Full wwPDB X-ray Structure Validation Report (i)

Jan 14, 2024 – 02:34 am GMT

PDB ID	:	6Z3C
Title	:	High resolution structure of RgNanOx
Authors	:	Naismith, J.H.; Lee, M.O.
Deposited on	:	2020-05-19
Resolution	:	1.74 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
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 (i)) were used in the production of this report:

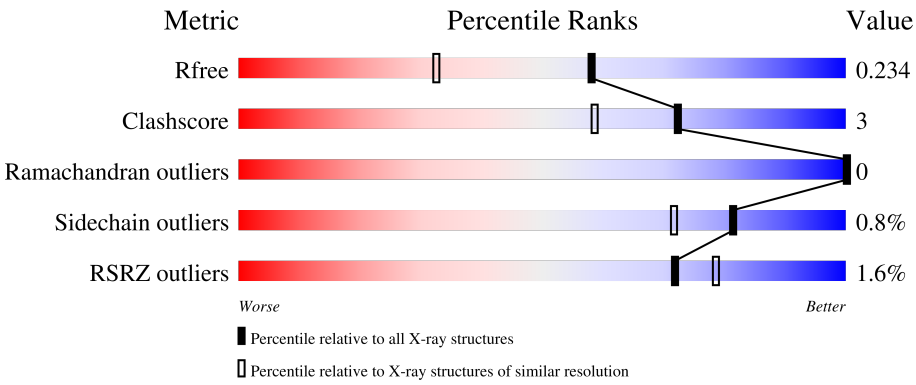
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.74 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	3764 (1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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	AAA	382	2% 93% 6%
1	BBB	382	% 91% 6%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7026 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.

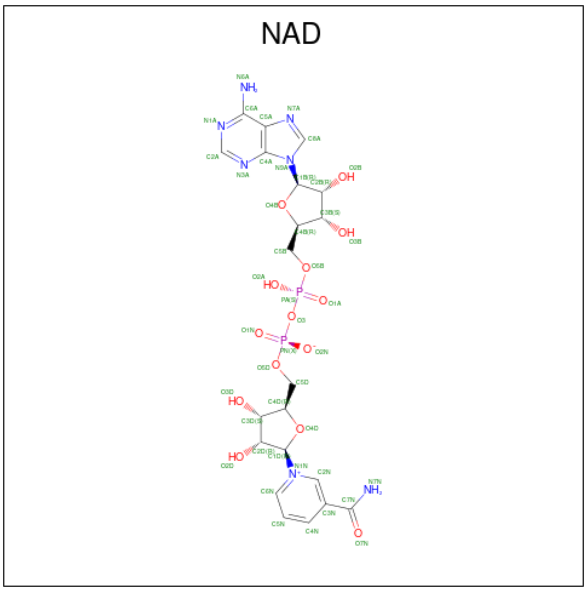
- Molecule 1 is a protein called Gfo/Idh/MocA family oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	379	3045	1916	520	580	29	0	10	0
1	BBB	376	3017	1902	512	574	29	0	7	0

There are 16 discrepancies between the modelled and reference sequences:

