wwPDB X-ray Structure Validation Summary Report (i)

Oct 22, 2024 – 07:36 PM EDT

PDB ID	:	4MPY
Title	:	1.85 Angstrom resolution crystal structure of betaine aldehyde dehydrogenase (betB) from Staphylococcus aureus (IDP00699) in complex with NAD+
Authors	:	Halavaty, A.S.; Minasov, G.; Shuvalova, L.; Winsor, J.; Peterson, S.N.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2013-09-14
Resolution	:	1.85 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 (i)) were used in the production of this report:

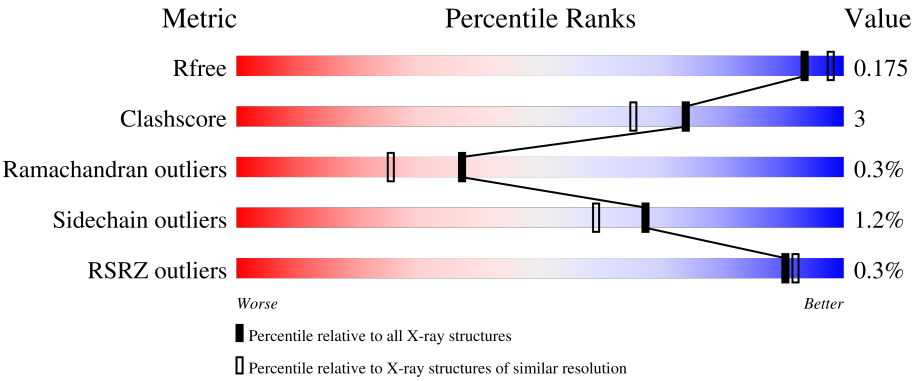
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 1.85 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}	164625	3097 (1.86-1.86)
Clashscore	180529	3359 (1.86-1.86)
Ramachandran outliers	177936	3335 (1.86-1.86)
Sidechain outliers	177891	3335 (1.86-1.86)
RSRZ outliers	164620	3097 (1.86-1.86)

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	A	520	90% 5% ·
1	B	520	% 91% 5% ·
1	C	520	90% 7% ·
1	D	520	89% 6% ·

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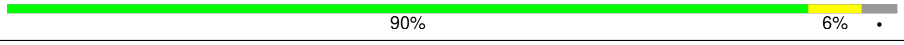
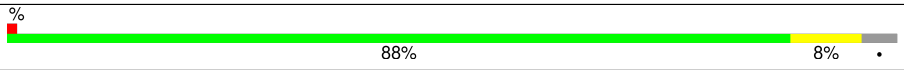
Mol	Chain	Length	Quality of chain
1	E	520	
1	F	520	
1	G	520	
1	H	520	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 37293 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 Betaine aldehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	500	Total	C	N	O	S	0	12	0
			3976	2503	671	785	17			
1	B	500	Total	C	N	O	S	0	10	0
			3966	2493	673	781	19			
1	C	503	Total	C	N	O	S	0	22	0
			4087	2573	687	807	20			
1	D	498	Total	C	N	O	S	0	13	0
			3969	2498	671	784	16			
1	E	501	Total	C	N	O	S	0	20	0
			4055	2552	682	801	20			
1	F	498	Total	C	N	O	S	0	21	0
			4035	2539	683	793	20			
1	G	503	Total	C	N	O	S	0	16	0
			4046	2545	687	792	22			
1	H	500	Total	C	N	O	S	0	22	0
			4066	2552	694	800	20			

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	expression tag	UNP Q5HCU0
A	-22	HIS	-	expression tag	UNP Q5HCU0
A	-21	HIS	-	expression tag	UNP Q5HCU0
A	-20	HIS	-	expression tag	UNP Q5HCU0
A	-19	HIS	-	expression tag	UNP Q5HCU0
A	-18	HIS	-	expression tag	UNP Q5HCU0
A	-17	HIS	-	expression tag	UNP Q5HCU0
A	-16	SER	-	expression tag	UNP Q5HCU0
A	-15	SER	-	expression tag	UNP Q5HCU0
A	-14	GLY	-	expression tag	UNP Q5HCU0
A	-13	VAL	-	expression tag	UNP Q5HCU0
A	-12	ASP	-	expression tag	UNP Q5HCU0
A	-11	LEU	-	expression tag	UNP Q5HCU0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	expression tag	UNP Q5HCU0
A	-9	THR	-	expression tag	UNP Q5HCU0
A	-8	GLU	-	expression tag	UNP Q5HCU0
A	-7	ASN	-	expression tag	UNP Q5HCU0
A	-6	LEU	-	expression tag	UNP Q5HCU0
A	-5	TYR	-	expression tag	UNP Q5HCU0
A	-4	PHE	-	expression tag	UNP Q5HCU0
A	-3	GLN	-	expression tag	UNP Q5HCU0
A	-2	SER	-	expression tag	UNP Q5HCU0
A	-1	ASN	-	expression tag	UNP Q5HCU0
A	0	ALA	-	expression tag	UNP Q5HCU0
B	-23	MET	-	expression tag	UNP Q5HCU0
B	-22	HIS	-	expression tag	UNP Q5HCU0
B	-21	HIS	-	expression tag	UNP Q5HCU0
B	-20	HIS	-	expression tag	UNP Q5HCU0
B	-19	HIS	-	expression tag	UNP Q5HCU0
B	-18	HIS	-	expression tag	UNP Q5HCU0
B	-17	HIS	-	expression tag	UNP Q5HCU0
B	-16	SER	-	expression tag	UNP Q5HCU0
B	-15	SER	-	expression tag	UNP Q5HCU0
B	-14	GLY	-	expression tag	UNP Q5HCU0
B	-13	VAL	-	expression tag	UNP Q5HCU0
B	-12	ASP	-	expression tag	UNP Q5HCU0
B	-11	LEU	-	expression tag	UNP Q5HCU0
B	-10	GLY	-	expression tag	UNP Q5HCU0
B	-9	THR	-	expression tag	UNP Q5HCU0
B	-8	GLU	-	expression tag	UNP Q5HCU0
B	-7	ASN	-	expression tag	UNP Q5HCU0
B	-6	LEU	-	expression tag	UNP Q5HCU0
B	-5	TYR	-	expression tag	UNP Q5HCU0
B	-4	PHE	-	expression tag	UNP Q5HCU0
B	-3	GLN	-	expression tag	UNP Q5HCU0
B	-2	SER	-	expression tag	UNP Q5HCU0
B	-1	ASN	-	expression tag	UNP Q5HCU0
B	0	ALA	-	expression tag	UNP Q5HCU0
C	-23	MET	-	expression tag	UNP Q5HCU0
C	-22	HIS	-	expression tag	UNP Q5HCU0
C	-21	HIS	-	expression tag	UNP Q5HCU0
C	-20	HIS	-	expression tag	UNP Q5HCU0
C	-19	HIS	-	expression tag	UNP Q5HCU0
C	-18	HIS	-	expression tag	UNP Q5HCU0
C	-17	HIS	-	expression tag	UNP Q5HCU0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	SER	-	expression tag	UNP Q5HCU0
C	-15	SER	-	expression tag	UNP Q5HCU0
C	-14	GLY	-	expression tag	UNP Q5HCU0
C	-13	VAL	-	expression tag	UNP Q5HCU0
C	-12	ASP	-	expression tag	UNP Q5HCU0
C	-11	LEU	-	expression tag	UNP Q5HCU0
C	-10	GLY	-	expression tag	UNP Q5HCU0
C	-9	THR	-	expression tag	UNP Q5HCU0
C	-8	GLU	-	expression tag	UNP Q5HCU0
C	-7	ASN	-	expression tag	UNP Q5HCU0
C	-6	LEU	-	expression tag	UNP Q5HCU0
C	-5	TYR	-	expression tag	UNP Q5HCU0
C	-4	PHE	-	expression tag	UNP Q5HCU0
C	-3	GLN	-	expression tag	UNP Q5HCU0
C	-2	SER	-	expression tag	UNP Q5HCU0
C	-1	ASN	-	expression tag	UNP Q5HCU0
C	0	ALA	-	expression tag	UNP Q5HCU0
D	-23	MET	-	expression tag	UNP Q5HCU0
D	-22	HIS	-	expression tag	UNP Q5HCU0
D	-21	HIS	-	expression tag	UNP Q5HCU0
D	-20	HIS	-	expression tag	UNP Q5HCU0
D	-19	HIS	-	expression tag	UNP Q5HCU0
D	-18	HIS	-	expression tag	UNP Q5HCU0
D	-17	HIS	-	expression tag	UNP Q5HCU0
D	-16	SER	-	expression tag	UNP Q5HCU0
D	-15	SER	-	expression tag	UNP Q5HCU0
D	-14	GLY	-	expression tag	UNP Q5HCU0
D	-13	VAL	-	expression tag	UNP Q5HCU0
D	-12	ASP	-	expression tag	UNP Q5HCU0
D	-11	LEU	-	expression tag	UNP Q5HCU0
D	-10	GLY	-	expression tag	UNP Q5HCU0
D	-9	THR	-	expression tag	UNP Q5HCU0
D	-8	GLU	-	expression tag	UNP Q5HCU0
D	-7	ASN	-	expression tag	UNP Q5HCU0
D	-6	LEU	-	expression tag	UNP Q5HCU0
D	-5	TYR	-	expression tag	UNP Q5HCU0
D	-4	PHE	-	expression tag	UNP Q5HCU0
D	-3	GLN	-	expression tag	UNP Q5HCU0
D	-2	SER	-	expression tag	UNP Q5HCU0
D	-1	ASN	-	expression tag	UNP Q5HCU0
D	0	ALA	-	expression tag	UNP Q5HCU0
E	-23	MET	-	expression tag	UNP Q5HCU0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-22	HIS	-	expression tag	UNP Q5HCU0
E	-21	HIS	-	expression tag	UNP Q5HCU0
E	-20	HIS	-	expression tag	UNP Q5HCU0
E	-19	HIS	-	expression tag	UNP Q5HCU0
E	-18	HIS	-	expression tag	UNP Q5HCU0
E	-17	HIS	-	expression tag	UNP Q5HCU0
E	-16	SER	-	expression tag	UNP Q5HCU0
E	-15	SER	-	expression tag	UNP Q5HCU0
E	-14	GLY	-	expression tag	UNP Q5HCU0
E	-13	VAL	-	expression tag	UNP Q5HCU0
E	-12	ASP	-	expression tag	UNP Q5HCU0
E	-11	LEU	-	expression tag	UNP Q5HCU0
E	-10	GLY	-	expression tag	UNP Q5HCU0
E	-9	THR	-	expression tag	UNP Q5HCU0
E	-8	GLU	-	expression tag	UNP Q5HCU0
E	-7	ASN	-	expression tag	UNP Q5HCU0
E	-6	LEU	-	expression tag	UNP Q5HCU0
E	-5	TYR	-	expression tag	UNP Q5HCU0
E	-4	PHE	-	expression tag	UNP Q5HCU0
E	-3	GLN	-	expression tag	UNP Q5HCU0
E	-2	SER	-	expression tag	UNP Q5HCU0
E	-1	ASN	-	expression tag	UNP Q5HCU0
E	0	ALA	-	expression tag	UNP Q5HCU0
F	-23	MET	-	expression tag	UNP Q5HCU0
F	-22	HIS	-	expression tag	UNP Q5HCU0
F	-21	HIS	-	expression tag	UNP Q5HCU0
F	-20	HIS	-	expression tag	UNP Q5HCU0
F	-19	HIS	-	expression tag	UNP Q5HCU0
F	-18	HIS	-	expression tag	UNP Q5HCU0
F	-17	HIS	-	expression tag	UNP Q5HCU0
F	-16	SER	-	expression tag	UNP Q5HCU0
F	-15	SER	-	expression tag	UNP Q5HCU0
F	-14	GLY	-	expression tag	UNP Q5HCU0
F	-13	VAL	-	expression tag	UNP Q5HCU0
F	-12	ASP	-	expression tag	UNP Q5HCU0
F	-11	LEU	-	expression tag	UNP Q5HCU0
F	-10	GLY	-	expression tag	UNP Q5HCU0
F	-9	THR	-	expression tag	UNP Q5HCU0
F	-8	GLU	-	expression tag	UNP Q5HCU0
F	-7	ASN	-	expression tag	UNP Q5HCU0
F	-6	LEU	-	expression tag	UNP Q5HCU0
F	-5	TYR	-	expression tag	UNP Q5HCU0

