

wwPDB X-ray Structure Validation Summary Report (i)

Jan 10, 2023 - 03:35 pm GMT

PDB ID	:	8BXX
Title	:	Crystal structure of formate dehydrogenase FDH2 enzyme from Granulicella
		mallensis MP5ACTX8 in complex with NAD and azide.
Authors	:	Robescu, M.S.; Rubini, R.; Filippini, F.; Bergantino, B.; Cendron, L.
Deposited on		
Resolution	:	1.97 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 A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

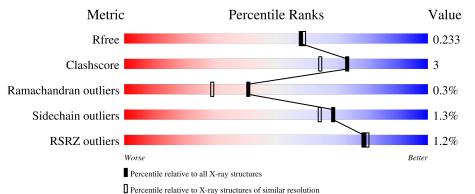
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.3
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.97 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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 >=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 <=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	AA	386	90%	5% •	
1	BB	386	% 85%	10% •	
1	CC	386	% 87%	9%	·
1	DD	386	88%	8%	•



8BXX

2 Entry composition (i)

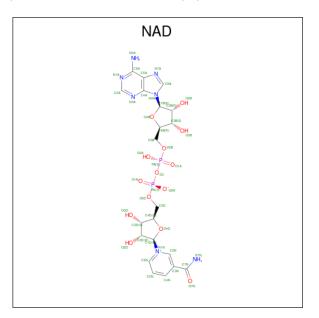
There are 5 unique types of molecules in this entry. The entry contains 12689 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	AA	370	Total	С	Ν	0	S	0	0	0
		0.0	2885	1841	493	539	12	Ŭ	Ŭ	
1	BB	370	Total	\mathbf{C}	Ν	Ο	\mathbf{S}	0	0	0
1	DD	510	2885	1841	493	539	12	0		0
1	CC	270	Total	С	Ν	0	S	0	0	0
		370	2885	1841	493	539	12	0	0	
1	DD	370	Total	С	Ν	0	S	0	2	0
	עע	570	2908	1856	498	542	12	0	Δ	0

• Molecule 1 is a protein called Formate dehydrogenase.

• Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf
0	АА	1	1 Total C N O P		0	0			
	AA	1	44	21	7	14	2	0	0
0	BB	1	Total	С	Ν	Ο	Р	0	0
	DD	1	44	21	7	14	2	0	U

Continued on next page...



 $\mathbf{2}$

DD

AltConf

0

0

Continuea from previous page										
Mol	Chain	Residues	Atoms					ZeroOcc		
2	CC	1	Total	C	N	0	Р	0		
			44	21	1	14	2			

Total

44

С

21

Ν

7

Continued from provious nage

1

 \bullet Molecule 3 is AZIDE ION (three-letter code: AZI) (formula: $\mathrm{N}_3)$ (labeled as "Ligand of Interest" by depositor).

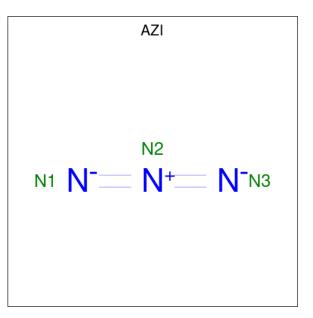
Р

2

0

Ο

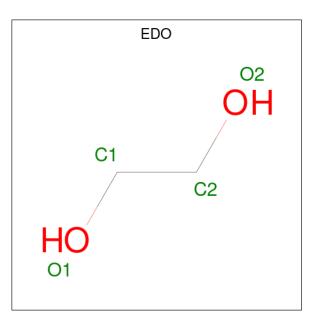
14



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	АА	1	Total N 3 3	0	0
3	BB	1	Total N 3 3	0	0
3	CC	1	Total N 3 3	0	0
3	DD	1	Total N 3 3	0	0

• Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
4	BB	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
4	CC	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
4	DD	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