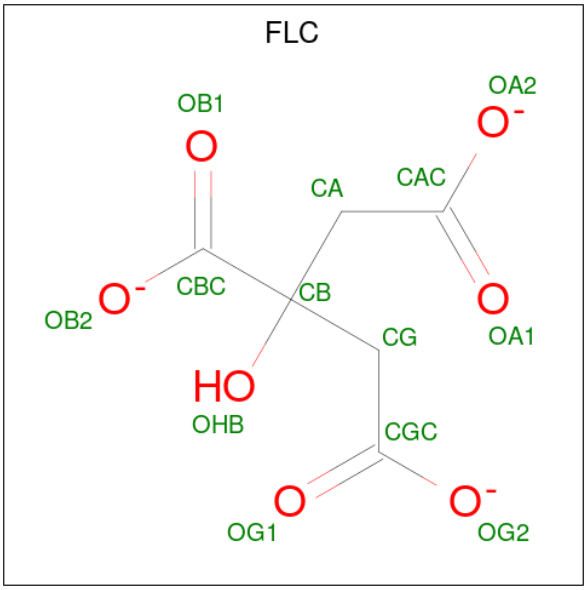
Chain	Residue	Modelled	Actual	Comment	Reference
AAA	1	GLY	-	expression tag	UNP A0A2N5NNS3
AAA	2	ALA	-	expression tag	UNP A0A2N5NNS3
AAA	3	MET	-	expression tag	UNP A0A2N5NNS3
AAA	4	ALA	-	expression tag	UNP A0A2N5NNS3
AAA	5	ASP	-	expression tag	UNP A0A2N5NNS3
AAA	6	ILE	-	expression tag	UNP A0A2N5NNS3
AAA	7	GLY	-	expression tag	UNP A0A2N5NNS3
AAA	8	SER	-	expression tag	UNP A0A2N5NNS3
BBB	1	GLY	-	expression tag	UNP A0A2N5NNS3
BBB	2	ALA	-	expression tag	UNP A0A2N5NNS3
BBB	3	MET	-	expression tag	UNP A0A2N5NNS3
BBB	4	ALA	-	expression tag	UNP A0A2N5NNS3
BBB	5	ASP	-	expression tag	UNP A0A2N5NNS3
BBB	6	ILE	-	expression tag	UNP A0A2N5NNS3
BBB	7	GLY	-	expression tag	UNP A0A2N5NNS3
BBB	8	SER	-	expression tag	UNP A0A2N5NNS3

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	AAA	1	44	21	7	14	2	0	0
			Total	C	N	O	P		
2	BBB	1	44	21	7	14	2	0	0

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	AAA	1	13	6	7	0	0
			Total	C	O		
3	BBB	1	13	6	7	0	0

- Molecule 4 is water.

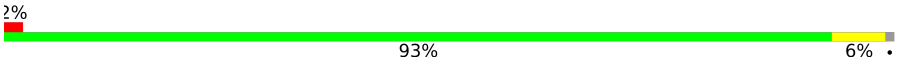
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	AAA	441	441	441	0	0
			Total	O		
4	BBB	409	409	409	0	0

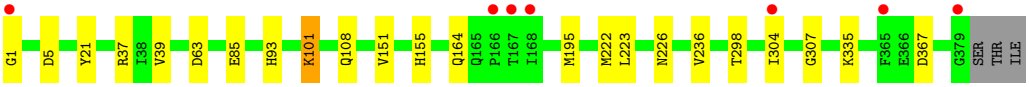
3 Residue-property plots (i)

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: Gfo/Idh/MocA family oxidoreductase

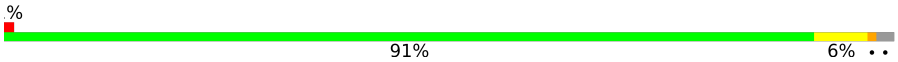
Chain AAA:

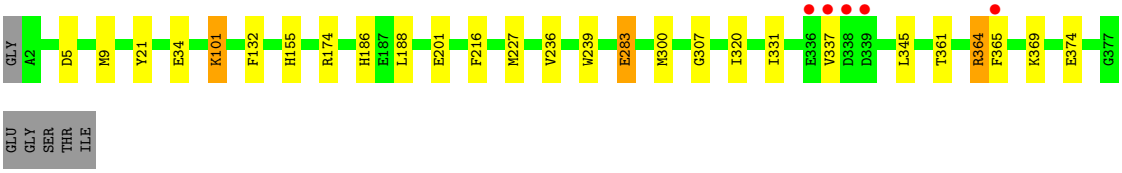




- Molecule 1: Gfo/Idh/MocA family oxidoreductase

Chain BBB:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	48.11Å 54.97Å 282.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.47 – 1.74 47.47 – 1.74	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.47-1.74) 99.8 (47.47-1.74)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.35 (at 1.74Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.182 , 0.223 0.196 , 0.234	Depositor DCC
R_{free} test set	3830 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	16.9	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 42.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.53$, $< L^2 > = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7026	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: NAD, FLC

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	AAA	0.71	0/3116	0.79	0/4200
1	BBB	0.73	1/3093 (0.0%)	0.79	0/4169
All	All	0.72	1/6209 (0.0%)	0.79	0/8369

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	BBB	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	283	GLU	CD-OE2	7.73	1.34	1.25

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	BBB	239	TRP	Peptide

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	AAA	3045	0	2940	15	0
1	BBB	3017	0	2902	27	1
2	AAA	44	0	26	0	0
2	BBB	44	0	26	0	0
3	AAA	13	0	5	0	0
3	BBB	13	0	5	0	0
4	AAA	441	0	0	3	0
4	BBB	409	0	0	3	1
All	All	7026	0	5904	41	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.

