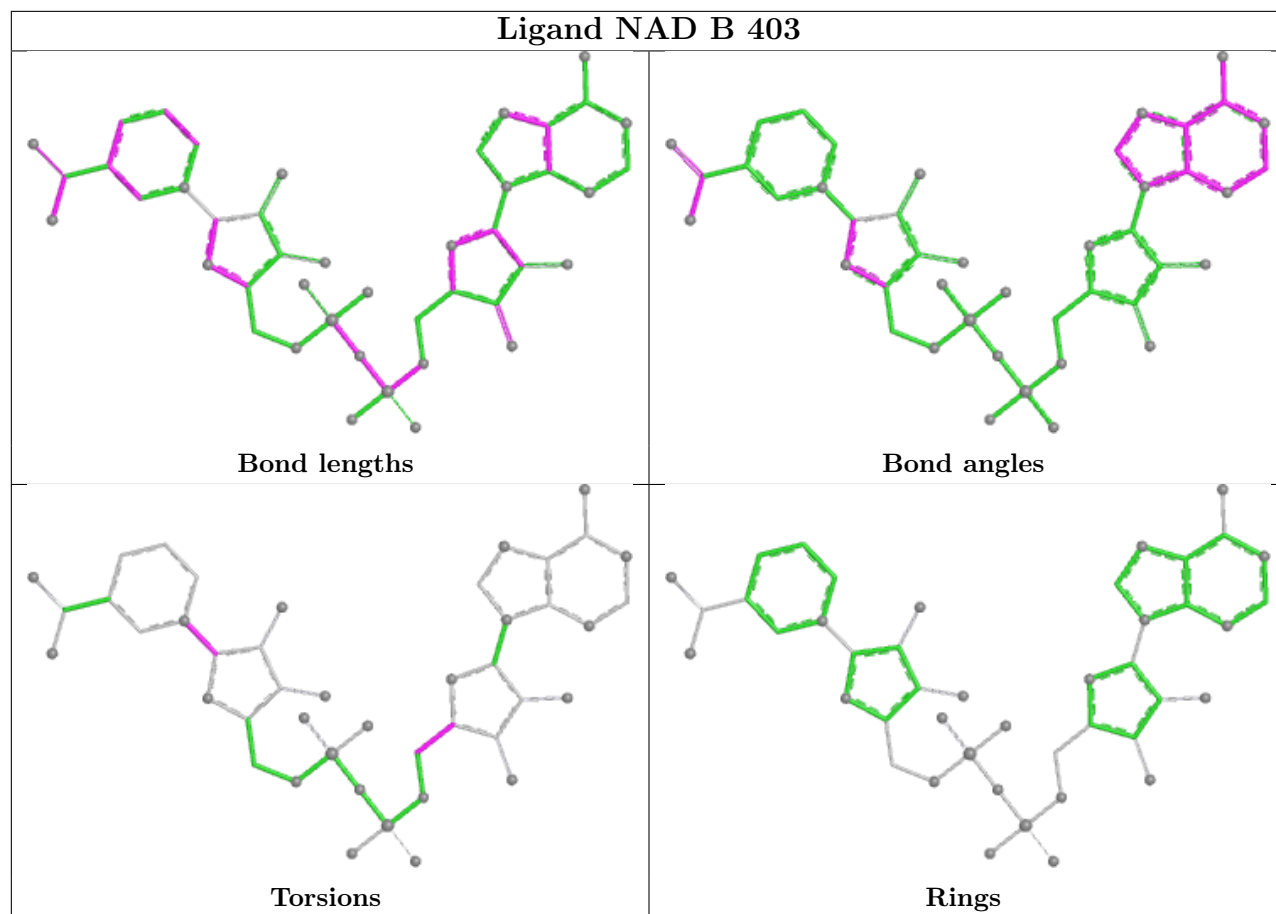
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