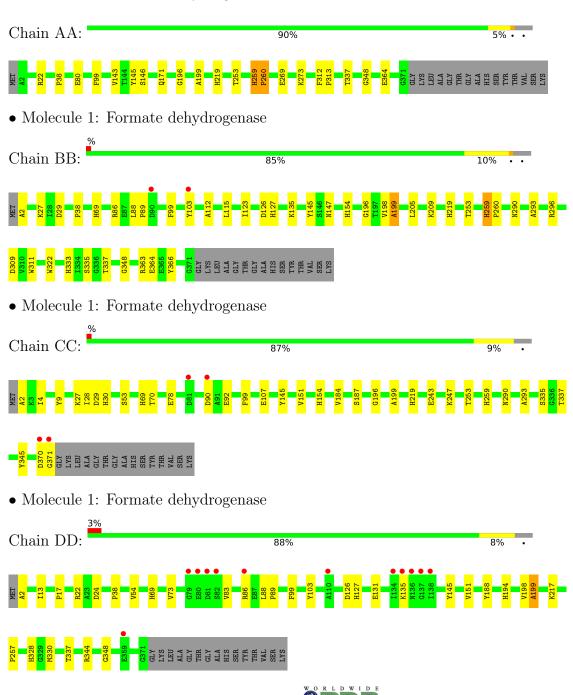
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	АА	239	Total O 239 239	0	0
5	BB	236	Total O 236 236	0	0
5	CC	243	Total O 243 243	0	0
5	DD	204	Total O 204 204	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Formate dehydrogenase

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	72.07Å 128.81Å 85.66Å	Depositor
a, b, c, α , β , γ	90.00° 100.40° 90.00°	Depositor
Resolution (Å)	62.10 - 1.97	Depositor
Resolution (A)	62.10 - 1.97	EDS
% Data completeness	97.8 (62.10-1.97)	Depositor
(in resolution range)	97.9 (62.10-1.97)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.38 (at 1.97 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
D D.	0.188 , 0.234	Depositor
R, R_{free}	0.186 , 0.233	DCC
R_{free} test set	5278 reflections $(4.98%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	15.5	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33, 41.1	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12689	wwPDB-VP
Average B, all atoms $(Å^2)$	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.14% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: NAD, EDO, AZI

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		Bo	nd lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	AA	0.48	1/2957~(0.0%)	0.77	0/4025	
1	BB	0.44	0/2957	0.76	0/4025	
1	CC	0.47	0/2957	0.77	0/4025	
1	DD	0.42	0/2981	0.75	0/4057	
All	All	0.46	1/11852~(0.0%)	0.76	0/16132	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	80	GLU	CD-OE2	-9.20	1.15	1.25

There are no bond angle outliers.

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	AA	2885	0	2868	15	0
1	BB	2885	0	2868	24	0
1	CC	2885	0	2868	19	0
1	DD	2908	0	2888	22	0
2	AA	44	0	26	0	0
2	BB	44	0	26	0	0

Continued on next page...



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	CC	44	0	26	2	0
2	DD	44	0	26	2	0
3	AA	3	0	0	0	0
3	BB	3	0	0	0	0
3	CC	3	0	0	0	0
3	DD	3	0	0	0	0
4	AA	4	0	6	0	0
4	BB	4	0	6	3	0
4	CC	4	0	6	0	0
4	DD	4	0	6	0	0
5	AA	239	0	0	4	0
5	BB	236	0	0	1	0
5	CC	243	0	0	7	0
5	DD	204	0	0	1	0
All	All	12689	0	11620	76	0

Continued from previous page...

