



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 03:35 PM UTC

PDB ID : 9ZAO / pdb_00009zao
Title : Crystal structure of a glyceraldehyde-3-phosphate dehydrogenase from *Neisseria gonorrhoeae* in complex with NAD (P1 form2)
Authors : Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2025-11-19
Resolution : 3.09 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

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

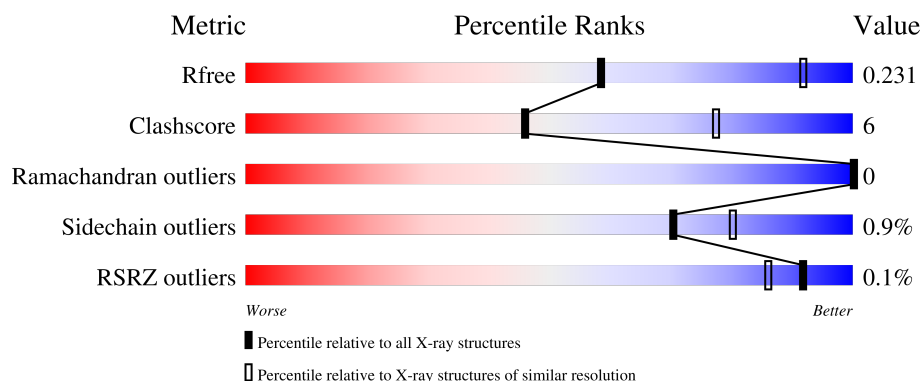
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.09 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



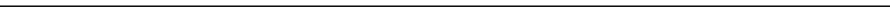
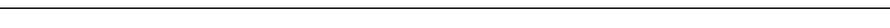
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	342	
1	B	342	
1	C	342	
1	D	342	

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Mol	Chain	Length	Quality of chain
1	E	342	 85% 12% .
1	F	342	 86% 11% .
1	G	342	 84% 13% .
1	H	342	 85% 12% .
1	I	342	 86% 11% .
1	J	342	 85% 13% .
1	K	342	 85% 13% .
1	L	342	 86% 11% .
1	M	342	 80% 14% 5%
1	N	342	 85% 12% . .
1	O	342	 79% 17% .
1	P	342	 % 80% 16% .
1	Q	342	 84% 13% .
1	R	342	 85% 13% .
1	S	342	 79% 18% . .
1	T	342	 % 84% 13% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 49857 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 Glyceraldehyde-3-phosphate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	0	0
			2475	1552	430	483	10			
1	B	334	Total	C	N	O	S	0	0	0
			2480	1555	431	484	10			
1	C	332	Total	C	N	O	S	0	0	0
			2469	1549	429	481	10			
1	D	334	Total	C	N	O	S	0	0	0
			2484	1557	431	486	10			
1	E	334	Total	C	N	O	S	0	0	0
			2491	1561	432	488	10			
1	F	334	Total	C	N	O	S	0	0	0
			2480	1555	431	484	10			
1	G	333	Total	C	N	O	S	0	0	0
			2470	1549	429	482	10			
1	H	333	Total	C	N	O	S	0	0	0
			2469	1550	428	481	10			
1	I	332	Total	C	N	O	S	0	0	0
			2453	1540	425	478	10			
1	J	334	Total	C	N	O	S	0	0	0
			2481	1555	428	488	10			
1	K	333	Total	C	N	O	S	0	0	0
			2475	1552	430	483	10			
1	L	333	Total	C	N	O	S	0	0	0
			2475	1552	430	483	10			
1	M	324	Total	C	N	O	S	0	0	0
			2407	1507	419	471	10			
1	N	333	Total	C	N	O	S	0	0	0
			2475	1552	430	483	10			
1	O	329	Total	C	N	O	S	0	0	0
			2439	1531	422	476	10			
1	P	328	Total	C	N	O	S	0	0	0
			2361	1473	409	469	10			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	333	Total	C	N	O	S	0	0	0
			2477	1554	428	485	10			
1	R	333	Total	C	N	O	S	0	0	0
			2468	1549	427	482	10			
1	S	333	Total	C	N	O	S	0	0	0
			2475	1552	430	483	10			
1	T	334	Total	C	N	O	S	0	0	0
			2477	1552	431	484	10			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP B4RPP8
A	-6	ALA	-	expression tag	UNP B4RPP8
A	-5	HIS	-	expression tag	UNP B4RPP8
A	-4	HIS	-	expression tag	UNP B4RPP8
A	-3	HIS	-	expression tag	UNP B4RPP8
A	-2	HIS	-	expression tag	UNP B4RPP8
A	-1	HIS	-	expression tag	UNP B4RPP8
A	0	HIS	-	expression tag	UNP B4RPP8
B	-7	MET	-	initiating methionine	UNP B4RPP8
B	-6	ALA	-	expression tag	UNP B4RPP8
B	-5	HIS	-	expression tag	UNP B4RPP8
B	-4	HIS	-	expression tag	UNP B4RPP8
B	-3	HIS	-	expression tag	UNP B4RPP8
B	-2	HIS	-	expression tag	UNP B4RPP8
B	-1	HIS	-	expression tag	UNP B4RPP8
B	0	HIS	-	expression tag	UNP B4RPP8
C	-7	MET	-	initiating methionine	UNP B4RPP8
C	-6	ALA	-	expression tag	UNP B4RPP8
C	-5	HIS	-	expression tag	UNP B4RPP8
C	-4	HIS	-	expression tag	UNP B4RPP8
C	-3	HIS	-	expression tag	UNP B4RPP8
C	-2	HIS	-	expression tag	UNP B4RPP8
C	-1	HIS	-	expression tag	UNP B4RPP8
C	0	HIS	-	expression tag	UNP B4RPP8
D	-7	MET	-	initiating methionine	UNP B4RPP8
D	-6	ALA	-	expression tag	UNP B4RPP8
D	-5	HIS	-	expression tag	UNP B4RPP8
D	-4	HIS	-	expression tag	UNP B4RPP8
D	-3	HIS	-	expression tag	UNP B4RPP8
D	-2	HIS	-	expression tag	UNP B4RPP8
D	-1	HIS	-	expression tag	UNP B4RPP8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	0	HIS	-	expression tag	UNP B4RPP8
E	-7	MET	-	initiating methionine	UNP B4RPP8
E	-6	ALA	-	expression tag	UNP B4RPP8
E	-5	HIS	-	expression tag	UNP B4RPP8
E	-4	HIS	-	expression tag	UNP B4RPP8
E	-3	HIS	-	expression tag	UNP B4RPP8
E	-2	HIS	-	expression tag	UNP B4RPP8
E	-1	HIS	-	expression tag	UNP B4RPP8
E	0	HIS	-	expression tag	UNP B4RPP8
F	-7	MET	-	initiating methionine	UNP B4RPP8
F	-6	ALA	-	expression tag	UNP B4RPP8
F	-5	HIS	-	expression tag	UNP B4RPP8
F	-4	HIS	-	expression tag	UNP B4RPP8
F	-3	HIS	-	expression tag	UNP B4RPP8
F	-2	HIS	-	expression tag	UNP B4RPP8
F	-1	HIS	-	expression tag	UNP B4RPP8
F	0	HIS	-	expression tag	UNP B4RPP8
G	-7	MET	-	initiating methionine	UNP B4RPP8
G	-6	ALA	-	expression tag	UNP B4RPP8
G	-5	HIS	-	expression tag	UNP B4RPP8
G	-4	HIS	-	expression tag	UNP B4RPP8
G	-3	HIS	-	expression tag	UNP B4RPP8
G	-2	HIS	-	expression tag	UNP B4RPP8
G	-1	HIS	-	expression tag	UNP B4RPP8
G	0	HIS	-	expression tag	UNP B4RPP8
H	-7	MET	-	initiating methionine	UNP B4RPP8
H	-6	ALA	-	expression tag	UNP B4RPP8
H	-5	HIS	-	expression tag	UNP B4RPP8
H	-4	HIS	-	expression tag	UNP B4RPP8
H	-3	HIS	-	expression tag	UNP B4RPP8
H	-2	HIS	-	expression tag	UNP B4RPP8
H	-1	HIS	-	expression tag	UNP B4RPP8
H	0	HIS	-	expression tag	UNP B4RPP8
I	-7	MET	-	initiating methionine	UNP B4RPP8
I	-6	ALA	-	expression tag	UNP B4RPP8
I	-5	HIS	-	expression tag	UNP B4RPP8
I	-4	HIS	-	expression tag	UNP B4RPP8
I	-3	HIS	-	expression tag	UNP B4RPP8
I	-2	HIS	-	expression tag	UNP B4RPP8
I	-1	HIS	-	expression tag	UNP B4RPP8
I	0	HIS	-	expression tag	UNP B4RPP8
J	-7	MET	-	initiating methionine	UNP B4RPP8