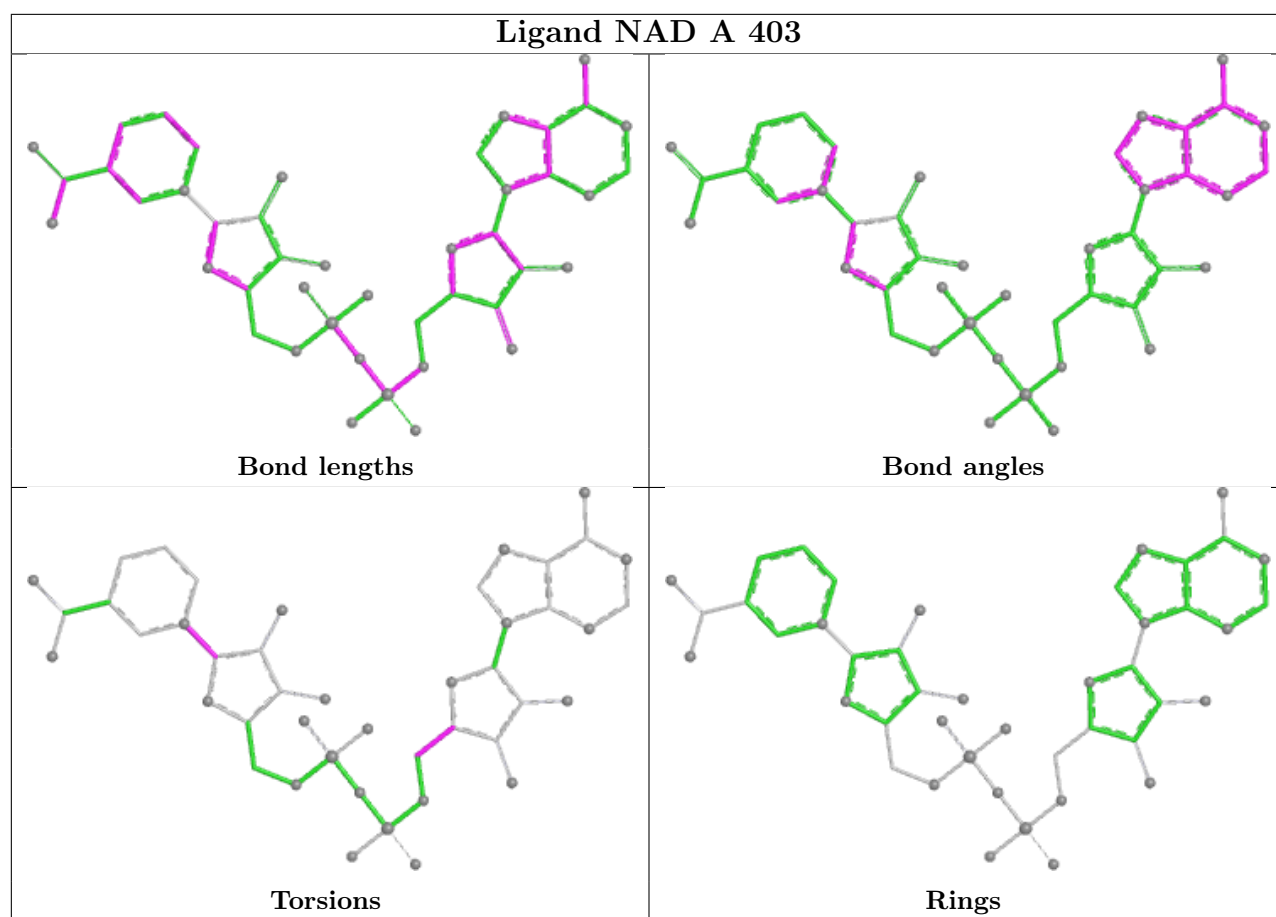












## 5.7 Other polymers [i](#)

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	377/378 (99%)	-0.39	3 (0%) 82 83	18, 26, 48, 75	2 (0%)
1	B	377/378 (99%)	-0.41	2 (0%) 87 87	18, 26, 48, 74	0
1	C	378/378 (100%)	-0.36	1 (0%) 90 90	18, 27, 53, 68	0
1	D	378/378 (100%)	-0.39	4 (1%) 78 79	18, 27, 45, 67	0
1	E	376/378 (99%)	-0.02	7 (1%) 66 68	23, 34, 57, 74	0
1	F	377/378 (99%)	-0.26	2 (0%) 87 87	19, 30, 47, 76	1 (0%)
All	All	2263/2268 (99%)	-0.30	19 (0%) 82 83	18, 28, 50, 76	3 (0%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1	MET	4.8
1	D	1	MET	3.2
1	D	2	SER	3.1
1	D	369	GLY	2.7
1	D	368	ALA	2.7

### 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 oligosaccharides 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.