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 76 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:AA:171:GLN:HG2	5:AA:709:HOH:O	1.40	1.18
1:BB:127:HIS:NE2	4:BB:403:EDO:H21	1.79	0.96
1:BB:364:GLU:HG3	5:BB:723:HOH:O	1.78	0.82
5:CC:634:HOH:O	1:DD:13:ILE:HD11	1.85	0.74
1:AA:259:HIS:HB2	1:AA:260:PRO:HD2	1.74	0.69

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	Perce	ntiles
1	AA	368/386~(95%)	349~(95%)	18 (5%)	1 (0%)	41	29
1	BB	368/386~(95%)	357~(97%)	10 (3%)	1 (0%)	41	29
1	CC	368/386~(95%)	355~(96%)	12 (3%)	1 (0%)	41	29
1	DD	370/386~(96%)	357~(96%)	12 (3%)	1 (0%)	41	29
All	All	1474/1544~(96%)	1418 (96%)	52~(4%)	4 (0%)	41	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AA	199	ALA
1	CC	199	ALA
1	DD	199	ALA
1	BB	199	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	AA	311/322~(97%)	307~(99%)	4 (1%)	69	64	
1	BB	311/322~(97%)	306~(98%)	5 (2%)	62	56	
1	CC	311/322~(97%)	306~(98%)	5 (2%)	62	56	
1	DD	313/322~(97%)	311~(99%)	2(1%)	86	85	
All	All	1246/1288~(97%)	1230~(99%)	16 (1%)	69	64	

5 of 16 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	DD	126	ASP
1	CC	345	TYR
1	BB	259	HIS
1	CC	253	THR
1	BB	253	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such



sidechains are listed below:

Mol	Chain	Res	Type
1	CC	30	HIS
1	CC	259	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
10101	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
4	EDO	BB	403	-	$3,\!3,\!3$	0.30	0	2,2,2	0.24	0
4	EDO	AA	403	-	3,3,3	0.21	0	2,2,2	0.46	0
3	AZI	BB	402	-	0,2,2	-	-	$0,\!1,\!1$	-	-
3	AZI	CC	402	-	0,2,2	-	-	$0,\!1,\!1$	-	-
3	AZI	DD	402	-	0,2,2	-	-	0,1,1	-	-
4	EDO	CC	403	-	3, 3, 3	0.23	0	$2,\!2,\!2$	0.23	0
4	EDO	DD	403	-	3,3,3	0.16	0	2,2,2	0.27	0
2	NAD	CC	401	-	42,48,48	0.97	2 (4%)	50,73,73	0.90	2 (4%)
2	NAD	AA	401	-	42,48,48	0.64	0	50,73,73	1.05	4 (8%)
3	AZI	AA	402	-	0,2,2	-	-	0,1,1	-	-



Mol Type 0	Chain	Dec	Res Link	Bond lengths			Bond angles			
	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
2	NAD	DD	401	-	42,48,48	0.80	2 (4%)	50,73,73	1.02	4 (8%)
2	NAD	BB	401	-	42,48,48	0.81	1 (2%)	50,73,73	0.81	1 (2%)

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	EDO	BB	403	-	-	1/1/1/1	-
4	EDO	AA	403	-	-	0/1/1/1	-
4	EDO	DD	403	-	-	0/1/1/1	-
4	EDO	CC	403	-	-	0/1/1/1	-
2	NAD	CC	401	-	-	2/26/62/62	0/5/5/5
2	NAD	BB	401	-	-	2/26/62/62	0/5/5/5
2	NAD	DD	401	-	-	3/26/62/62	0/5/5/5
2	NAD	AA	401	-	_	2/26/62/62	0/5/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
2	CC	401	NAD	C2N-N1N	4.30	1.40	1.35
2	BB	401	NAD	C2N-N1N	3.43	1.39	1.35
2	CC	401	NAD	O4D-C1D	3.24	1.45	1.41
2	DD	401	NAD	C2N-N1N	2.44	1.37	1.35
2	DD	401	NAD	O4D-C1D	2.19	1.44	1.41

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
2	DD	401	NAD	C6N-N1N-C2N	-3.28	118.99	121.97
2	AA	401	NAD	C6N-N1N-C2N	-2.96	119.27	121.97
2	CC	401	NAD	C5A-C6A-N6A	2.96	124.85	120.35
2	AA	401	NAD	C5A-C6A-N6A	2.83	124.65	120.35
2	DD	401	NAD	C5A-C6A-N6A	2.66	124.40	120.35

There are no chirality outliers.