All (41) 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:AAA:226[A]:ASN:OD1	4:AAA:501:HOH:O	2.13	0.66
1:BBB:337:VAL:CG1	1:BBB:345:LEU:HD12	2.27	0.64
1:AAA:85:GLU:HG3	4:AAA:917:HOH:O	1.98	0.62
1:BBB:337:VAL:HG11	1:BBB:345:LEU:HD12	1.84	0.59
1:BBB:201[A]:GLU:OE2	1:BBB:369:LYS:HD2	2.03	0.58
1:BBB:188:LEU:HD11	1:BBB:227[B]:MET:HE1	1.86	0.58
1:BBB:101:LYS:HE2	1:BBB:186:HIS:NE2	2.18	0.58
1:BBB:101:LYS:HD2	1:BBB:101:LYS:C	2.25	0.56
1:BBB:365[C]:PHE:N	1:BBB:365[C]:PHE:HD1	2.03	0.56
1:BBB:365[C]:PHE:N	1:BBB:365[C]:PHE:CD1	2.73	0.56
1:AAA:298:THR:HG22	1:AAA:304:ILE:CG2	2.39	0.53
1:BBB:21:TYR:CD2	1:BBB:307:GLY:HA3	2.43	0.53
1:AAA:63:ASP:OD1	1:AAA:93:HIS:HE1	1.92	0.52
1:AAA:21:TYR:CD2	1:AAA:307:GLY:HA3	2.46	0.51
1:AAA:164:GLN:NE2	4:AAA:502:HOH:O	2.17	0.51
1:BBB:188:LEU:CD1	1:BBB:227[B]:MET:HE1	2.40	0.51
1:BBB:361:THR:O	1:BBB:365[C]:PHE:CD1	2.64	0.50
1:AAA:37:ARG:NH1	1:AAA:39:VAL:HG12	2.27	0.50
1:BBB:201[A]:GLU:OE2	1:BBB:369:LYS:CD	2.61	0.49
1:BBB:331:ILE:HD12	1:BBB:337:VAL:HG22	1.94	0.49
1:BBB:9[A]:MET:HE1	1:BBB:34:GLU:HB3	1.96	0.47
1:BBB:5:ASP:HB2	1:BBB:9[B]:MET:SD	2.55	0.47
1:BBB:364:ARG:HD3	1:BBB:365[C]:PHE:CD1	2.50	0.46
1:BBB:155:HIS:HA	1:BBB:236:VAL:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:155:HIS:HA	1:AAA:236:VAL:O	2.17	0.44
1:BBB:320:ILE:HA	1:BBB:320:ILE:HD12	1.75	0.44
1:BBB:188:LEU:CD1	1:BBB:227[B]:MET:CE	2.96	0.43
1:AAA:367:ASP:OD1	1:BBB:369:LYS:NZ	2.51	0.43
1:BBB:101:LYS:HE2	1:BBB:186:HIS:HE2	1.82	0.43
1:BBB:174:ARG:NH2	1:BBB:365[C]:PHE:CE2	2.87	0.42
1:AAA:101:LYS:O	1:AAA:101:LYS:HD3	2.19	0.42
1:BBB:283:GLU:OE2	4:BBB:501:HOH:O	2.22	0.42
1:AAA:222:MET:C	1:AAA:223[B]:LEU:HD12	2.41	0.41
1:AAA:335:LYS:HE3	1:AAA:335:LYS:HB3	1.88	0.41
1:BBB:21:TYR:CG	1:BBB:307:GLY:HA3	2.56	0.41
1:BBB:132:PHE:O	1:BBB:320:ILE:HD11	2.21	0.41
1:BBB:216:PHE:O	4:BBB:502:HOH:O	2.22	0.41
1:AAA:1:GLY:HA3	1:AAA:5:ASP:OD2	2.21	0.41
1:AAA:151:VAL:HG12	1:AAA:195[B]:MET:SD	2.61	0.41
1:AAA:223[B]:LEU:HD12	1:AAA:223[B]:LEU:N	2.35	0.41
1:BBB:374:GLU:OE2	4:BBB:503:HOH:O	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:9[B]:MET:CE	4:BBB:664:HOH:O[3_545]	1.62	0.58