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-6	ALA	-	expression tag	UNP B4RPP8
J	-5	HIS	-	expression tag	UNP B4RPP8
J	-4	HIS	-	expression tag	UNP B4RPP8
J	-3	HIS	-	expression tag	UNP B4RPP8
J	-2	HIS	-	expression tag	UNP B4RPP8
J	-1	HIS	-	expression tag	UNP B4RPP8
J	0	HIS	-	expression tag	UNP B4RPP8
K	-7	MET	-	initiating methionine	UNP B4RPP8
K	-6	ALA	-	expression tag	UNP B4RPP8
K	-5	HIS	-	expression tag	UNP B4RPP8
K	-4	HIS	-	expression tag	UNP B4RPP8
K	-3	HIS	-	expression tag	UNP B4RPP8
K	-2	HIS	-	expression tag	UNP B4RPP8
K	-1	HIS	-	expression tag	UNP B4RPP8
K	0	HIS	-	expression tag	UNP B4RPP8
L	-7	MET	-	initiating methionine	UNP B4RPP8
L	-6	ALA	-	expression tag	UNP B4RPP8
L	-5	HIS	-	expression tag	UNP B4RPP8
L	-4	HIS	-	expression tag	UNP B4RPP8
L	-3	HIS	-	expression tag	UNP B4RPP8
L	-2	HIS	-	expression tag	UNP B4RPP8
L	-1	HIS	-	expression tag	UNP B4RPP8
L	0	HIS	-	expression tag	UNP B4RPP8
M	-7	MET	-	initiating methionine	UNP B4RPP8
M	-6	ALA	-	expression tag	UNP B4RPP8
M	-5	HIS	-	expression tag	UNP B4RPP8
M	-4	HIS	-	expression tag	UNP B4RPP8
M	-3	HIS	-	expression tag	UNP B4RPP8
M	-2	HIS	-	expression tag	UNP B4RPP8
M	-1	HIS	-	expression tag	UNP B4RPP8
M	0	HIS	-	expression tag	UNP B4RPP8
N	-7	MET	-	initiating methionine	UNP B4RPP8
N	-6	ALA	-	expression tag	UNP B4RPP8
N	-5	HIS	-	expression tag	UNP B4RPP8
N	-4	HIS	-	expression tag	UNP B4RPP8
N	-3	HIS	-	expression tag	UNP B4RPP8
N	-2	HIS	-	expression tag	UNP B4RPP8
N	-1	HIS	-	expression tag	UNP B4RPP8
N	0	HIS	-	expression tag	UNP B4RPP8
O	-7	MET	-	initiating methionine	UNP B4RPP8
O	-6	ALA	-	expression tag	UNP B4RPP8
O	-5	HIS	-	expression tag	UNP B4RPP8