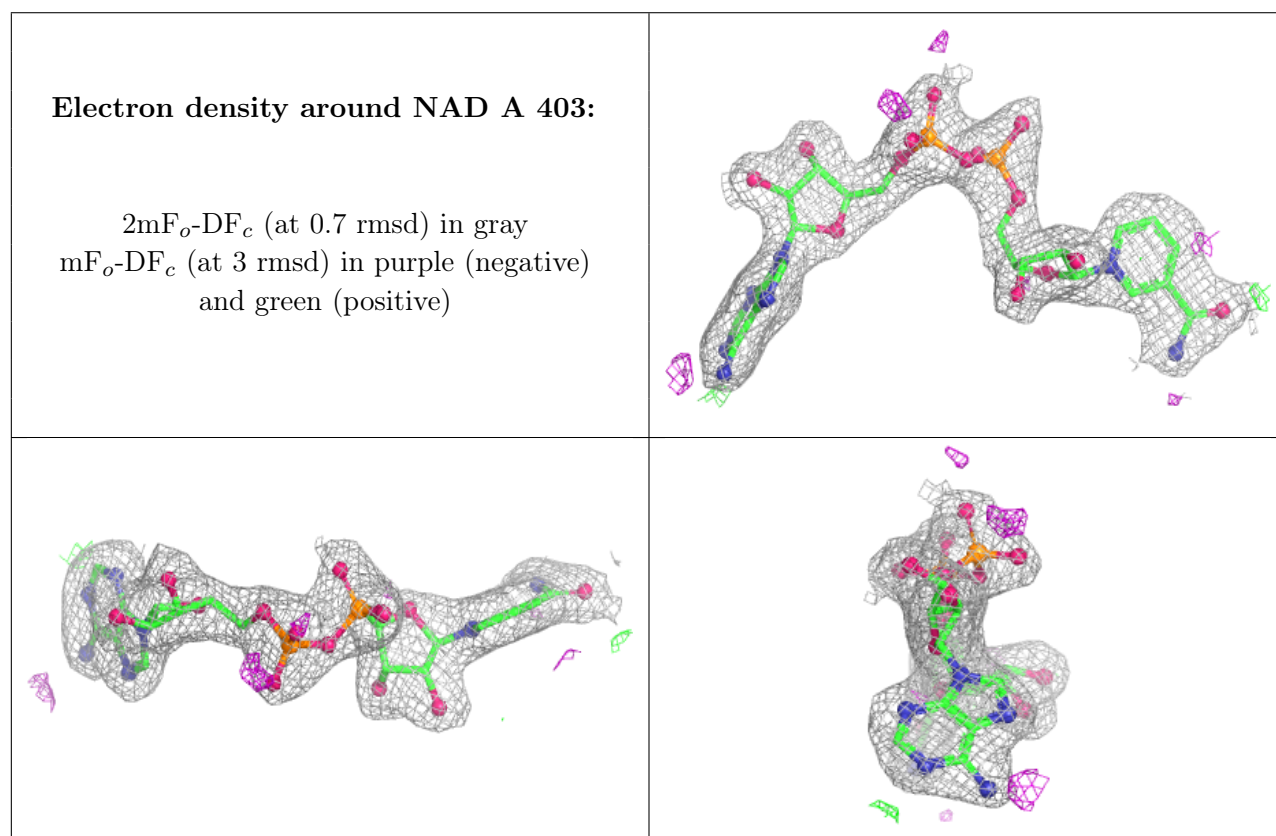
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	PEG	A	405	7/7	0.80	0.21	27,36,41,46	0
4	PEG	F	405	7/7	0.81	0.14	36,41,46,49	0
4	PEG	F	404	7/7	0.83	0.12	30,36,41,43	0
4	PEG	A	404	6/7	0.85	0.14	31,33,38,47	0
4	PEG	E	404	7/7	0.87	0.15	39,40,47,48	0
4	PEG	C	405	7/7	0.87	0.12	29,31,38,40	0
4	PEG	D	405	6/7	0.87	0.12	35,38,42,47	0
5	CL	C	406	1/1	0.87	0.10	61,61,61,61	0
4	PEG	D	406	7/7	0.89	0.12	37,38,45,47	0
4	PEG	B	405	6/7	0.89	0.13	34,38,40,43	0
4	PEG	C	404	7/7	0.89	0.12	34,38,39,43	0
4	PEG	A	406	7/7	0.89	0.10	29,35,41,44	0
4	PEG	A	407	7/7	0.89	0.10	30,34,37,39	0
4	PEG	B	404	7/7	0.91	0.10	27,29,33,36	0
4	PEG	D	404	7/7	0.92	0.10	36,38,41,46	0
4	PEG	E	405	6/7	0.93	0.10	36,38,41,42	0
2	ZN	C	401	1/1	0.94	0.07	53,53,53,53	1
5	CL	F	407	1/1	0.95	0.08	51,51,51,51	0
6	MG	F	408	1/1	0.95	0.10	44,44,44,44	0
3	NAD	A	403	44/44	0.96	0.07	22,28,32,37	0
5	CL	F	406	1/1	0.96	0.09	52,52,52,52	0
3	NAD	D	403	44/44	0.96	0.06	21,30,36,39	0
3	NAD	E	403	44/44	0.96	0.07	23,31,38,41	0
3	NAD	F	403	44/44	0.97	0.06	23,30,36,42	0
5	CL	C	407	1/1	0.97	0.11	40,40,40,40	0
3	NAD	C	403	44/44	0.97	0.06	19,25,30,31	0
2	ZN	F	401	1/1	0.97	0.06	60,60,60,60	1
3	NAD	B	403	44/44	0.97	0.06	18,26,30,32	0
2	ZN	E	402	1/1	0.98	0.03	28,28,28,28	0
2	ZN	A	402	1/1	0.99	0.02	25,25,25,25	0
2	ZN	D	402	1/1	0.99	0.02	24,24,24,24	0
2	ZN	A	401	1/1	1.00	0.02	33,33,33,33	0
2	ZN	F	402	1/1	1.00	0.02	25,25,25,25	0
2	ZN	C	402	1/1	1.00	0.02	24,24,24,24	0
2	ZN	D	401	1/1	1.00	0.03	33,33,33,33	0
2	ZN	B	401	1/1	1.00	0.01	32,32,32,32	0
2	ZN	E	401	1/1	1.00	0.04	38,38,38,38	0