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-4	PHE	-	expression tag	UNP Q5HCU0
F	-3	GLN	-	expression tag	UNP Q5HCU0
F	-2	SER	-	expression tag	UNP Q5HCU0
F	-1	ASN	-	expression tag	UNP Q5HCU0
F	0	ALA	-	expression tag	UNP Q5HCU0
G	-23	MET	-	expression tag	UNP Q5HCU0
G	-22	HIS	-	expression tag	UNP Q5HCU0
G	-21	HIS	-	expression tag	UNP Q5HCU0
G	-20	HIS	-	expression tag	UNP Q5HCU0
G	-19	HIS	-	expression tag	UNP Q5HCU0
G	-18	HIS	-	expression tag	UNP Q5HCU0
G	-17	HIS	-	expression tag	UNP Q5HCU0
G	-16	SER	-	expression tag	UNP Q5HCU0
G	-15	SER	-	expression tag	UNP Q5HCU0
G	-14	GLY	-	expression tag	UNP Q5HCU0
G	-13	VAL	-	expression tag	UNP Q5HCU0
G	-12	ASP	-	expression tag	UNP Q5HCU0
G	-11	LEU	-	expression tag	UNP Q5HCU0
G	-10	GLY	-	expression tag	UNP Q5HCU0
G	-9	THR	-	expression tag	UNP Q5HCU0
G	-8	GLU	-	expression tag	UNP Q5HCU0
G	-7	ASN	-	expression tag	UNP Q5HCU0
G	-6	LEU	-	expression tag	UNP Q5HCU0
G	-5	TYR	-	expression tag	UNP Q5HCU0
G	-4	PHE	-	expression tag	UNP Q5HCU0
G	-3	GLN	-	expression tag	UNP Q5HCU0
G	-2	SER	-	expression tag	UNP Q5HCU0
G	-1	ASN	-	expression tag	UNP Q5HCU0
G	0	ALA	-	expression tag	UNP Q5HCU0
H	-23	MET	-	expression tag	UNP Q5HCU0
H	-22	HIS	-	expression tag	UNP Q5HCU0
H	-21	HIS	-	expression tag	UNP Q5HCU0
H	-20	HIS	-	expression tag	UNP Q5HCU0
H	-19	HIS	-	expression tag	UNP Q5HCU0
H	-18	HIS	-	expression tag	UNP Q5HCU0
H	-17	HIS	-	expression tag	UNP Q5HCU0
H	-16	SER	-	expression tag	UNP Q5HCU0
H	-15	SER	-	expression tag	UNP Q5HCU0
H	-14	GLY	-	expression tag	UNP Q5HCU0
H	-13	VAL	-	expression tag	UNP Q5HCU0
H	-12	ASP	-	expression tag	UNP Q5HCU0
H	-11	LEU	-	expression tag	UNP Q5HCU0

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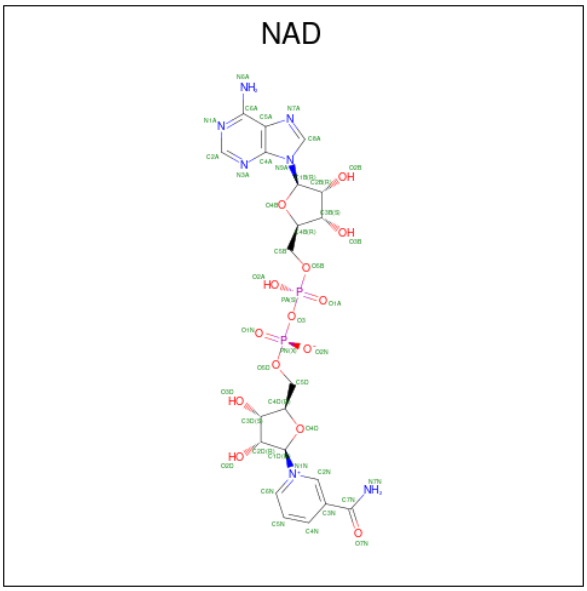
Chain	Residue	Modelled	Actual	Comment	Reference
H	-10	GLY	-	expression tag	UNP Q5HCU0
H	-9	THR	-	expression tag	UNP Q5HCU0
H	-8	GLU	-	expression tag	UNP Q5HCU0
H	-7	ASN	-	expression tag	UNP Q5HCU0
H	-6	LEU	-	expression tag	UNP Q5HCU0
H	-5	TYR	-	expression tag	UNP Q5HCU0
H	-4	PHE	-	expression tag	UNP Q5HCU0
H	-3	GLN	-	expression tag	UNP Q5HCU0
H	-2	SER	-	expression tag	UNP Q5HCU0
H	-1	ASN	-	expression tag	UNP Q5HCU0
H	0	ALA	-	expression tag	UNP Q5HCU0

- 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
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Na	0	0
			2	2		
3	B	2	Total	Na	0	0
			2	2		
3	C	2	Total	Na	0	0
			2	2		
3	D	2	Total	Na	0	0
			2	2		
3	E	4	Total	Na	0	0
			4	4		
3	F	3	Total	Na	0	0
			3	3		
3	G	2	Total	Na	0	0
			2	2		
3	H	2	Total	Na	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	458	Total	O	0	14
			468	468		
4	B	501	Total	O	0	18
			516	516		
4	C	597	Total	O	0	32
			620	620		
4	D	577	Total	O	0	28
			599	599		
4	E	641	Total	O	0	32
			665	665		
4	F	646	Total	O	0	22
			667	667		

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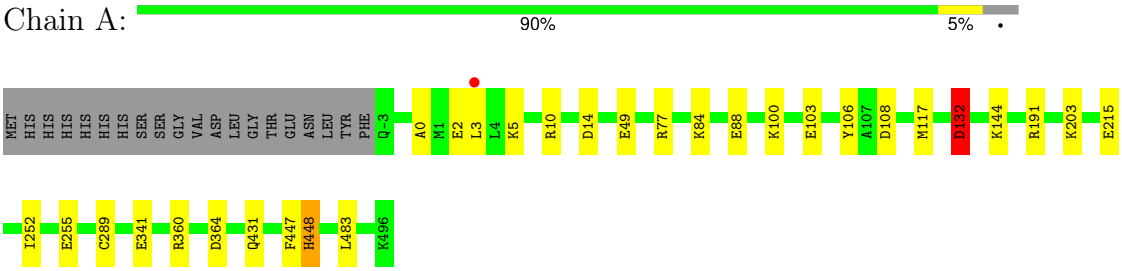
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	560	Total O 571 571	0	14
4	H	594	Total O 616 616	0	30

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.

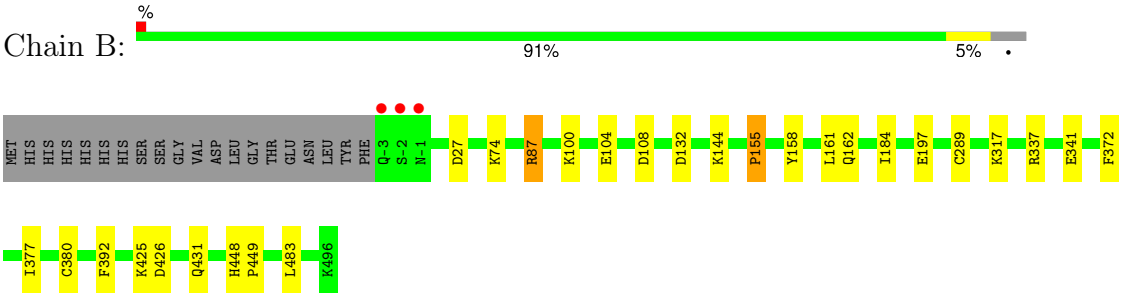
• Molecule 1: Betaine aldehyde dehydrogenase

Chain A:



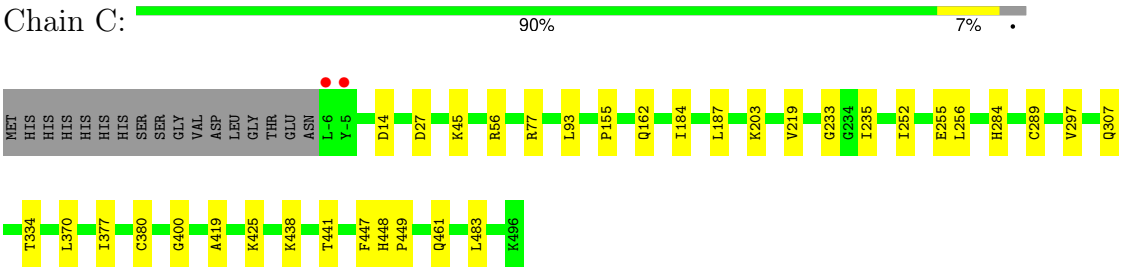
• Molecule 1: Betaine aldehyde dehydrogenase

Chain B:



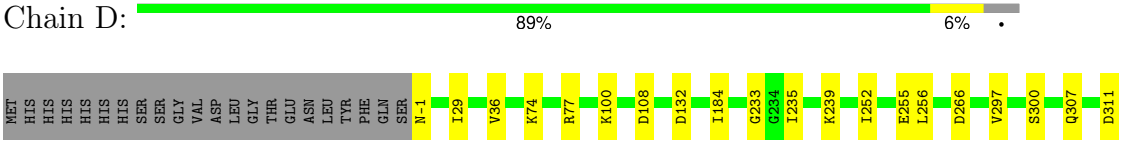
• Molecule 1: Betaine aldehyde dehydrogenase

Chain C:



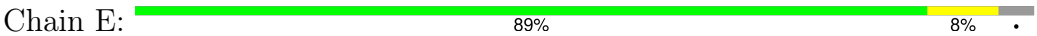
• Molecule 1: Betaine aldehyde dehydrogenase

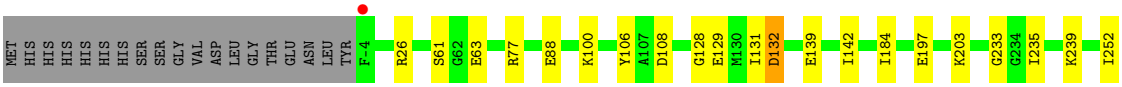
Chain D:

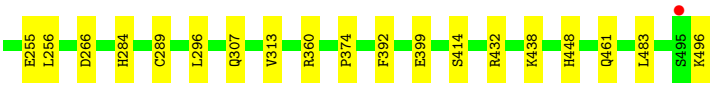


• Molecule 1: Betaine aldehyde dehydrogenase

Chain E:

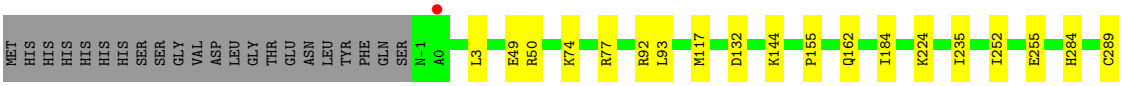






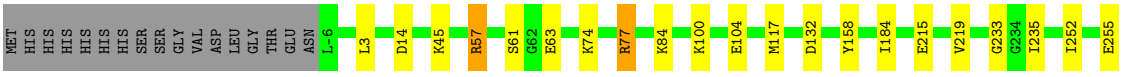
• Molecule 1: Betaine aldehyde dehydrogenase

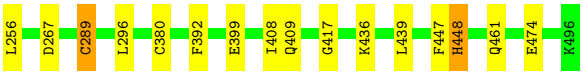
Chain F:



• Molecule 1: Betaine aldehyde dehydrogenase

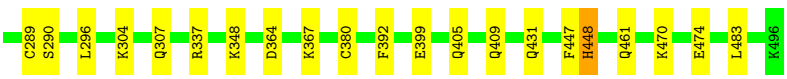
Chain G:





• Molecule 1: Betaine aldehyde dehydrogenase

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	99.87Å 159.15Å 122.99Å 90.00° 94.79° 90.00°	Depositor
Resolution (Å)	24.98 – 1.85 24.98 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.7 (24.98-1.85) 99.7 (24.98-1.85)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.17 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.126 , 0.167 0.140 , 0.175	Depositor DCC
R_{free} test set	9843 reflections (3.04%)	wwPDB-VP
Wilson B-factor (Å^2)	15.9	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 50.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	37293	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 19.16% 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: CME, NAD, NA

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	0.58	0/4036	0.80	2/5452 (0.0%)
1	B	0.60	1/4016 (0.0%)	0.82	4/5425 (0.1%)
1	C	0.62	1/4139 (0.0%)	0.84	2/5593 (0.0%)
1	D	0.63	1/4029 (0.0%)	0.82	1/5442 (0.0%)
1	E	0.65	1/4106 (0.0%)	0.83	3/5546 (0.1%)
1	F	0.64	1/4085 (0.0%)	0.84	2/5515 (0.0%)
1	G	0.61	1/4098 (0.0%)	0.83	5/5532 (0.1%)
1	H	0.62	1/4116 (0.0%)	0.81	2/5556 (0.0%)
All	All	0.62	7/32625 (0.0%)	0.82	21/44061 (0.0%)

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	G	0	1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	184	ILE	C-O	5.84	1.34	1.23
1	D	184	ILE	C-O	5.78	1.34	1.23
1	G	184	ILE	C-O	5.77	1.34	1.23
1	H	184	ILE	C-O	5.77	1.34	1.23
1	E	184	ILE	C-O	5.71	1.34	1.23

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	432	ARG	NE-CZ-NH1	7.17	123.88	120.30
1	G	57[A]	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	G	57[B]	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	F	312	ARG	NE-CZ-NH1	5.97	123.28	120.30
1	F	50	ARG	NE-CZ-NH2	-5.83	117.39	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	77[A]	ARG	Sidechain

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	3976	0	3914	20	0
1	B	3966	0	3902	22	0
1	C	4087	0	4010	20	0
1	D	3969	0	3907	23	0
1	E	4055	0	3980	34	0
1	F	4035	0	3974	27	0
1	G	4046	0	3980	31	0
1	H	4066	0	3998	43	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	C	44	0	26	0	0
2	D	44	0	26	0	0
2	E	44	0	26	0	0
2	F	44	0	26	0	0
2	G	44	0	26	0	0
2	H	44	0	26	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	4	0	0	0	0
3	F	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	2	0	0	0	0
3	H	2	0	0	0	0
4	A	468	0	0	13	0
4	B	516	0	0	6	0
4	C	620	0	0	8	0
4	D	599	0	0	9	0
4	E	665	0	0	5	0
4	F	667	0	0	11	0
4	G	571	0	0	11	0
4	H	616	0	0	19	0
All	All	37293	0	31873	197	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 197 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:D:235[A]:ILE:HD11	1:D:461:GLN:OE1	1.46	1.14
1:H:337[B]:ARG:HG2	1:H:337[B]:ARG:HH11	1.20	1.00
1:C:235[B]:ILE:HD11	1:C:461:GLN:OE1	1.63	0.98
1:H:307:GLN:HG2	4:H:685:HOH:O	1.68	0.90
1:E:235[B]:ILE:HD11	1:E:461:GLN:OE1	1.76	0.86

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	509/520 (98%)	498 (98%)	10 (2%)	1 (0%)	44	32
1	B	506/520 (97%)	498 (98%)	6 (1%)	2 (0%)	30	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	521/520 (100%)	512 (98%)	8 (2%)	1 (0%)	44 32
1	D	508/520 (98%)	498 (98%)	8 (2%)	2 (0%)	30 18
1	E	517/520 (99%)	506 (98%)	10 (2%)	1 (0%)	44 32
1	F	515/520 (99%)	505 (98%)	8 (2%)	2 (0%)	30 18
1	G	515/520 (99%)	506 (98%)	8 (2%)	1 (0%)	44 32
1	H	518/520 (100%)	507 (98%)	10 (2%)	1 (0%)	44 32
All	All	4109/4160 (99%)	4030 (98%)	68 (2%)	11 (0%)	37 25

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	448	HIS
1	B	448	HIS
1	C	448	HIS
1	D	448	HIS
1	E	448	HIS

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	425/431 (99%)	422 (99%)	3 (1%)	81 78
1	B	422/431 (98%)	417 (99%)	5 (1%)	67 59
1	C	437/431 (101%)	434 (99%)	3 (1%)	81 78
1	D	424/431 (98%)	419 (99%)	5 (1%)	67 59
1	E	433/431 (100%)	426 (98%)	7 (2%)	58 46
1	F	430/431 (100%)	424 (99%)	6 (1%)	62 53
1	G	431/431 (100%)	425 (99%)	6 (1%)	62 53
1	H	434/431 (101%)	424 (98%)	10 (2%)	45 31
All	All	3436/3448 (100%)	3391 (99%)	45 (1%)	67 55

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	364[B]	ASP
1	H	77[A]	ARG
1	G	132	ASP
1	G	380[A]	CYS
1	H	117[A]	MET

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

Mol	Chain	Res	Type
1	H	-1	ASN
1	H	307	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)

14 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	CME	F	289[A]	1	8,9,10	0.89	0	6,9,11	2.25	2 (33%)
1	CME	B	289[B]	1	8,9,10	0.82	0	6,9,11	2.26	2 (33%)
1	CME	E	289[B]	1	8,9,10	0.82	0	6,9,11	2.75	1 (16%)
1	CME	B	289[A]	1	8,9,10	0.79	0	6,9,11	0.83	0
1	CME	E	289[A]	1	8,9,10	0.82	0	6,9,11	0.81	0
1	CME	G	289[B]	1	8,9,10	0.90	0	6,9,11	2.26	2 (33%)
1	CME	G	289[A]	1	8,9,10	0.87	0	6,9,11	1.22	1 (16%)
1	CME	D	289	1	8,9,10	0.88	0	6,9,11	1.11	0
1	CME	C	289[B]	1	8,9,10	0.76	0	6,9,11	2.54	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	CME	H	289[B]	1	8,9,10	0.86	0	6,9,11	2.59	2 (33%)
1	CME	F	289[B]	1	8,9,10	0.82	0	6,9,11	0.61	0
1	CME	A	289	1	8,9,10	0.79	0	6,9,11	3.50	3 (50%)
1	CME	H	289[A]	1	8,9,10	0.89	0	6,9,11	1.00	0
1	CME	C	289[A]	1	8,9,10	0.74	0	6,9,11	1.21	1 (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
1	CME	F	289[A]	1	-	1/5/8/10	-
1	CME	B	289[B]	1	-	1/5/8/10	-
1	CME	E	289[B]	1	-	1/5/8/10	-
1	CME	B	289[A]	1	-	3/5/8/10	-
1	CME	E	289[A]	1	-	3/5/8/10	-
1	CME	G	289[B]	1	-	1/5/8/10	-
1	CME	G	289[A]	1	-	2/5/8/10	-
1	CME	D	289	1	-	4/5/8/10	-
1	CME	C	289[B]	1	-	1/5/8/10	-
1	CME	H	289[B]	1	-	0/5/8/10	-
1	CME	F	289[B]	1	-	2/5/8/10	-
1	CME	A	289	1	-	1/5/8/10	-
1	CME	H	289[A]	1	-	3/5/8/10	-
1	CME	C	289[A]	1	-	3/5/8/10	-

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	289	CME	CB-SG-SD	7.42	123.07	103.86
1	E	289[B]	CME	CB-SG-SD	6.16	119.80	103.86
1	C	289[B]	CME	CB-SG-SD	5.79	118.86	103.86
1	H	289[B]	CME	CB-SG-SD	5.42	117.88	103.86
1	B	289[B]	CME	CB-SG-SD	4.64	115.86	103.86

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	289	CME	CZ-CE-SD-SG
1	B	289[A]	CME	CE-SD-SG-CB
1	C	289[A]	CME	CE-SD-SG-CB
1	C	289[A]	CME	SD-CE-CZ-OH
1	E	289[A]	CME	CE-SD-SG-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	G	289[B]	CME	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 27 ligands modelled in this entry, 19 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAD	H	501	-	42,48,48	1.40	4 (9%)	50,73,73	1.23	5 (10%)
2	NAD	A	501	-	42,48,48	1.29	4 (9%)	50,73,73	1.38	4 (8%)
2	NAD	E	501	-	42,48,48	1.33	4 (9%)	50,73,73	1.58	11 (22%)
2	NAD	G	501	-	42,48,48	1.39	6 (14%)	50,73,73	1.56	9 (18%)
2	NAD	D	501	-	42,48,48	1.38	4 (9%)	50,73,73	1.36	8 (16%)
2	NAD	F	501	-	42,48,48	1.30	3 (7%)	50,73,73	1.32	9 (18%)
2	NAD	B	501	-	42,48,48	0.96	3 (7%)	50,73,73	1.36	7 (14%)
2	NAD	C	501	-	42,48,48	1.16	2 (4%)	50,73,73	1.43	7 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	H	501	-	-	4/26/62/62	0/5/5/5
2	NAD	A	501	-	-	8/26/62/62	0/5/5/5
2	NAD	E	501	-	-	5/26/62/62	0/5/5/5
2	NAD	G	501	-	-	7/26/62/62	0/5/5/5
2	NAD	D	501	-	-	5/26/62/62	0/5/5/5
2	NAD	F	501	-	-	5/26/62/62	0/5/5/5
2	NAD	B	501	-	-	5/26/62/62	0/5/5/5
2	NAD	C	501	-	-	5/26/62/62	0/5/5/5

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	NAD	O7N-C7N	5.47	1.34	1.24
2	F	501	NAD	PA-O3	5.38	1.65	1.59
2	A	501	NAD	O7N-C7N	5.22	1.33	1.24
2	H	501	NAD	O7N-C7N	4.98	1.33	1.24
2	E	501	NAD	O7N-C7N	4.73	1.32	1.24