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	AAA	387/382 (101%)	376 (97%)	11 (3%)	0	100	100
1	BBB	382/382 (100%)	373 (98%)	9 (2%)	0	100	100
All	All	769/764 (101%)	749 (97%)	20 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	AAA	322/315 (102%)	320 (99%)	2 (1%)	86	79
1	BBB	319/315 (101%)	315 (99%)	4 (1%)	69	52
All	All	641/630 (102%)	635 (99%)	6 (1%)	81	67

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	101	LYS
1	AAA	108	GLN
1	BBB	101	LYS
1	BBB	300[A]	MET
1	BBB	300[B]	MET
1	BBB	364	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

4 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	FLC	BBB	402	-	12,12,12	1.28	1 (8%)	17,17,17	1.15	1 (5%)
3	FLC	AAA	402	-	12,12,12	1.37	2 (16%)	17,17,17	1.69	3 (17%)
2	NAD	BBB	401	-	42,48,48	0.74	1 (2%)	50,73,73	0.94	2 (4%)
2	NAD	AAA	401	-	42,48,48	0.70	0	50,73,73	0.95	3 (6%)

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	FLC	BBB	402	-	-	0/16/16/16	-
3	FLC	AAA	402	-	-	2/16/16/16	-
2	NAD	BBB	401	-	-	7/26/62/62	0/5/5/5
2	NAD	AAA	401	-	-	4/26/62/62	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	AAA	402	FLC	CB-CBC	2.72	1.56	1.53
3	AAA	402	FLC	OA2-CAC	-2.61	1.22	1.30
3	BBB	402	FLC	CB-CBC	2.42	1.55	1.53
2	BBB	401	NAD	C8A-N7A	-2.12	1.30	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	AAA	402	FLC	OB1-CBC-CB	-4.33	116.12	122.25
3	AAA	402	FLC	OB2-CBC-CB	3.28	118.75	113.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	BBB	402	FLC	OB1-CBC-CB	-3.18	117.75	122.25
2	AAA	401	NAD	C6N-N1N-C2N	-3.07	119.18	121.97
2	BBB	401	NAD	C5A-C6A-N6A	2.25	123.77	120.35
2	AAA	401	NAD	C5A-C6A-N6A	2.12	123.58	120.35
2	BBB	401	NAD	C3N-C7N-N7N	-2.10	115.22	117.75
2	AAA	401	NAD	O4B-C1B-C2B	-2.08	103.89	106.93
3	AAA	402	FLC	OG1-CGC-CG	-2.05	116.95	122.94

There are no chirality outliers.

All (13) torsion outliers are listed below:

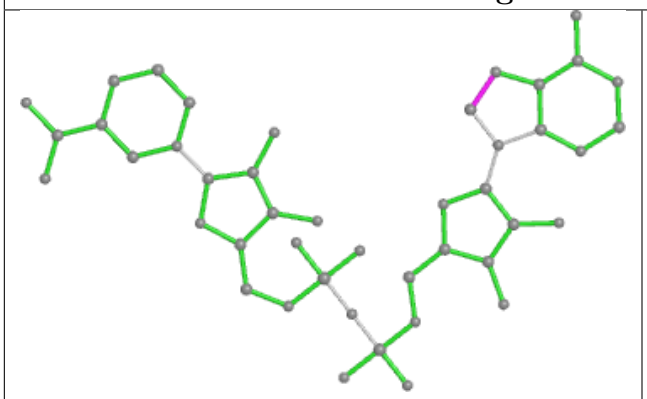
Mol	Chain	Res	Type	Atoms
2	AAA	401	NAD	O4D-C1D-N1N-C6N
2	BBB	401	NAD	C5D-O5D-PN-O2N
2	BBB	401	NAD	O4D-C1D-N1N-C2N
2	BBB	401	NAD	O4D-C1D-N1N-C6N
3	AAA	402	FLC	CB-CA-CAC-OA1
3	AAA	402	FLC	CB-CA-CAC-OA2
2	BBB	401	NAD	C5D-O5D-PN-O3
2	BBB	401	NAD	C5D-O5D-PN-O1N
2	AAA	401	NAD	C5D-O5D-PN-O3
2	BBB	401	NAD	C2D-C1D-N1N-C2N
2	AAA	401	NAD	O4B-C4B-C5B-O5B
2	AAA	401	NAD	C5D-O5D-PN-O1N
2	BBB	401	NAD	O4B-C4B-C5B-O5B

There are no ring outliers.

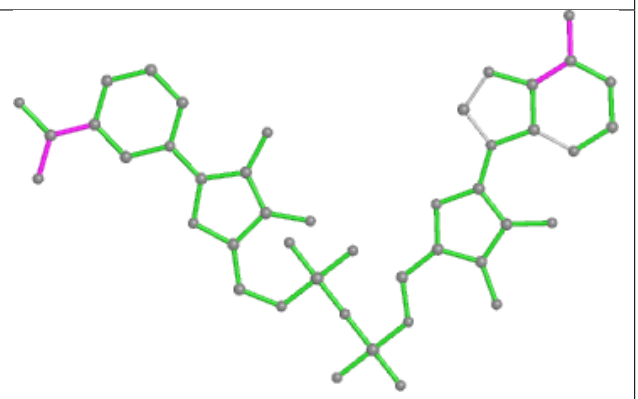
No monomer is involved in short contacts.

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.