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-4	HIS	-	expression tag	UNP B4RPP8
O	-3	HIS	-	expression tag	UNP B4RPP8
O	-2	HIS	-	expression tag	UNP B4RPP8
O	-1	HIS	-	expression tag	UNP B4RPP8
O	0	HIS	-	expression tag	UNP B4RPP8
P	-7	MET	-	initiating methionine	UNP B4RPP8
P	-6	ALA	-	expression tag	UNP B4RPP8
P	-5	HIS	-	expression tag	UNP B4RPP8
P	-4	HIS	-	expression tag	UNP B4RPP8
P	-3	HIS	-	expression tag	UNP B4RPP8
P	-2	HIS	-	expression tag	UNP B4RPP8
P	-1	HIS	-	expression tag	UNP B4RPP8
P	0	HIS	-	expression tag	UNP B4RPP8
Q	-7	MET	-	initiating methionine	UNP B4RPP8
Q	-6	ALA	-	expression tag	UNP B4RPP8
Q	-5	HIS	-	expression tag	UNP B4RPP8
Q	-4	HIS	-	expression tag	UNP B4RPP8
Q	-3	HIS	-	expression tag	UNP B4RPP8
Q	-2	HIS	-	expression tag	UNP B4RPP8
Q	-1	HIS	-	expression tag	UNP B4RPP8
Q	0	HIS	-	expression tag	UNP B4RPP8
R	-7	MET	-	initiating methionine	UNP B4RPP8
R	-6	ALA	-	expression tag	UNP B4RPP8
R	-5	HIS	-	expression tag	UNP B4RPP8
R	-4	HIS	-	expression tag	UNP B4RPP8
R	-3	HIS	-	expression tag	UNP B4RPP8
R	-2	HIS	-	expression tag	UNP B4RPP8
R	-1	HIS	-	expression tag	UNP B4RPP8
R	0	HIS	-	expression tag	UNP B4RPP8
S	-7	MET	-	initiating methionine	UNP B4RPP8
S	-6	ALA	-	expression tag	UNP B4RPP8
S	-5	HIS	-	expression tag	UNP B4RPP8
S	-4	HIS	-	expression tag	UNP B4RPP8
S	-3	HIS	-	expression tag	UNP B4RPP8
S	-2	HIS	-	expression tag	UNP B4RPP8
S	-1	HIS	-	expression tag	UNP B4RPP8
S	0	HIS	-	expression tag	UNP B4RPP8
T	-7	MET	-	initiating methionine	UNP B4RPP8
T	-6	ALA	-	expression tag	UNP B4RPP8
T	-5	HIS	-	expression tag	UNP B4RPP8
T	-4	HIS	-	expression tag	UNP B4RPP8
T	-3	HIS	-	expression tag	UNP B4RPP8

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Chain	Residue	Modelled	Actual	Comment	Reference
T	-2	HIS	-	expression tag	UNP B4RPP8
T	-1	HIS	-	expression tag	UNP B4RPP8
T	0	HIS	-	expression tag	UNP B4RPP8

- # NAD

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	B	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	D	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	E	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	F	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	H	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	I	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	J	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	K	1	Total 44	C 21	N 7	O 14	P 2	0	0



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	L	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	N	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	Q	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	T	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

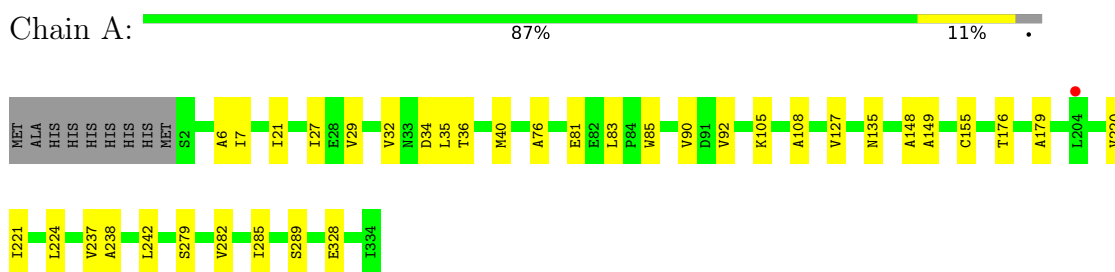
- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		
3	C	1	Total	Na	0	0
			1	1		
3	G	1	Total	Na	0	0
			1	1		
3	O	1	Total	Na	0	0
			1	1		

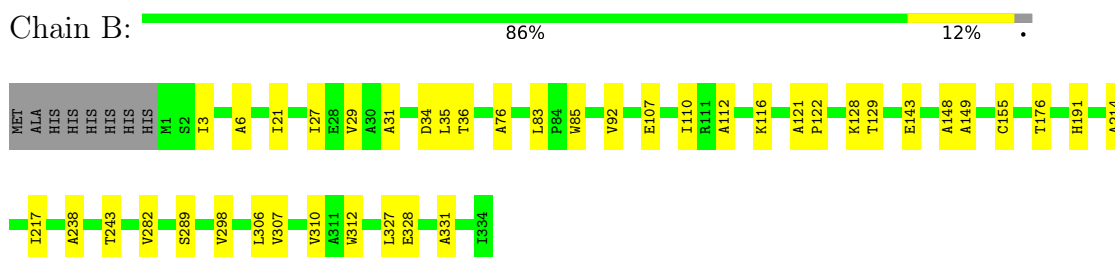
3 Residue-property plots [i](#)

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.