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	501	NAD	N3A-C2A-N1A	-5.48	121.23	128.67
2	C	501	NAD	N3A-C2A-N1A	-5.22	121.59	128.67
2	D	501	NAD	N3A-C2A-N1A	-4.86	122.07	128.67
2	G	501	NAD	N3A-C2A-N1A	-4.71	122.28	128.67
2	A	501	NAD	N3A-C2A-N1A	-4.68	122.31	128.67

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

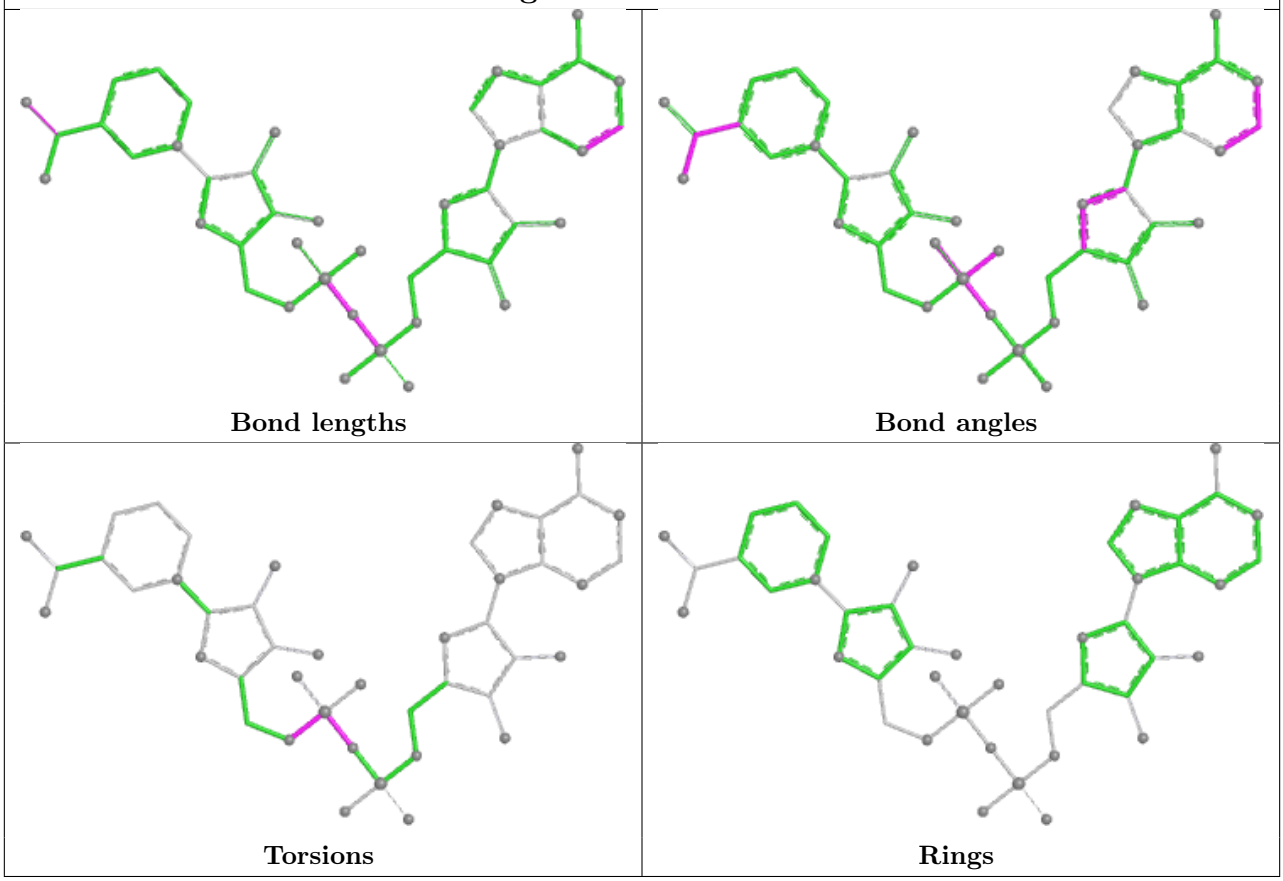
Mol	Chain	Res	Type	Atoms
2	A	501	NAD	C5D-O5D-PN-O2N
2	B	501	NAD	C5D-O5D-PN-O3
2	B	501	NAD	C5D-O5D-PN-O2N
2	C	501	NAD	C5D-O5D-PN-O3
2	C	501	NAD	C5D-O5D-PN-O2N

There are no ring outliers.

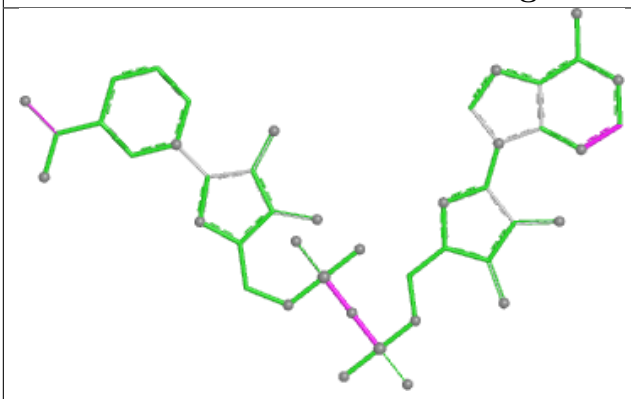
No monomer is involved in short contacts.

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.