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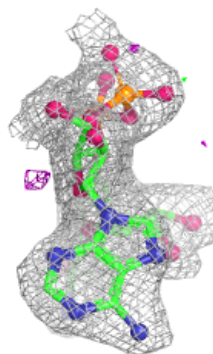
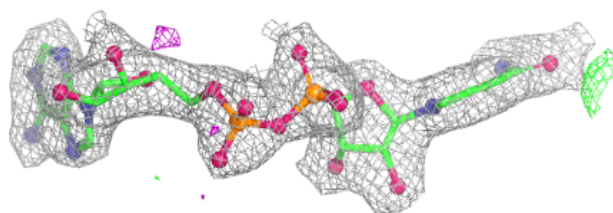
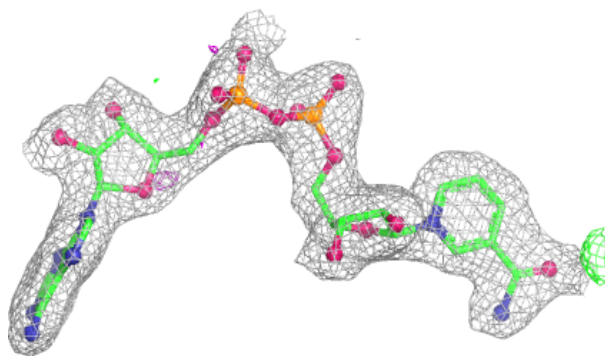
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	B	402	1/1	1.00	0.02	19,19,19,19	0

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.