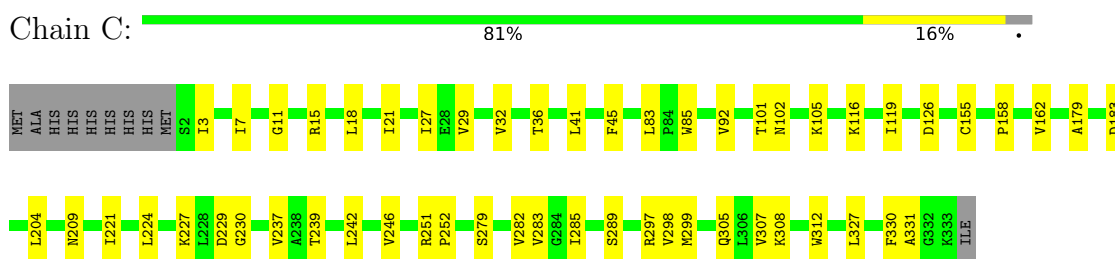
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase



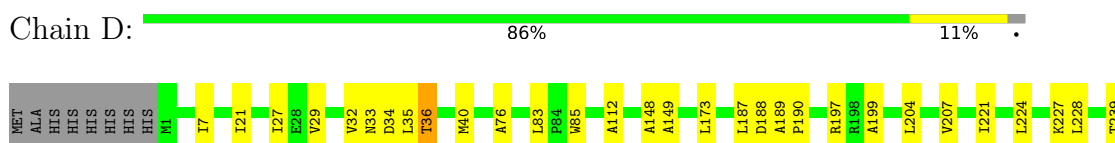
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase





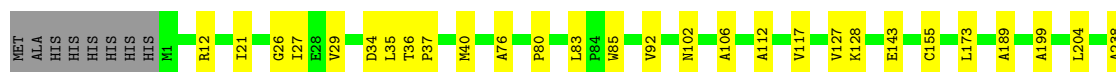
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain E: 85% 12% .



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain F: 86% 11% .



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain G: 84% 13% .



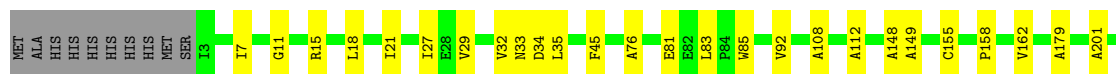
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain H: 85% 12% .



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

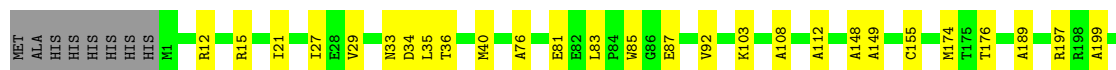
Chain I: 86% 11% .





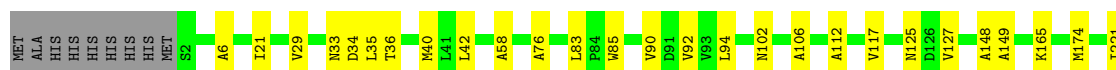
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain J: 85% 13% .



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain K: 85% 13% .



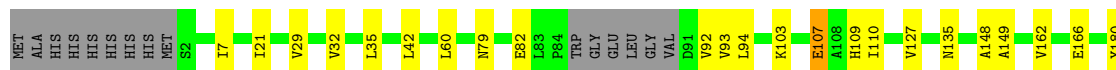
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain L: 86% 11% .



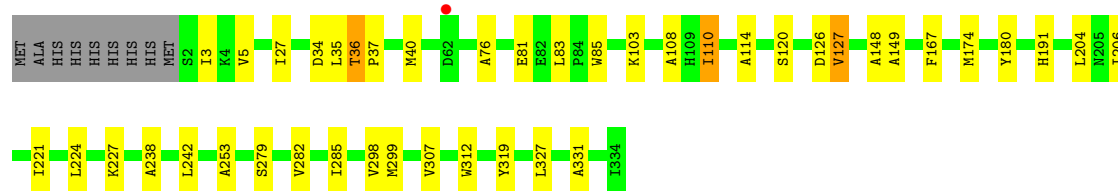
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain M: 80% 14% 5%



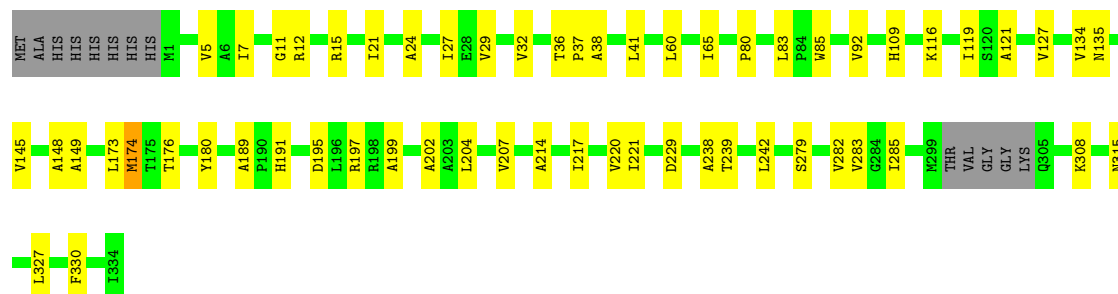
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain N: 85% 12% . .



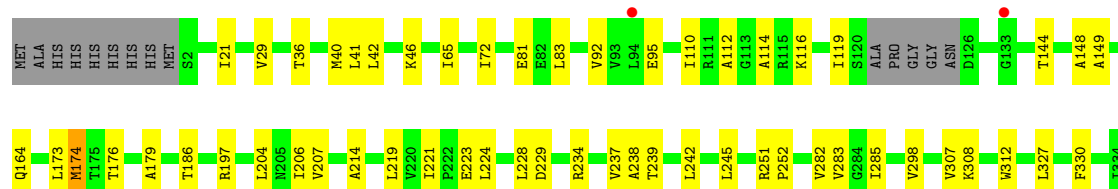
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain O: 79% 17% .