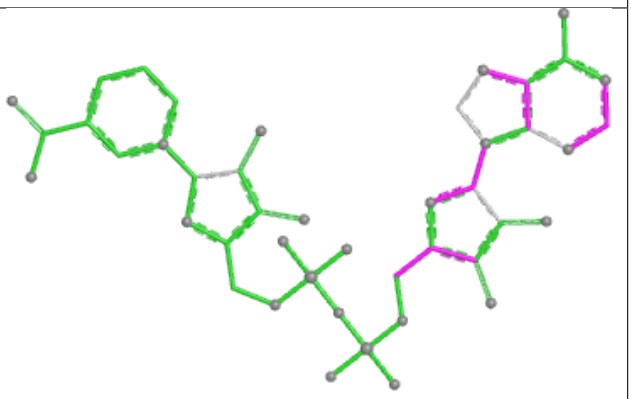
Ligand NAD H 501



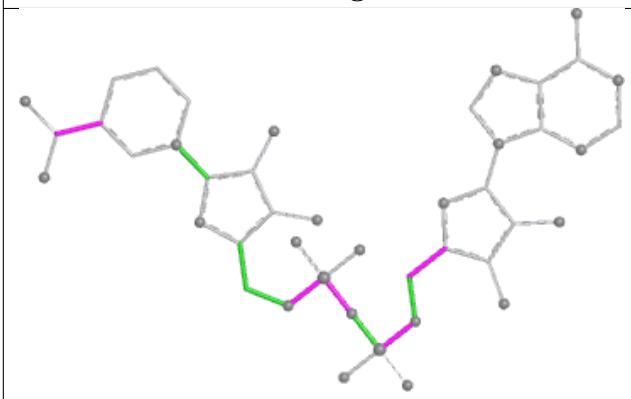
Ligand NAD A 501



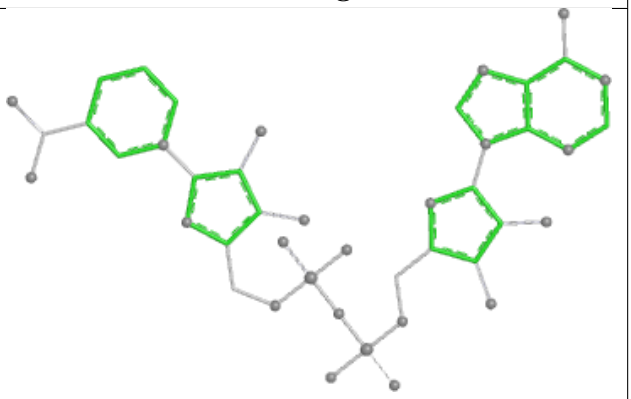
Bond lengths



Bond angles

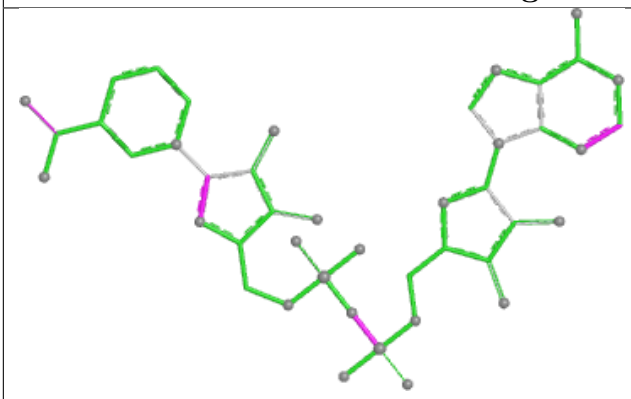


Torsions

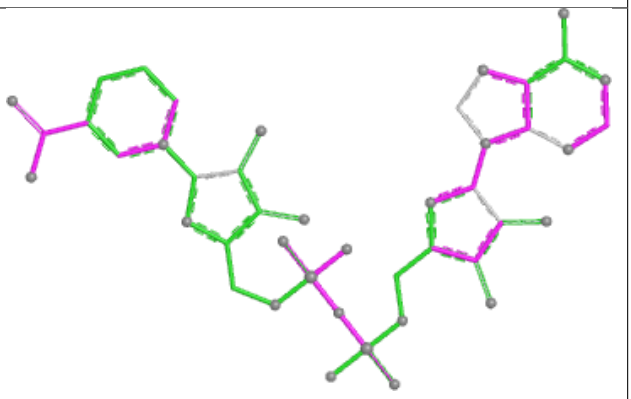


Rings

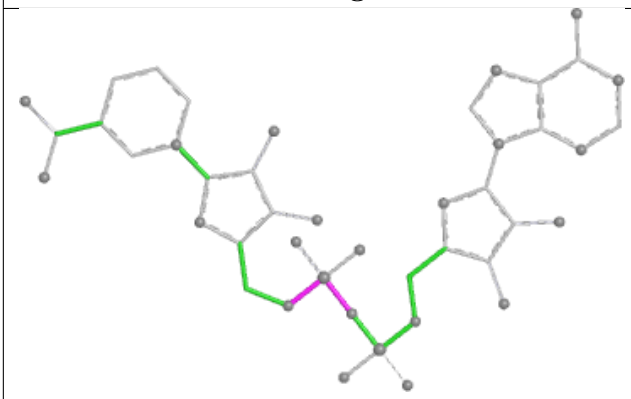
Ligand NAD E 501



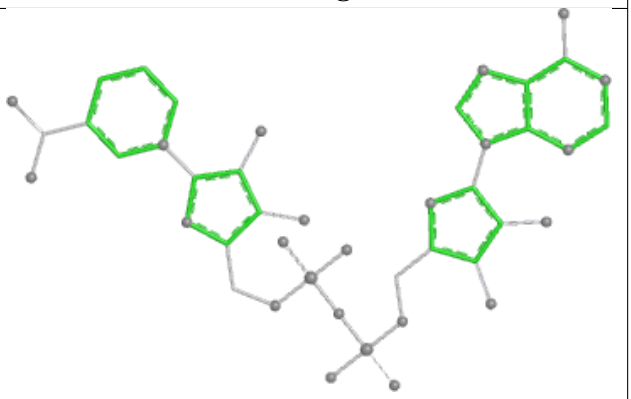
Bond lengths



Bond angles

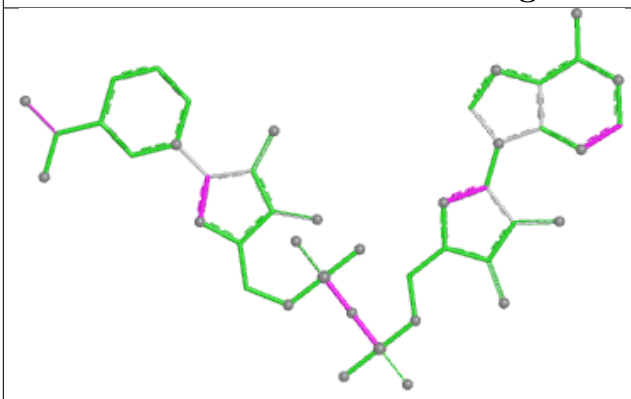


Torsions

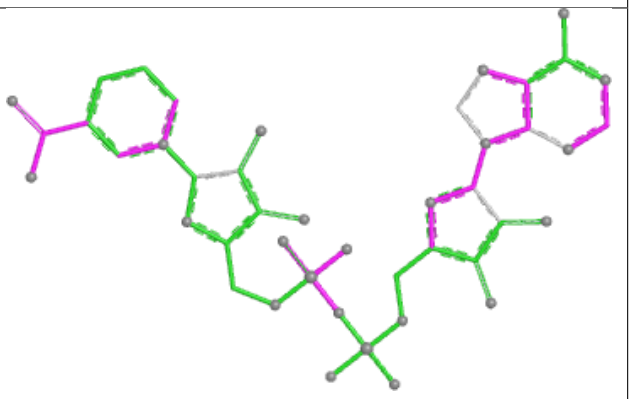


Rings

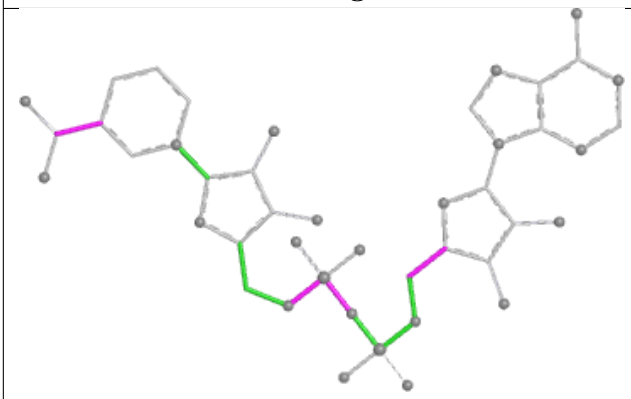
Ligand NAD G 501



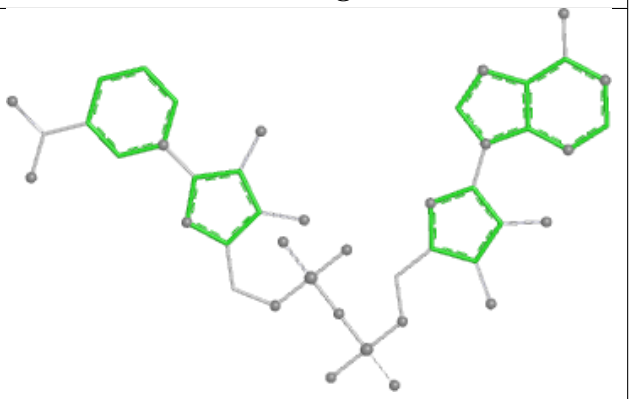
Bond lengths



Bond angles

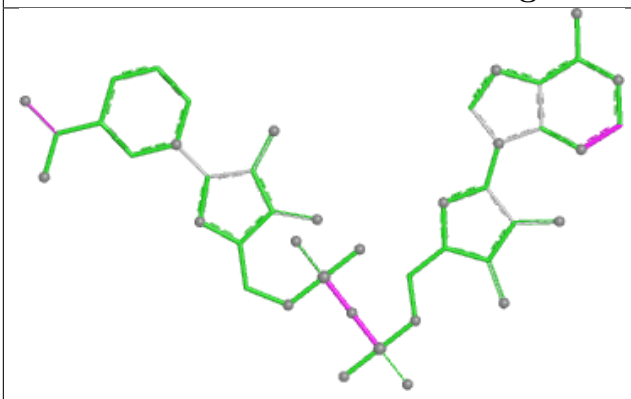


Torsions

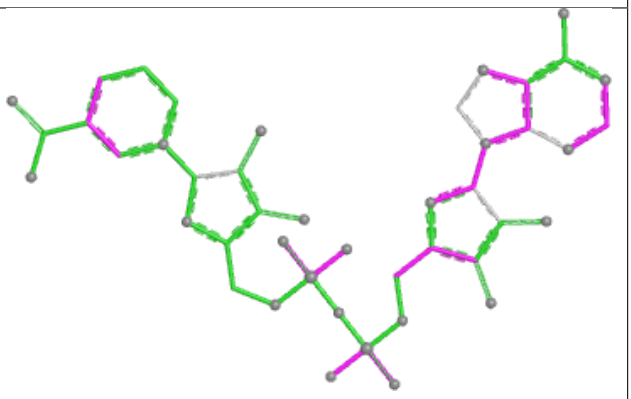


Rings

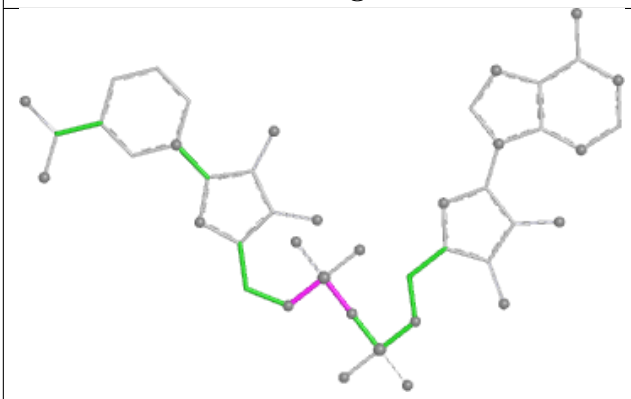
Ligand NAD D 501



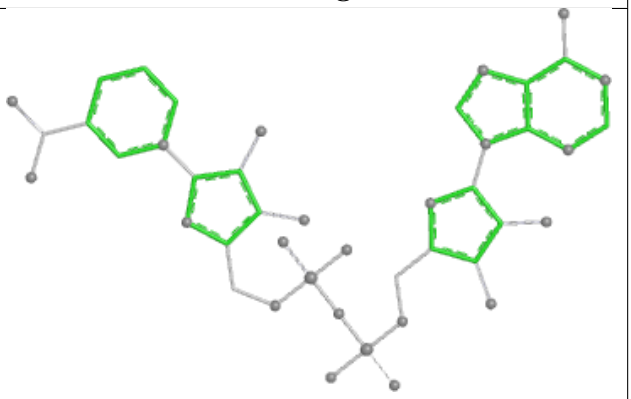
Bond lengths



Bond angles

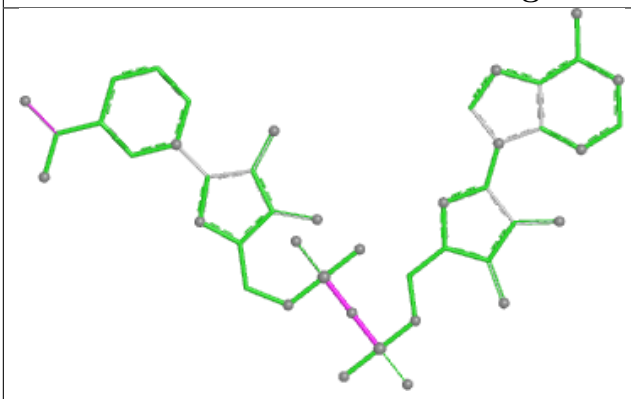


Torsions

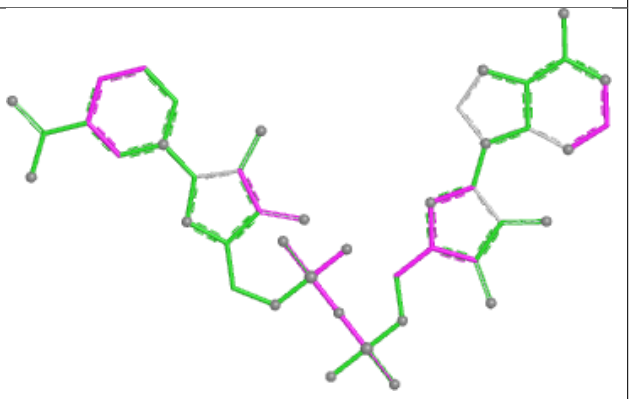


Rings

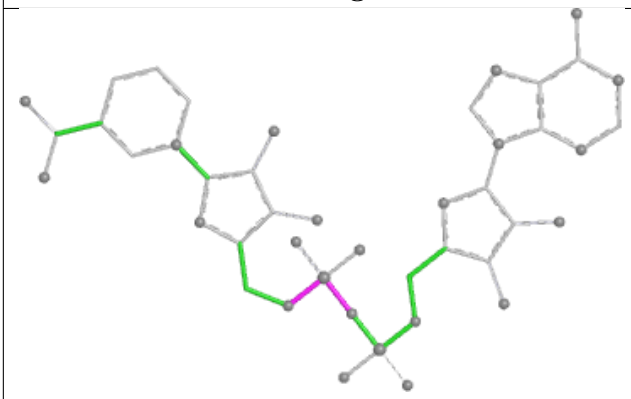
Ligand NAD F 501



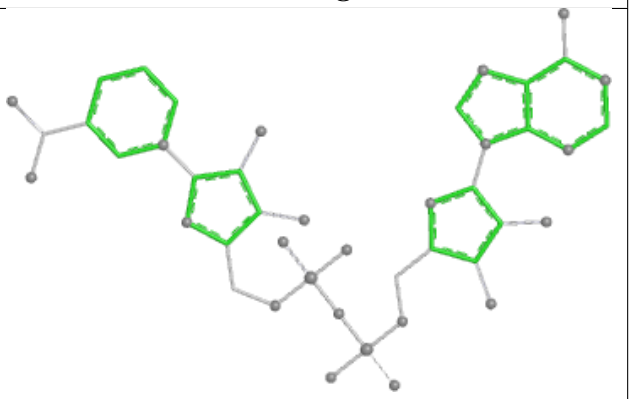
Bond lengths



Bond angles

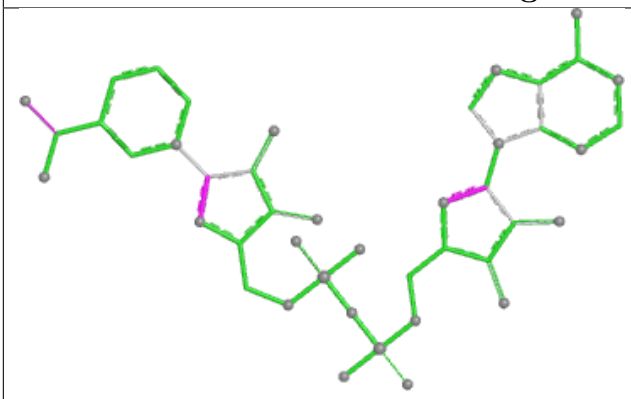


Torsions

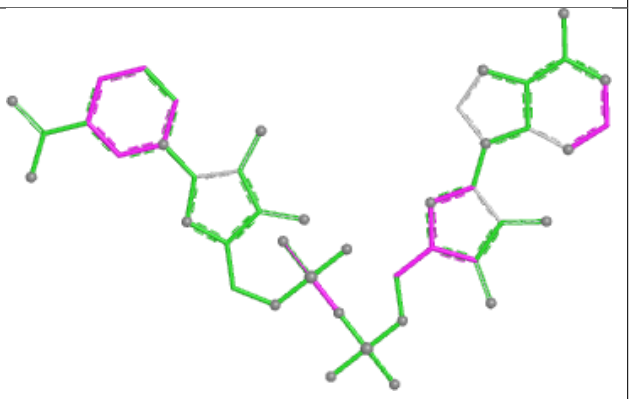


Rings

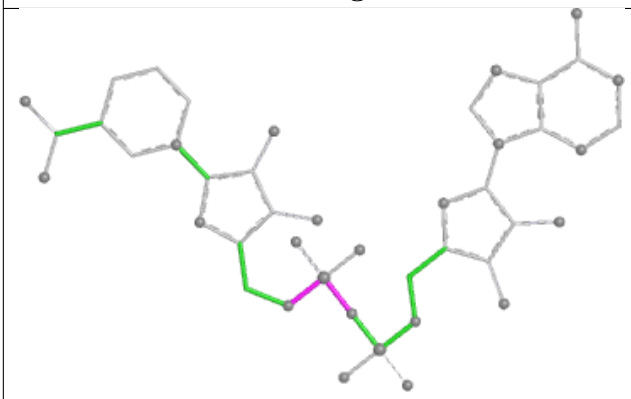
Ligand NAD B 501



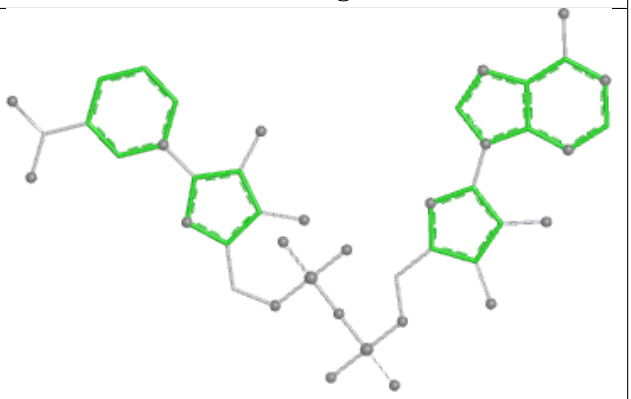
Bond lengths



Bond angles

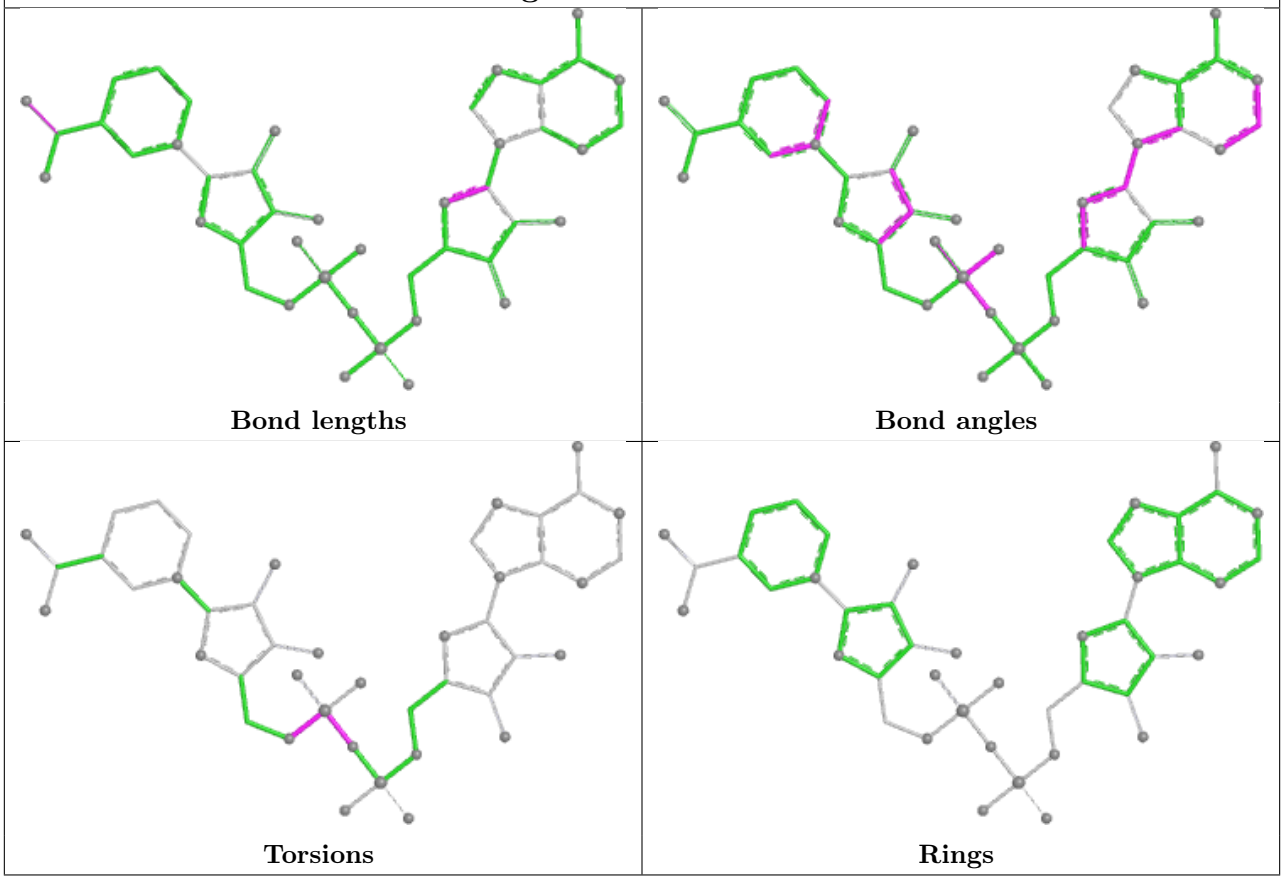


Torsions



Rings

Ligand NAD C 501



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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{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	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	499/520 (95%)	-0.53	1 (0%) 92 93	6, 22, 41, 77	12 (2%)
1	B	499/520 (95%)	-0.71	3 (0%) 85 88	7, 17, 34, 88	9 (1%)
1	C	502/520 (96%)	-0.83	2 (0%) 89 91	6, 14, 28, 60	21 (4%)
1	D	497/520 (95%)	-0.75	0 100 100	6, 16, 32, 57	13 (2%)
1	E	500/520 (96%)	-0.83	2 (0%) 89 91	5, 14, 28, 60	19 (3%)
1	F	497/520 (95%)	-0.87	1 (0%) 92 93	5, 13, 25, 67	20 (4%)
1	G	502/520 (96%)	-0.73	0 100 100	6, 17, 31, 49	15 (2%)
1	H	499/520 (95%)	-0.73	3 (0%) 85 88	6, 15, 30, 71	21 (4%)
All	All	3995/4160 (96%)	-0.75	12 (0%) 90 92	5, 16, 33, 88	130 (3%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	-6	LEU	4.4