5 of 10 torsion outliers are listed below:



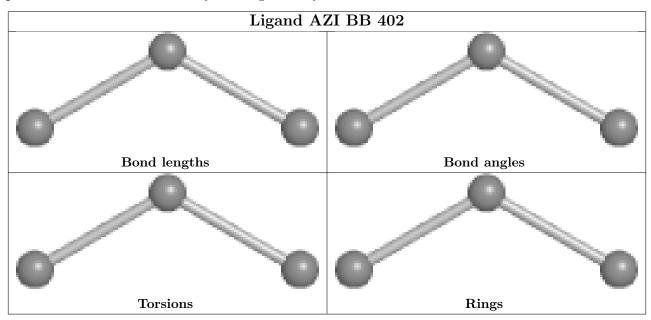
Mol	Chain	Res	Type	Atoms
2	AA	401	NAD	O4D-C1D-N1N-C6N
2	BB	401	NAD	O4D-C1D-N1N-C6N
2	CC	401	NAD	O4D-C1D-N1N-C6N
2	DD	401	NAD	O4D-C1D-N1N-C6N
2	DD	401	NAD	O4B-C4B-C5B-O5B

There are no ring outliers.

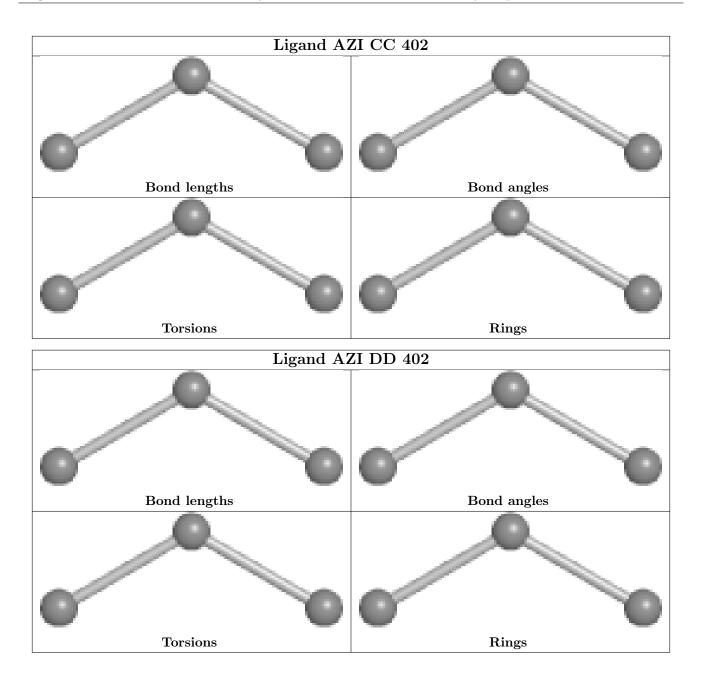
3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	BB	403	EDO	3	0
2	CC	401	NAD	2	0
2	DD	401	NAD	2	0

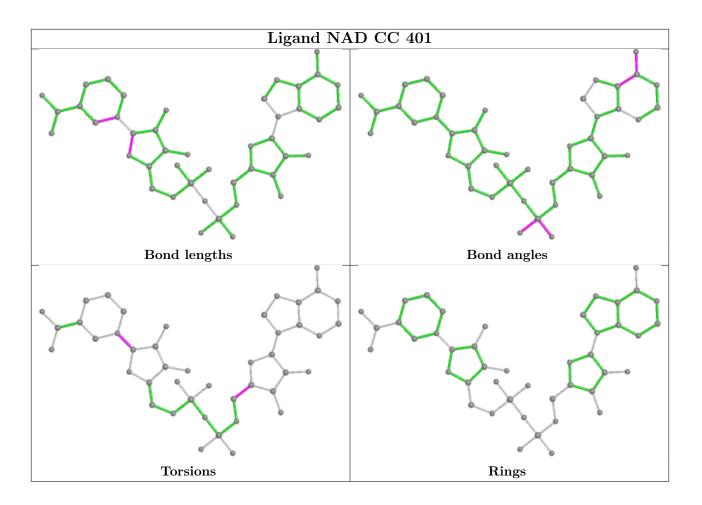
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