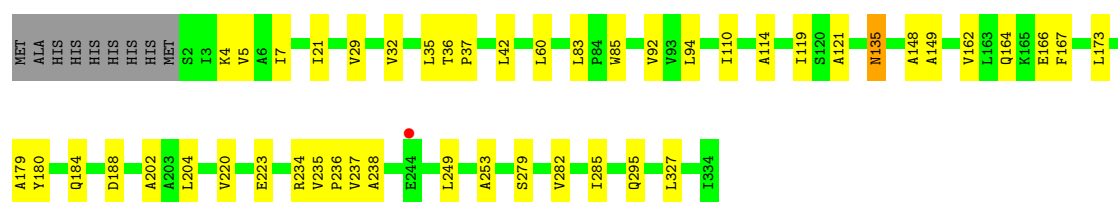
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain P: 80% 16% .



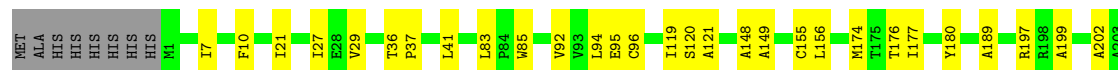
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain Q: 84% 13% .



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain R: 85% 13% .





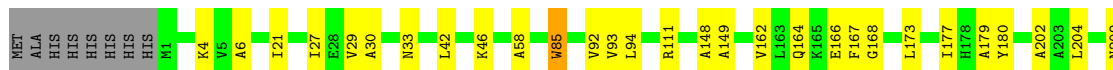
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain S: 79% 18% . .



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase

Chain T: 84% 13% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	76.36Å 139.72Å 222.70Å 76.30° 87.32° 88.12°	Depositor
Resolution (Å)	48.29 – 3.09 48.29 – 3.09	Depositor EDS
% Data completeness (in resolution range)	97.5 (48.29-3.09) 97.5 (48.29-3.09)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 3.07Å)	Xtriage
Refinement program	PHENIX (dev_5438: ???)	Depositor
R, R_{free}	0.181 , 0.234 0.183 , 0.231	Depositor DCC
R_{free} test set	7920 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	84.9	Xtriage
Anisotropy	0.296	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 84.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.049 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	49857	wwPDB-VP
Average B, all atoms (Å ²)	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.26	0/2512	0.44	0/3410
1	B	0.26	0/2517	0.45	0/3417
1	C	0.29	0/2506	0.48	0/3403
1	D	0.27	0/2521	0.46	0/3422
1	E	0.26	0/2528	0.47	0/3430
1	F	0.25	0/2517	0.45	0/3417
1	G	0.29	0/2507	0.49	0/3406
1	H	0.22	0/2506	0.40	0/3402
1	I	0.22	0/2490	0.42	0/3382
1	J	0.25	0/2518	0.45	0/3419
1	K	0.22	0/2512	0.43	0/3410
1	L	0.22	0/2512	0.42	0/3410
1	M	0.20	0/2441	0.41	0/3314
1	N	0.20	0/2512	0.40	0/3410
1	O	0.23	0/2475	0.45	0/3361
1	P	0.19	0/2392	0.41	0/3257
1	Q	0.19	0/2514	0.42	0/3412
1	R	0.19	0/2505	0.39	0/3403
1	S	0.21	0/2512	0.41	0/3410
1	T	0.17	0/2514	0.39	0/3413
All	All	0.23	0/50011	0.43	0/67908

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2475	0	2467	21	0
1	B	2480	0	2472	27	0
1	C	2469	0	2465	32	0
1	D	2484	0	2476	29	0
1	E	2491	0	2489	29	0
1	F	2480	0	2472	33	0
1	G	2470	0	2459	30	0
1	H	2469	0	2459	29	0
1	I	2453	0	2434	27	0
1	J	2481	0	2467	27	0
1	K	2475	0	2467	27	0
1	L	2475	0	2467	26	0
1	M	2407	0	2397	32	0
1	N	2475	0	2467	31	0
1	O	2439	0	2421	47	0
1	P	2361	0	2262	40	0
1	Q	2477	0	2471	33	0
1	R	2468	0	2459	33	0
1	S	2475	0	2467	49	0
1	T	2477	0	2463	34	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	D	44	0	26	0	0
2	E	44	0	26	1	0
2	F	44	0	26	2	0
2	H	44	0	26	1	0
2	I	44	0	26	0	0
2	J	44	0	26	1	0
2	K	44	0	26	0	0
2	L	44	0	26	1	0
2	N	44	0	26	0	0
2	Q	44	0	26	0	0
2	T	44	0	26	1	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	G	1	0	0	0	0
3	O	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	49857	0	49339	572	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 6.

The worst 5 of 572 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:N:5:VAL:HG23	1:N:27:ILE:HD11	1.45	0.98
1:B:36:THR:HG21	1:D:190:PRO:HB3	1.53	0.90
1:M:135:ASN:OD1	1:M:220:VAL:HG13	1.75	0.86
1:P:221:ILE:HG21	1:P:224:LEU:HD12	1.59	0.83
1:A:279:SER:O	1:A:282:VAL:HG12	1.79	0.83