1	H	3	LEU	4.2
1	E	-4	PHE	3.1
1	H	0	ALA	2.7
1	B	-2	SER	2.5

6.2 Non-standard residues in protein, DNA, RNA chains

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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CME	H	289[A]	10/11	0.89	0.12	20,23,40,41	10

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CME	H	289[B]	10/11	0.89	0.12	20,24,31,31	10
1	CME	A	289	10/11	0.90	0.12	24,29,42,49	0
1	CME	D	289	10/11	0.93	0.11	17,24,43,59	0
1	CME	G	289[A]	10/11	0.93	0.10	20,22,34,35	10
1	CME	G	289[B]	10/11	0.93	0.10	20,24,35,35	10
1	CME	C	289[A]	10/11	0.93	0.10	14,16,31,32	10
1	CME	C	289[B]	10/11	0.93	0.10	13,15,24,25	10
1	CME	B	289[B]	10/11	0.94	0.08	15,18,25,26	10
1	CME	B	289[A]	10/11	0.94	0.08	15,18,30,32	10
1	CME	F	289[A]	10/11	0.94	0.08	14,18,30,34	10
1	CME	F	289[B]	10/11	0.94	0.08	13,15,24,26	10
1	CME	E	289[A]	10/11	0.95	0.11	15,19,34,35	10
1	CME	E	289[B]	10/11	0.95	0.11	15,19,31,31	10

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	NA	E	503	1/1	0.83	0.15	31,31,31,31	0
3	NA	E	502	1/1	0.90	0.19	32,32,32,32	0
2	NAD	A	501	44/44	0.93	0.08	20,27,35,44	0
3	NA	G	503	1/1	0.94	0.07	19,19,19,19	0
2	NAD	H	501	44/44	0.95	0.06	18,23,28,31	0
2	NAD	G	501	44/44	0.95	0.07	19,24,28,30	0
2	NAD	D	501	44/44	0.96	0.06	17,22,28,28	0
3	NA	C	503	1/1	0.96	0.08	16,16,16,16	0
3	NA	D	503	1/1	0.96	0.06	18,18,18,18	0
3	NA	A	503	1/1	0.97	0.06	19,19,19,19	0
3	NA	D	502	1/1	0.97	0.05	12,12,12,12	0
3	NA	A	502	1/1	0.98	0.06	17,17,17,17	0
2	NAD	E	501	44/44	0.98	0.04	12,15,18,19	0
2	NAD	C	501	44/44	0.98	0.04	12,14,18,18	0
3	NA	E	505	1/1	0.98	0.04	16,16,16,16	0

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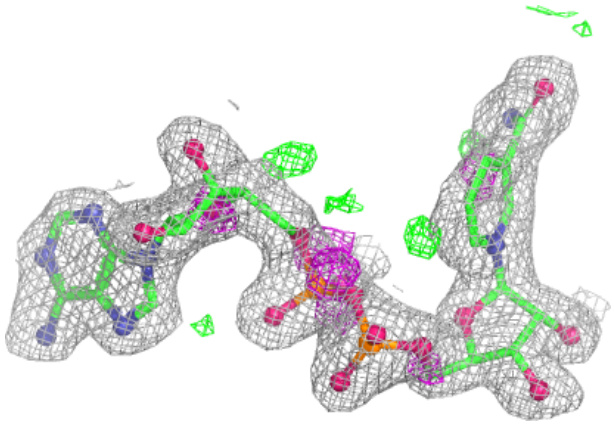
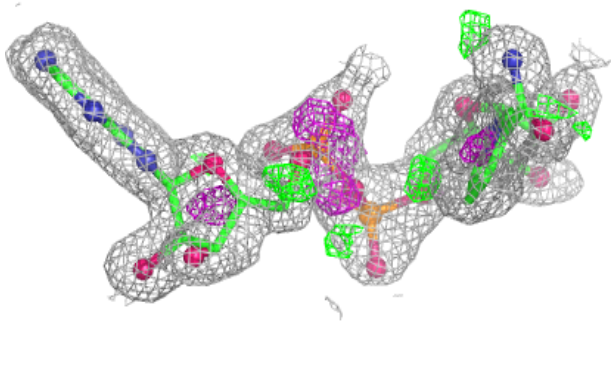
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NA	F	502	1/1	0.98	0.19	26,26,26,26	0
3	NA	F	503	1/1	0.98	0.05	14,14,14,14	0
2	NAD	B	501	44/44	0.98	0.05	13,17,19,22	0
3	NA	H	503	1/1	0.98	0.08	16,16,16,16	0
3	NA	B	503	1/1	0.99	0.03	17,17,17,17	0
3	NA	C	502	1/1	0.99	0.06	11,11,11,11	0
3	NA	G	502	1/1	0.99	0.07	15,15,15,15	0
2	NAD	F	501	44/44	0.99	0.04	11,14,16,18	0
3	NA	H	502	1/1	0.99	0.10	14,14,14,14	0
3	NA	B	502	1/1	0.99	0.04	13,13,13,13	0
3	NA	E	504	1/1	1.00	0.04	10,10,10,10	0
3	NA	F	504	1/1	1.00	0.02	8,8,8,8	0