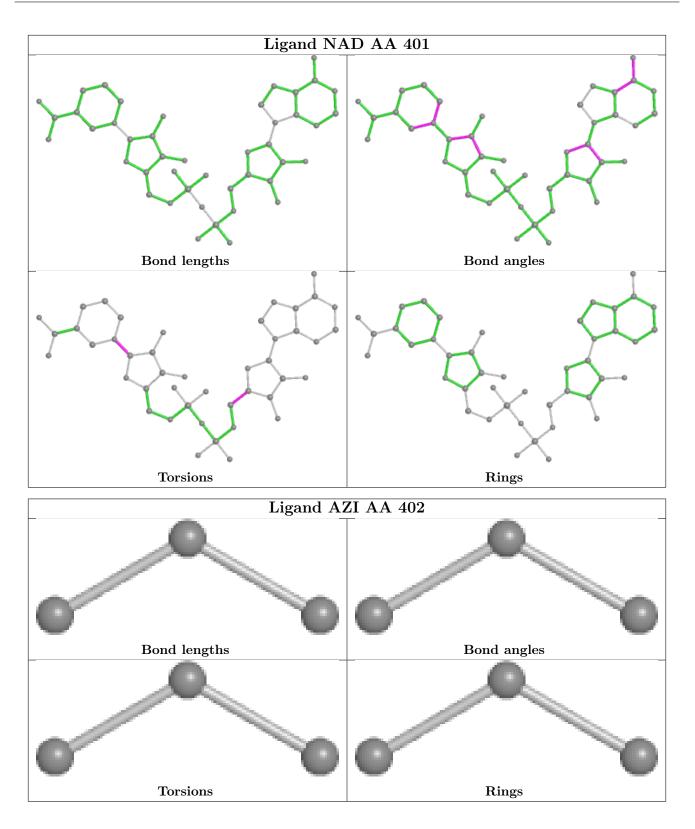




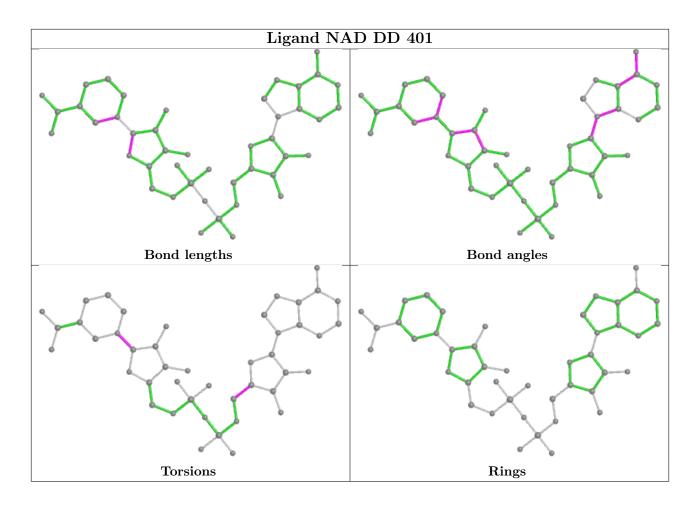




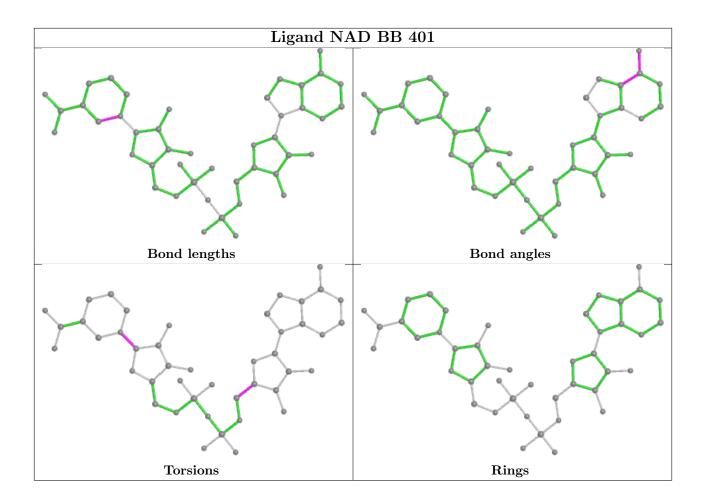












5.7 Other polymers (i)

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^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q<0.9
1	AA	370/386~(95%)	-0.04	0 100 100	5, 13, 26, 37	0
1	BB	370/386~(95%)	-0.01	2 (0%) 91 91	6, 13, 27, 44	0
1	CC	370/386~(95%)	-0.11	4 (1%) 80 82	4, 10, 24, 57	0