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	331/342 (97%)	320 (97%)	11 (3%)	0	100	100
1	B	332/342 (97%)	323 (97%)	9 (3%)	0	100	100
1	C	330/342 (96%)	320 (97%)	10 (3%)	0	100	100
1	D	332/342 (97%)	322 (97%)	10 (3%)	0	100	100
1	E	332/342 (97%)	323 (97%)	9 (3%)	0	100	100
1	F	332/342 (97%)	321 (97%)	11 (3%)	0	100	100
1	G	331/342 (97%)	320 (97%)	11 (3%)	0	100	100
1	H	331/342 (97%)	324 (98%)	7 (2%)	0	100	100
1	I	330/342 (96%)	319 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	332/342 (97%)	323 (97%)	9 (3%)	0	100	100
1	K	331/342 (97%)	321 (97%)	10 (3%)	0	100	100
1	L	331/342 (97%)	322 (97%)	9 (3%)	0	100	100
1	M	320/342 (94%)	312 (98%)	8 (2%)	0	100	100
1	N	331/342 (97%)	322 (97%)	9 (3%)	0	100	100
1	O	325/342 (95%)	316 (97%)	9 (3%)	0	100	100
1	P	324/342 (95%)	314 (97%)	10 (3%)	0	100	100
1	Q	331/342 (97%)	321 (97%)	10 (3%)	0	100	100
1	R	331/342 (97%)	321 (97%)	10 (3%)	0	100	100
1	S	331/342 (97%)	321 (97%)	10 (3%)	0	100	100
1	T	332/342 (97%)	322 (97%)	10 (3%)	0	100	100
All	All	6600/6840 (96%)	6407 (97%)	193 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	258/273 (94%)	254 (98%)	4 (2%)	55	75
1	B	258/273 (94%)	257 (100%)	1 (0%)	84	86
1	C	258/273 (94%)	256 (99%)	2 (1%)	73	81
1	D	259/273 (95%)	258 (100%)	1 (0%)	84	86
1	E	261/273 (96%)	259 (99%)	2 (1%)	73	81
1	F	258/273 (94%)	256 (99%)	2 (1%)	73	81
1	G	257/273 (94%)	254 (99%)	3 (1%)	63	78
1	H	256/273 (94%)	254 (99%)	2 (1%)	73	81
1	I	253/273 (93%)	252 (100%)	1 (0%)	84	86
1	J	259/273 (95%)	255 (98%)	4 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	258/273 (94%)	253 (98%)	5 (2%)	50	73
1	L	258/273 (94%)	258 (100%)	0	100	100
1	M	252/273 (92%)	249 (99%)	3 (1%)	63	78
1	N	258/273 (94%)	254 (98%)	4 (2%)	55	75
1	O	253/273 (93%)	252 (100%)	1 (0%)	84	86
1	P	233/273 (85%)	231 (99%)	2 (1%)	70	80
1	Q	259/273 (95%)	257 (99%)	2 (1%)	73	81
1	R	257/273 (94%)	256 (100%)	1 (0%)	84	86
1	S	258/273 (94%)	255 (99%)	3 (1%)	63	78
1	T	257/273 (94%)	253 (98%)	4 (2%)	55	75
All	All	5120/5460 (94%)	5073 (99%)	47 (1%)	70	80

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	193	LYS
1	P	174	MET
1	M	297	ARG
1	N	127	VAL
1	Q	4	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	77	ASN
1	T	209	ASN
1	P	184	GLN
1	Q	209	ASN
1	H	43	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 4 are monoatomic - leaving 13 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	Q	401	-	46,48,48	1.05	3 (6%)	64,73,73	0.81	2 (3%)
2	NAD	N	401	-	46,48,48	1.11	3 (6%)	64,73,73	1.00	7 (10%)
2	NAD	K	401	-	46,48,48	1.22	2 (4%)	64,73,73	0.85	1 (1%)
2	NAD	A	401	-	46,48,48	1.14	3 (6%)	64,73,73	0.90	2 (3%)
2	NAD	F	401	-	46,48,48	1.09	3 (6%)	64,73,73	1.00	5 (7%)
2	NAD	I	401	-	46,48,48	1.15	3 (6%)	64,73,73	1.05	6 (9%)
2	NAD	T	401	-	46,48,48	1.19	3 (6%)	64,73,73	0.84	2 (3%)
2	NAD	E	401	-	46,48,48	1.20	2 (4%)	64,73,73	0.94	1 (1%)
2	NAD	L	401	-	46,48,48	1.21	3 (6%)	64,73,73	0.97	5 (7%)
2	NAD	J	401	-	46,48,48	1.33	3 (6%)	64,73,73	1.00	6 (9%)
2	NAD	B	401	-	46,48,48	1.17	3 (6%)	64,73,73	1.03	4 (6%)
2	NAD	H	401	-	46,48,48	1.30	3 (6%)	64,73,73	0.99	4 (6%)
2	NAD	D	401	-	46,48,48	1.33	2 (4%)	64,73,73	0.88	2 (3%)

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	Q	401	-	-	6/30/62/62	0/5/5/5
2	NAD	N	401	-	-	12/30/62/62	0/5/5/5
2	NAD	K	401	-	-	12/30/62/62	0/5/5/5
2	NAD	A	401	-	-	13/30/62/62	0/5/5/5
2	NAD	F	401	-	-	9/30/62/62	0/5/5/5
2	NAD	I	401	-	-	12/30/62/62	0/5/5/5
2	NAD	T	401	-	-	10/30/62/62	0/5/5/5
2	NAD	E	401	-	-	9/30/62/62	0/5/5/5
2	NAD	L	401	-	-	13/30/62/62	0/5/5/5
2	NAD	J	401	-	-	11/30/62/62	0/5/5/5
2	NAD	B	401	-	-	11/30/62/62	0/5/5/5
2	NAD	H	401	-	-	10/30/62/62	0/5/5/5
2	NAD	D	401	-	-	12/30/62/62	0/5/5/5

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	NAD	PA-O3	6.34	1.66	1.59
2	H	401	NAD	PA-O3	6.05	1.66	1.59
2	J	401	NAD	PA-O3	5.89	1.65	1.59
2	K	401	NAD	PA-O3	5.72	1.65	1.59
2	T	401	NAD	PA-O3	5.66	1.65	1.59

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	NAD	O3-PA-O1A	-3.19	101.12	110.70
2	B	401	NAD	O7N-C7N-N7N	2.90	126.81	122.62
2	F	401	NAD	C3N-C7N-N7N	-2.72	114.38	117.74
2	F	401	NAD	O2A-PA-O1A	2.72	125.08	112.44
2	I	401	NAD	O7N-C7N-N7N	2.71	126.53	122.62

There are no chirality outliers.