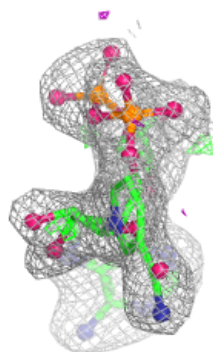
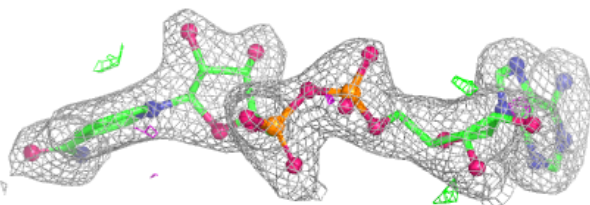
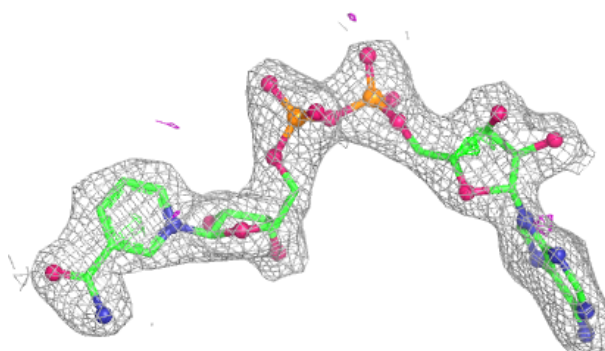