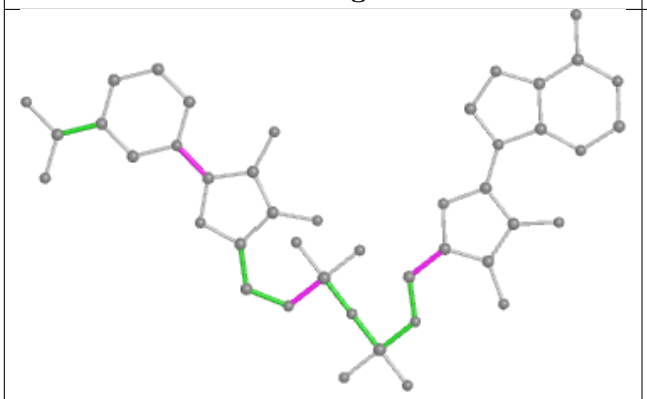
Ligand NAD BBB 401



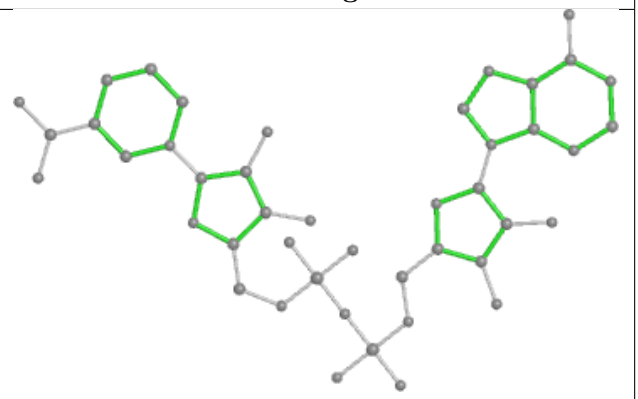
Bond lengths



Bond angles

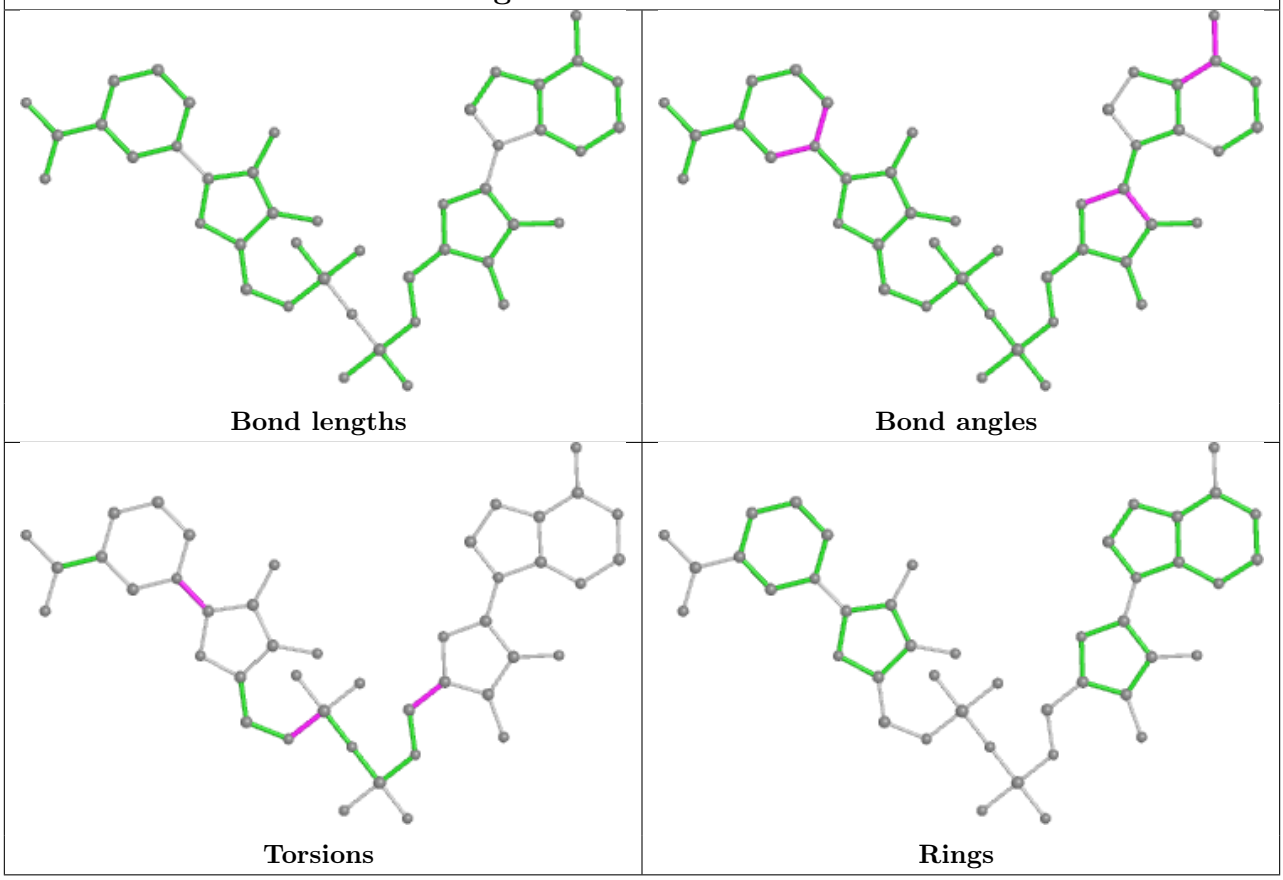


Torsions



Rings

Ligand NAD AAA 401



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	AAA	379/382 (99%)	-0.10	7 (1%)	68	74	9, 14, 32, 63	0
1	BBB	376/382 (98%)	-0.00	5 (1%)	77	82	9, 17, 36, 68	0
All	All	755/764 (98%)	-0.05	12 (1%)	72	78	9, 15, 34, 68	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	337	VAL	4.6
1	BBB	365[A]	PHE	4.4
1	BBB	338[A]	ASP	4.3
1	AAA	1	GLY	4.1
1	AAA	379	GLY	3.4
1	BBB	336	GLU	3.3
1	AAA	365[A]	PHE	3.1
1	AAA	166	PRO	3.1
1	AAA	168[A]	ILE	3.1
1	AAA	167	THR	2.8
1	BBB	339	ASP	2.8
1	AAA	304	ILE	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