5 of 140 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	NAD	C5B-O5B-PA-O1A
2	A	401	NAD	C5B-O5B-PA-O2A
2	A	401	NAD	O4B-C4B-C5B-O5B

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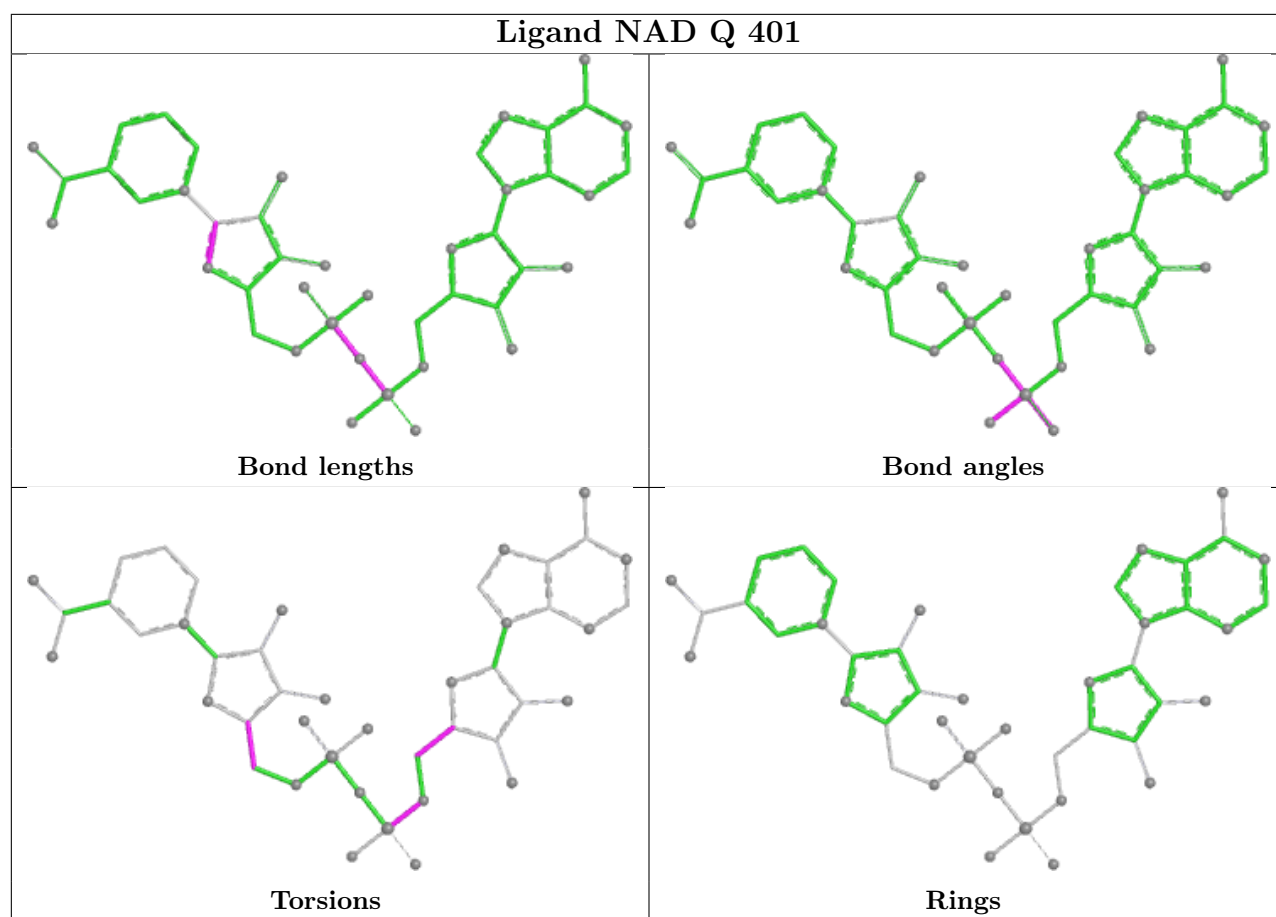
Mol	Chain	Res	Type	Atoms
2	A	401	NAD	C5D-O5D-PN-O1N
2	A	401	NAD	C5D-O5D-PN-O2N