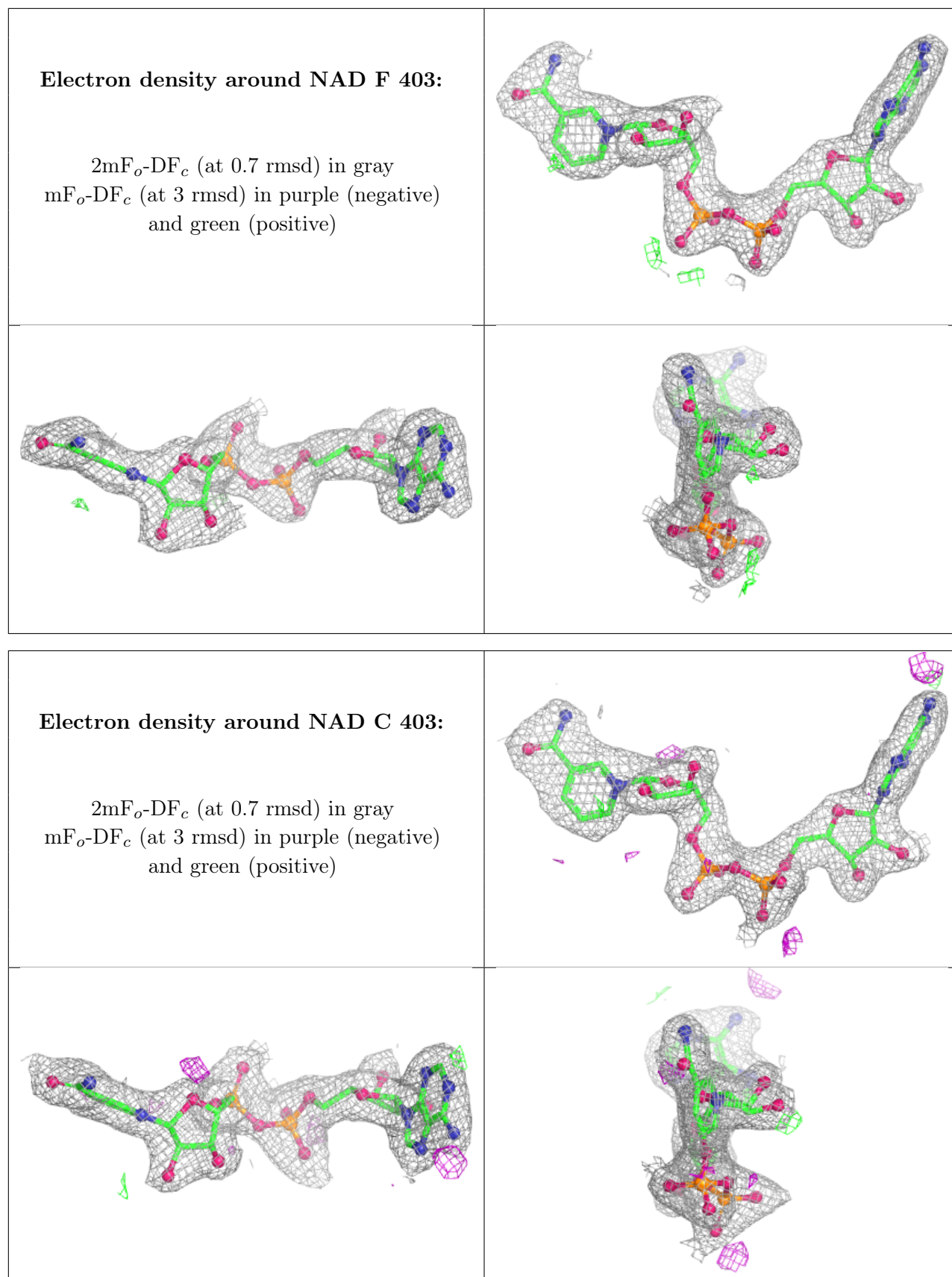
**Electron density around NAD D 403:**

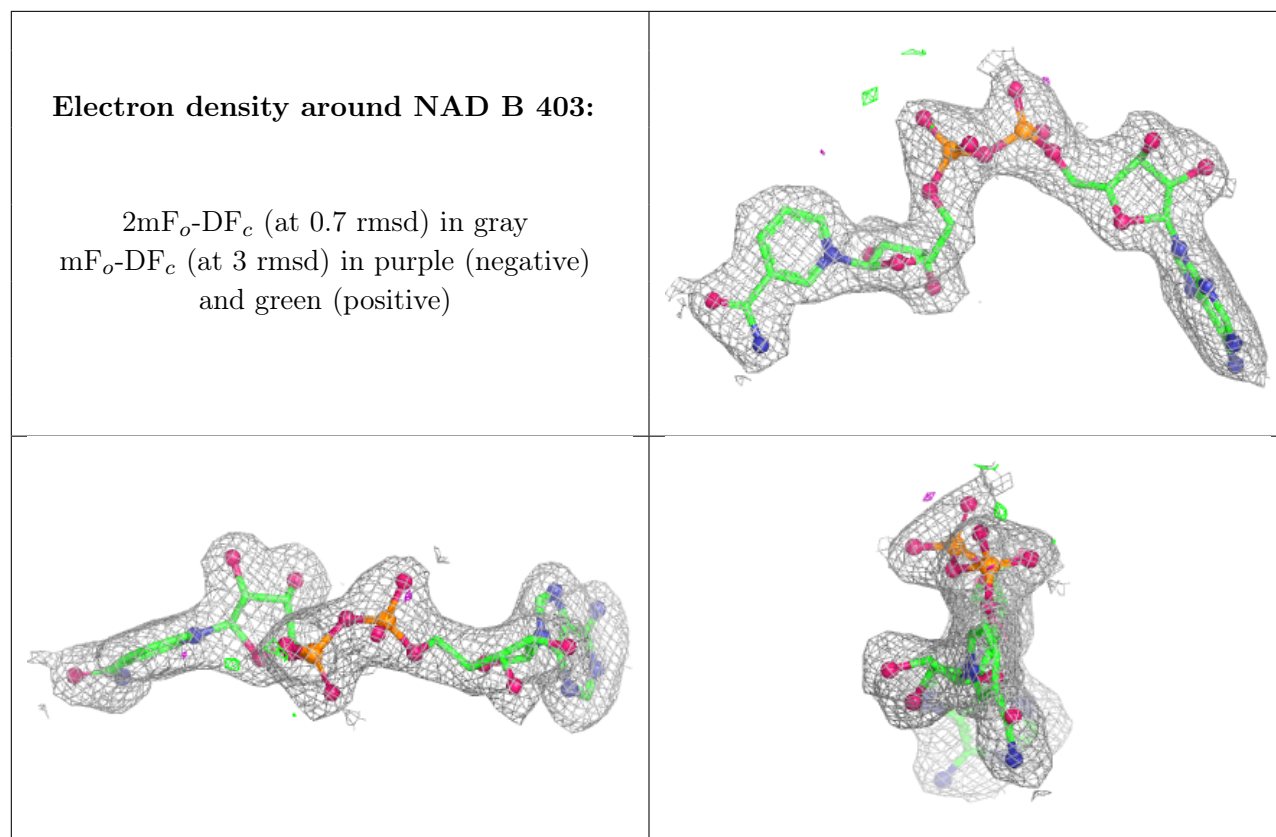
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around NAD E 403:**

$2mF_o-DF_c$  (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.