1	DD	370/386~(95%)	0.11	12 (3%) 47 50	6, 13, 38, 55	0
All	All	1480/1544~(95%)	-0.01	18 (1%) 79 80	4, 12, 30, 57	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	DD	134	ILE	3.4
1	DD	137	GLY	2.9
1	DD	86[A]	ARG	2.9
1	DD	80	GLU	2.9
1	CC	371	GLY	2.9

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 monosaccharides in this entry.

6.4 Ligands (i)

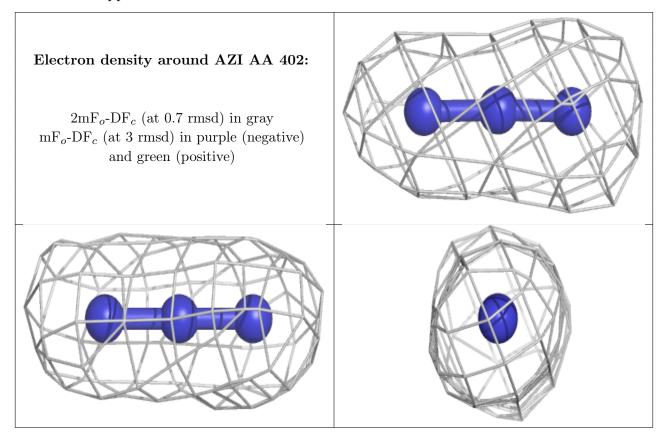
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.