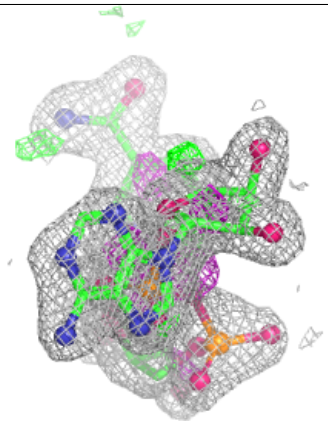
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAD A 501:

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

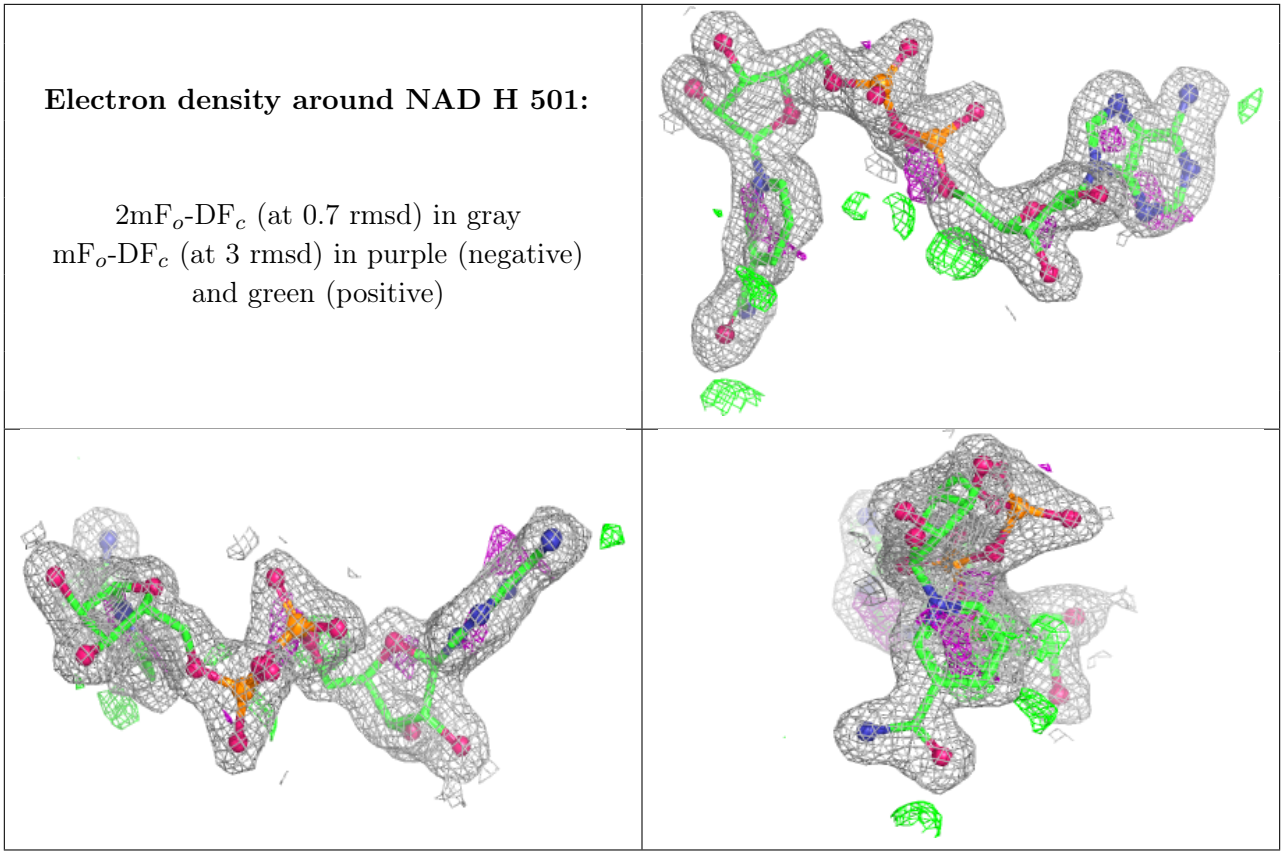






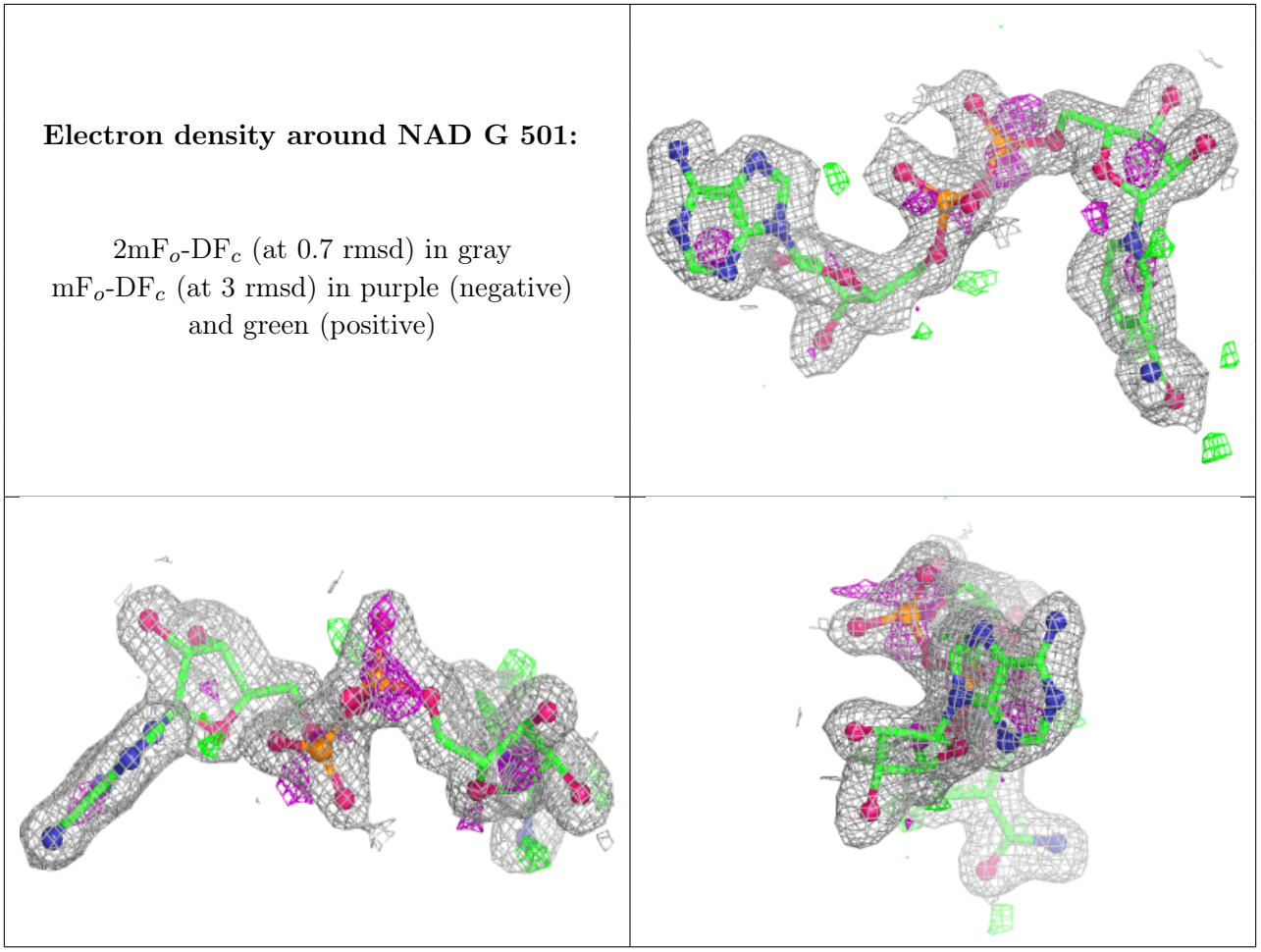
Electron density around NAD H 501:

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



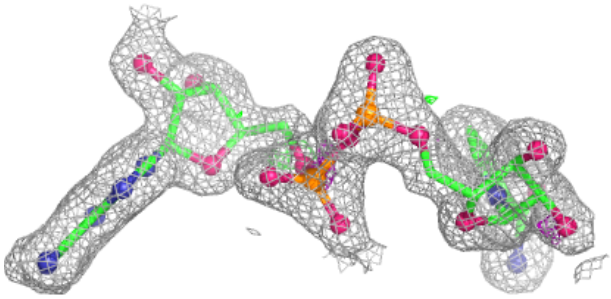
Electron density around NAD G 501:

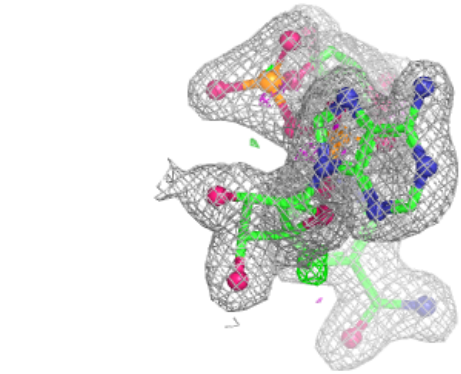
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

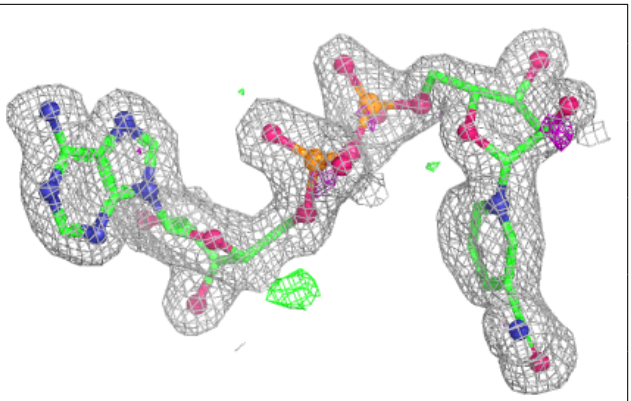


Electron density around NAD D 501:

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

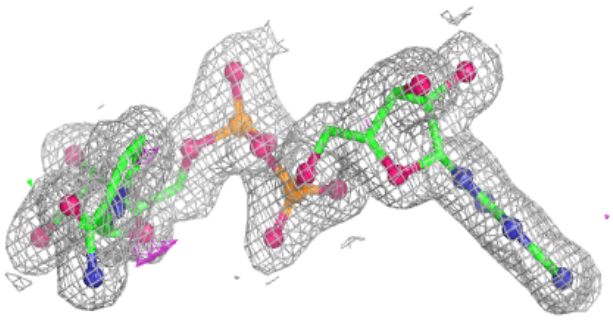


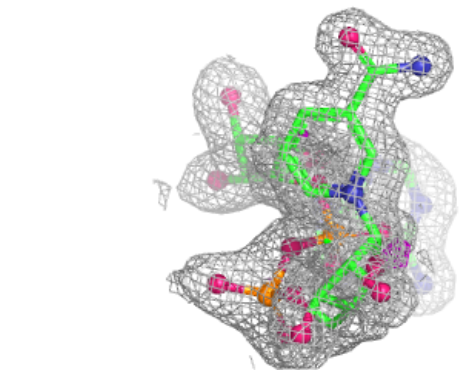


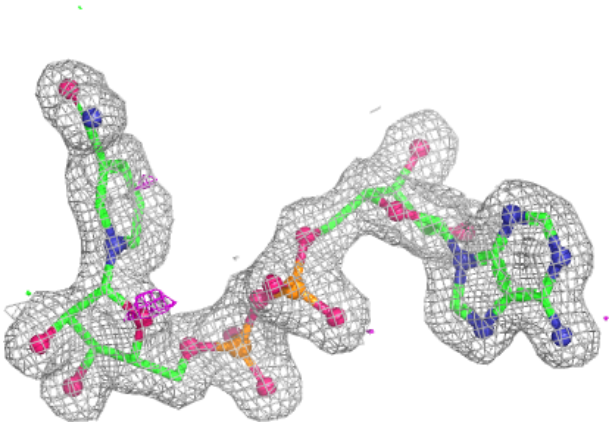


Electron density around NAD E 501:

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

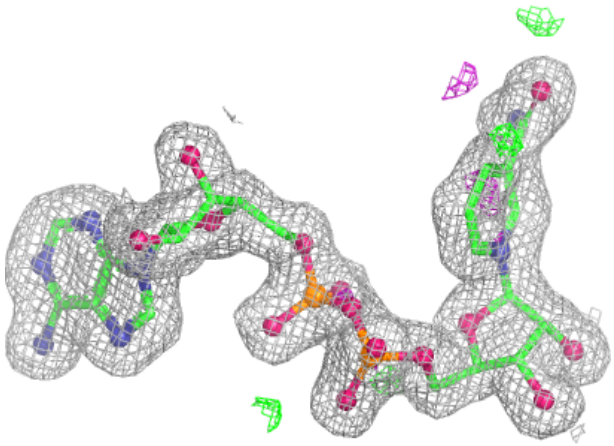


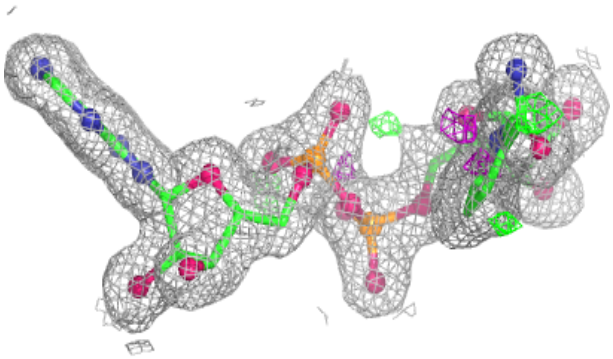


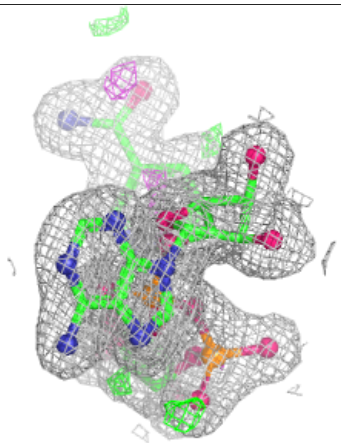


Electron density around NAD C 501:

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

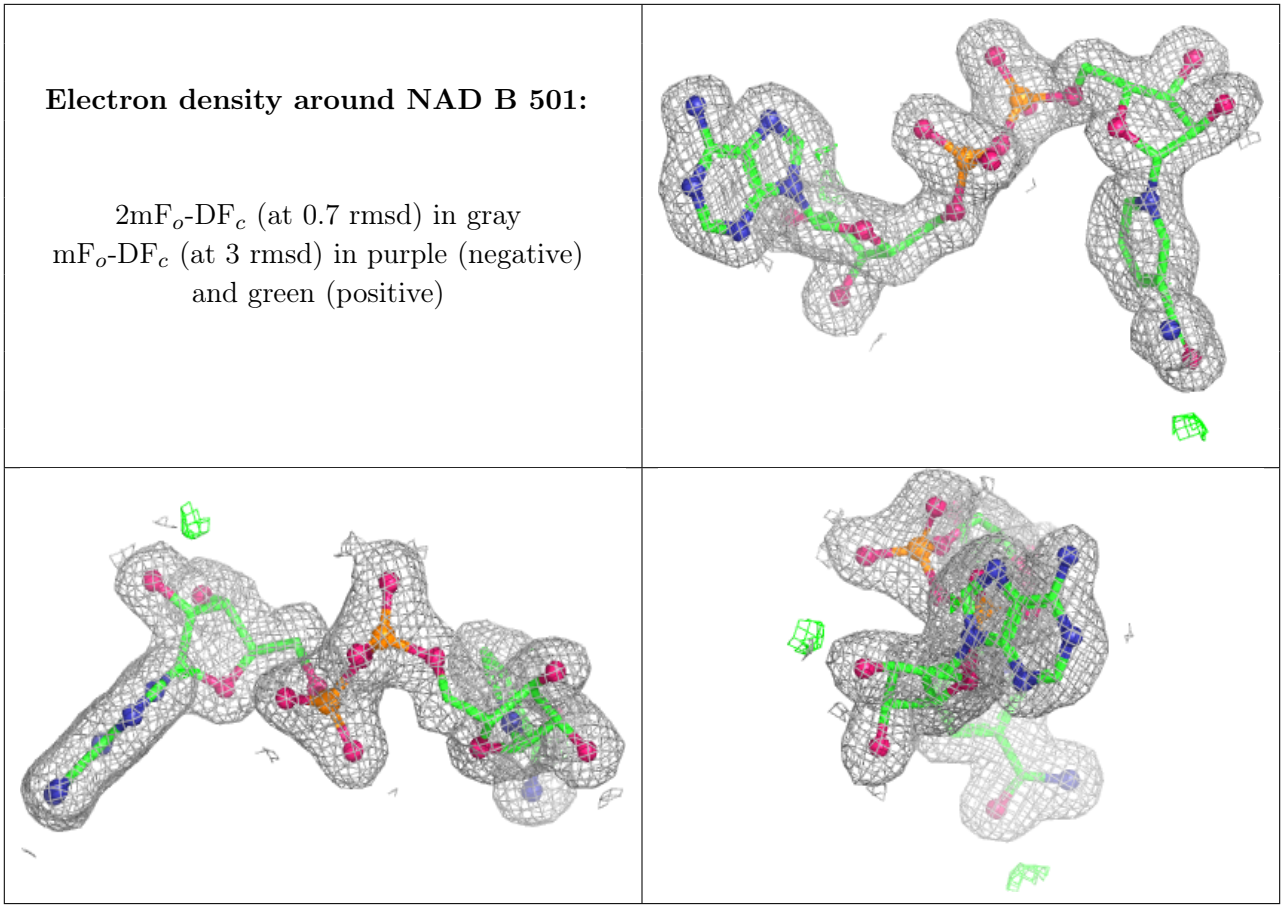






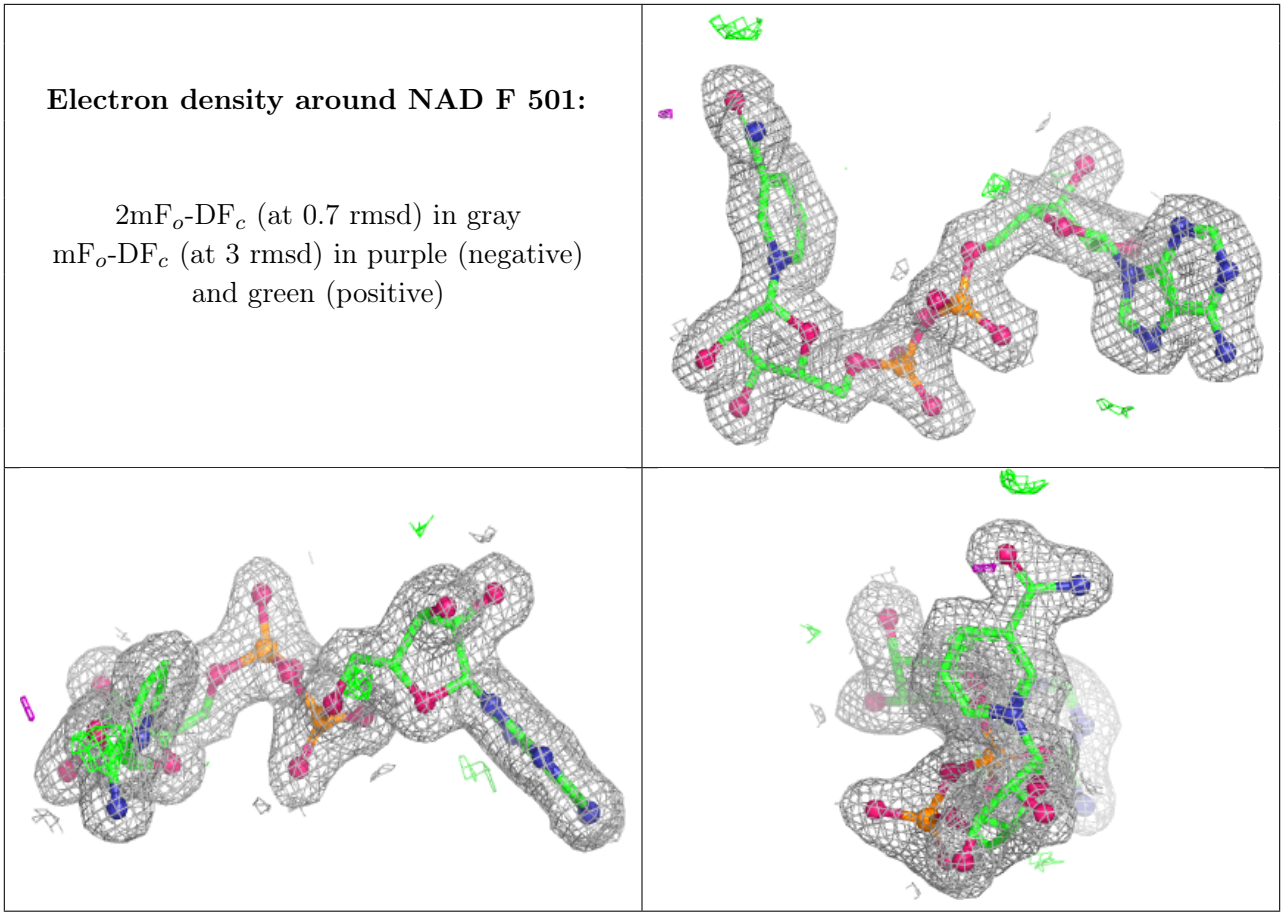
Electron density around NAD B 501:

$2mF_o$-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 F 501:

$2mF_o$-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

There are no such residues in this entry.