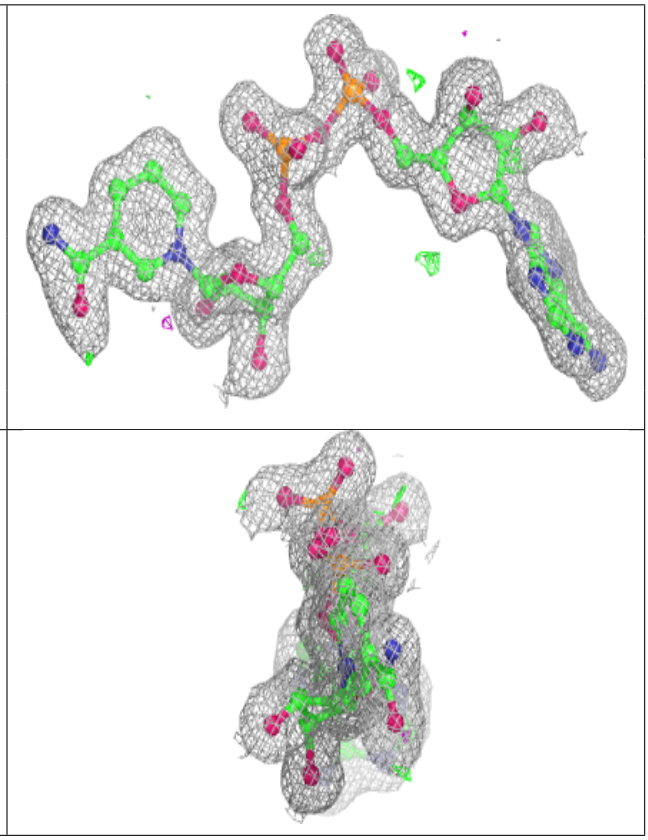
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	FLC	AAA	402	13/13	0.93	0.10	14,18,27,28	0
3	FLC	BBB	402	13/13	0.94	0.09	15,20,24,25	0
2	NAD	BBB	401	44/44	0.96	0.08	9,15,21,24	0
2	NAD	AAA	401	44/44	0.97	0.07	10,12,16,22	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.

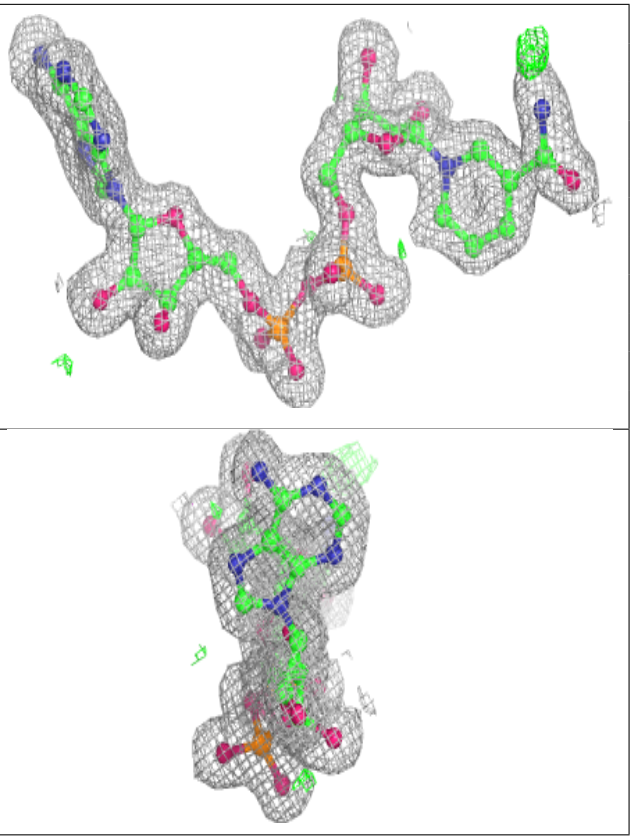
Electron density around NAD BBB 401:

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 AAA 401:

$2mF_o$-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.