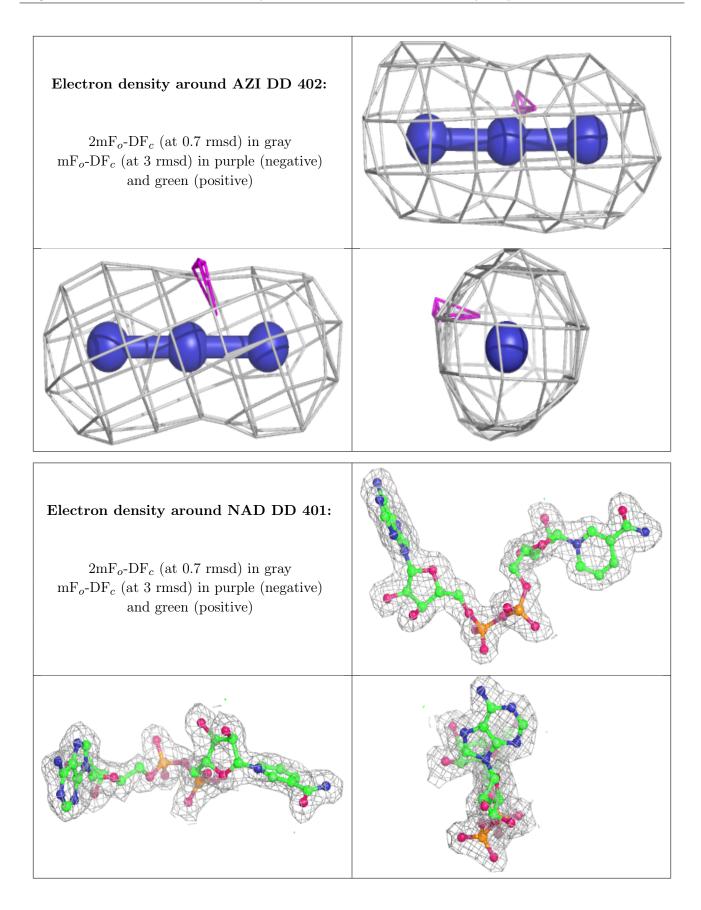
8BXX

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
4	EDO	BB	403	4/4	0.82	0.22	24,31,34,34	0
4	EDO	AA	403	4/4	0.93	0.17	$21,\!27,\!27,\!29$	0
3	AZI	AA	402	3/3	0.94	0.11	$12,\!12,\!13,\!14$	0
4	EDO	DD	403	4/4	0.94	0.18	$25,\!30,\!31,\!31$	0
3	AZI	DD	402	3/3	0.95	0.10	$12,\!12,\!12,\!14$	0
2	NAD	DD	401	44/44	0.95	0.10	$9,\!12,\!18,\!18$	0
2	NAD	AA	401	44/44	0.96	0.09	$8,\!11,\!14,\!15$	0
4	EDO	CC	403	4/4	0.96	0.17	$14,\!15,\!16,\!17$	0
2	NAD	BB	401	44/44	0.96	0.09	$10,\!13,\!17,\!18$	0
3	AZI	BB	402	3/3	0.97	0.08	11,11,12,12	0
2	NAD	CC	401	44/44	0.97	0.09	6, 8, 12, 13	0
3	AZI	CC	402	3/3	0.98	0.10	$6,\!6,\!6,\!6$	0

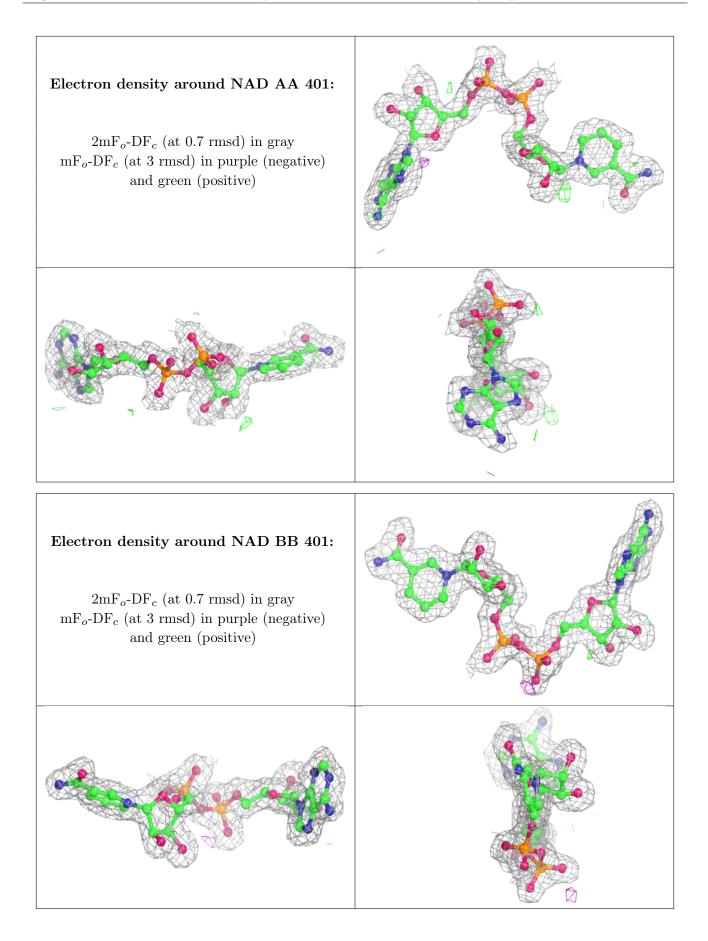
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



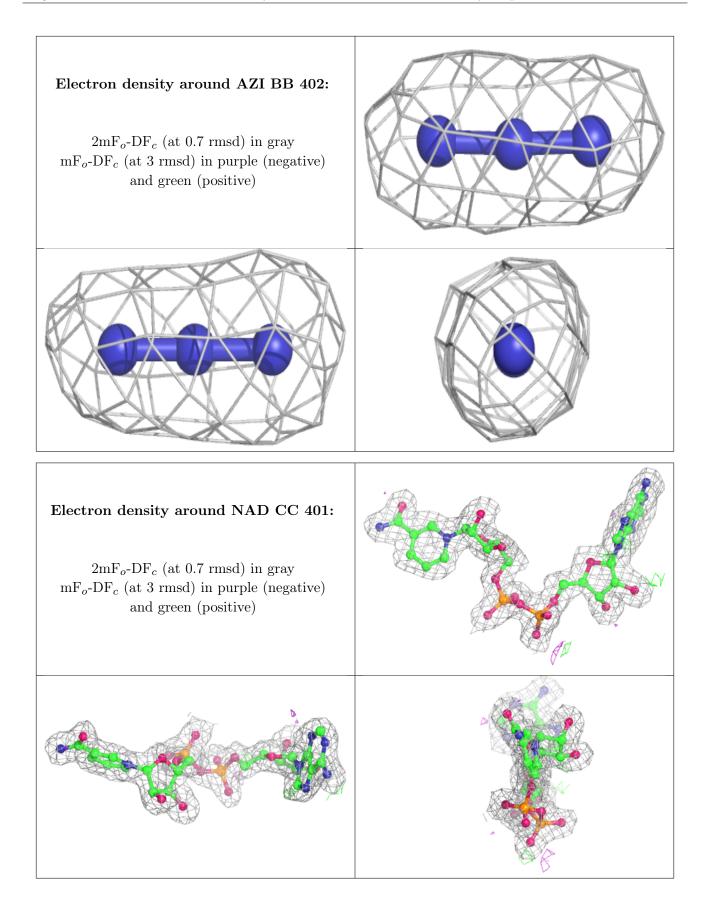




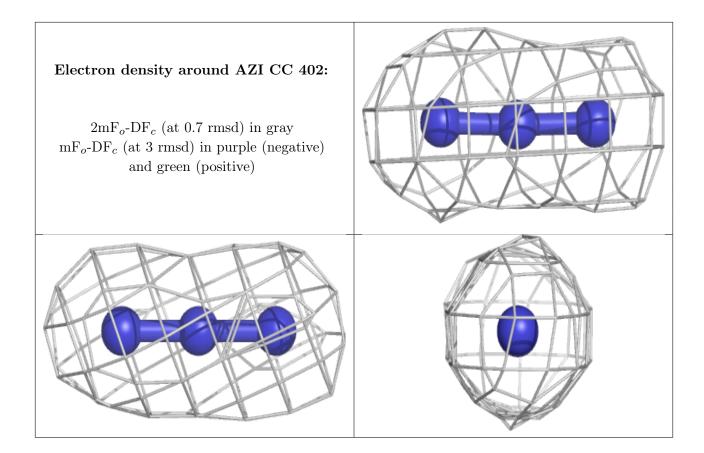












6.5 Other polymers (i)

There are no such residues in this entry.