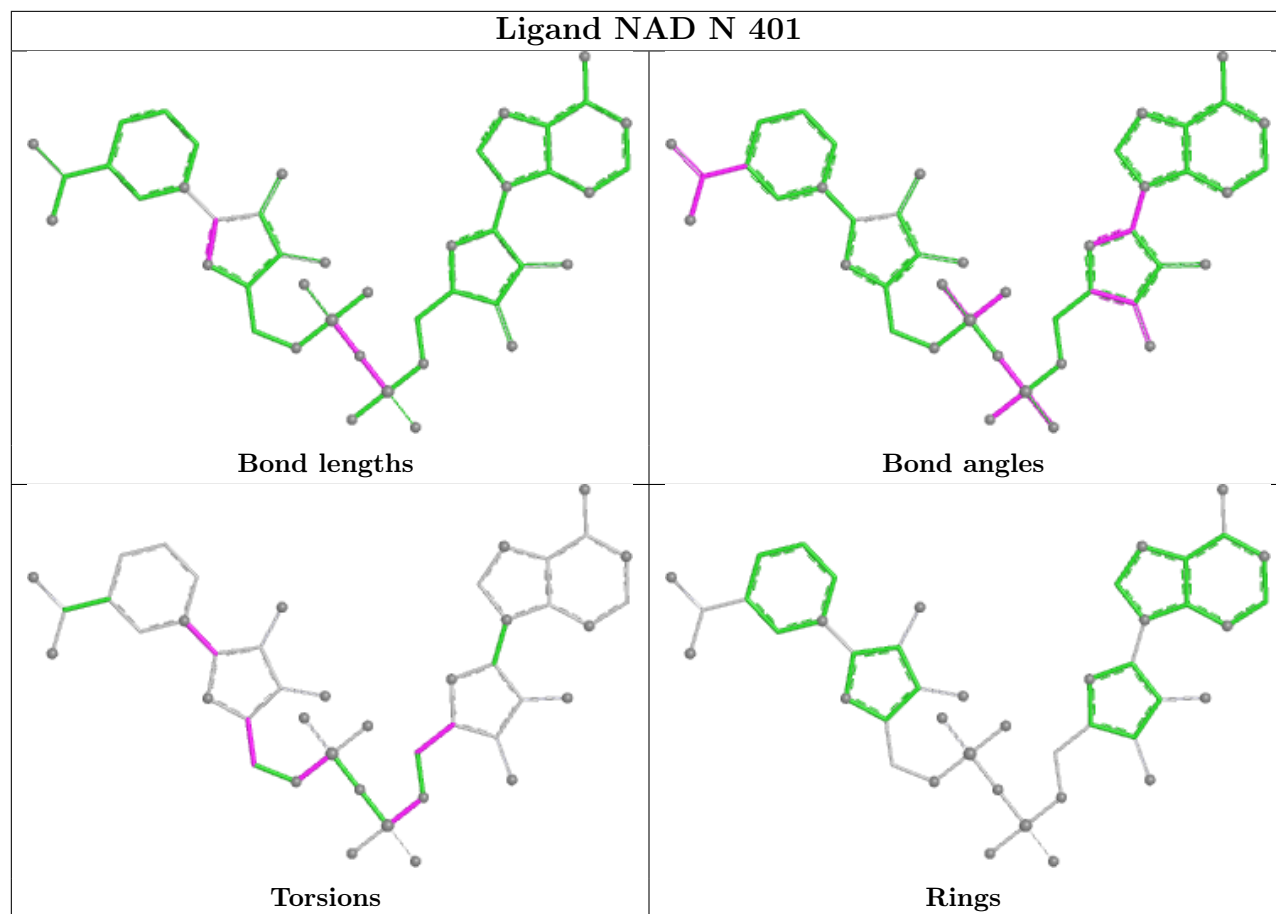
There are no ring outliers.

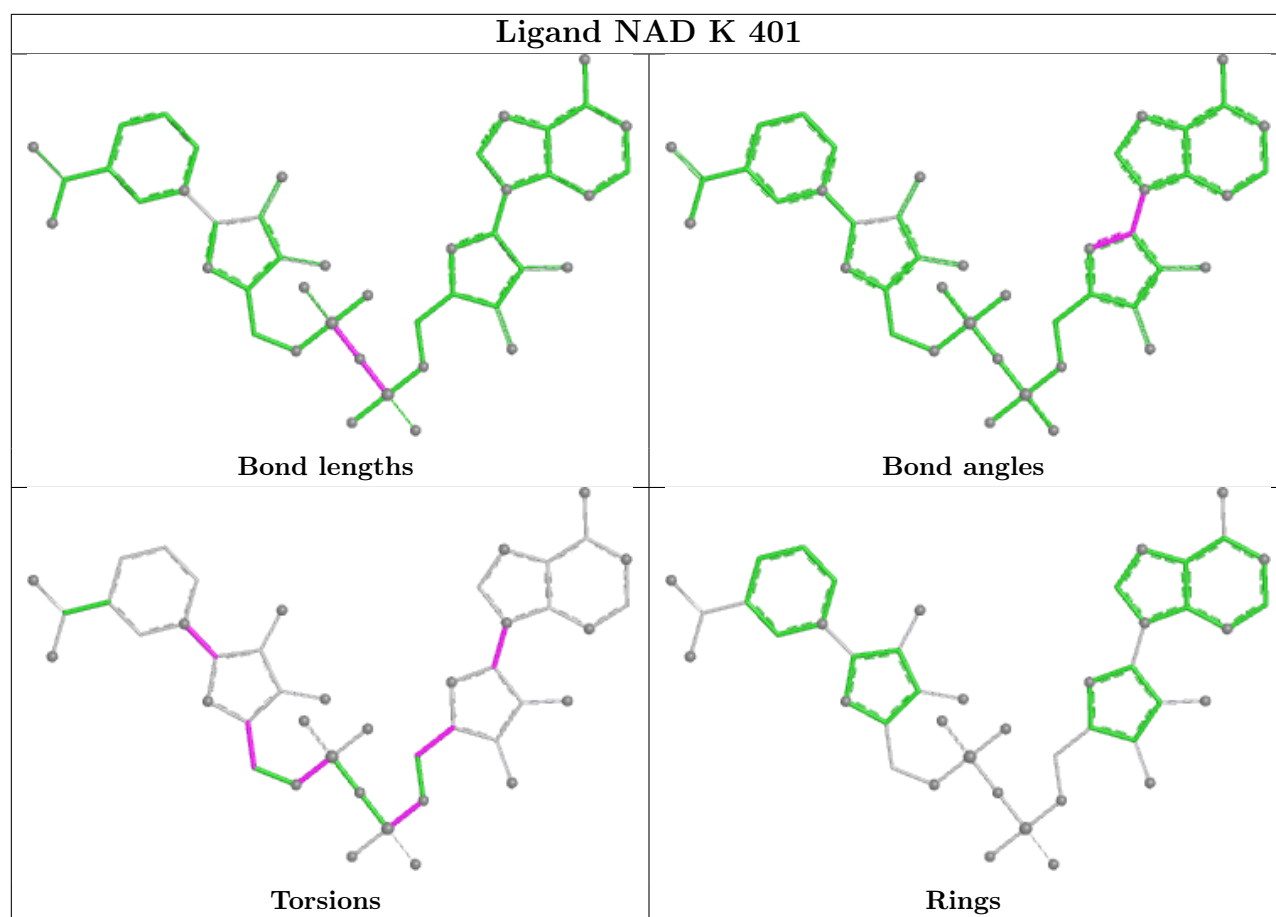
6 monomers are involved in 7 short contacts:

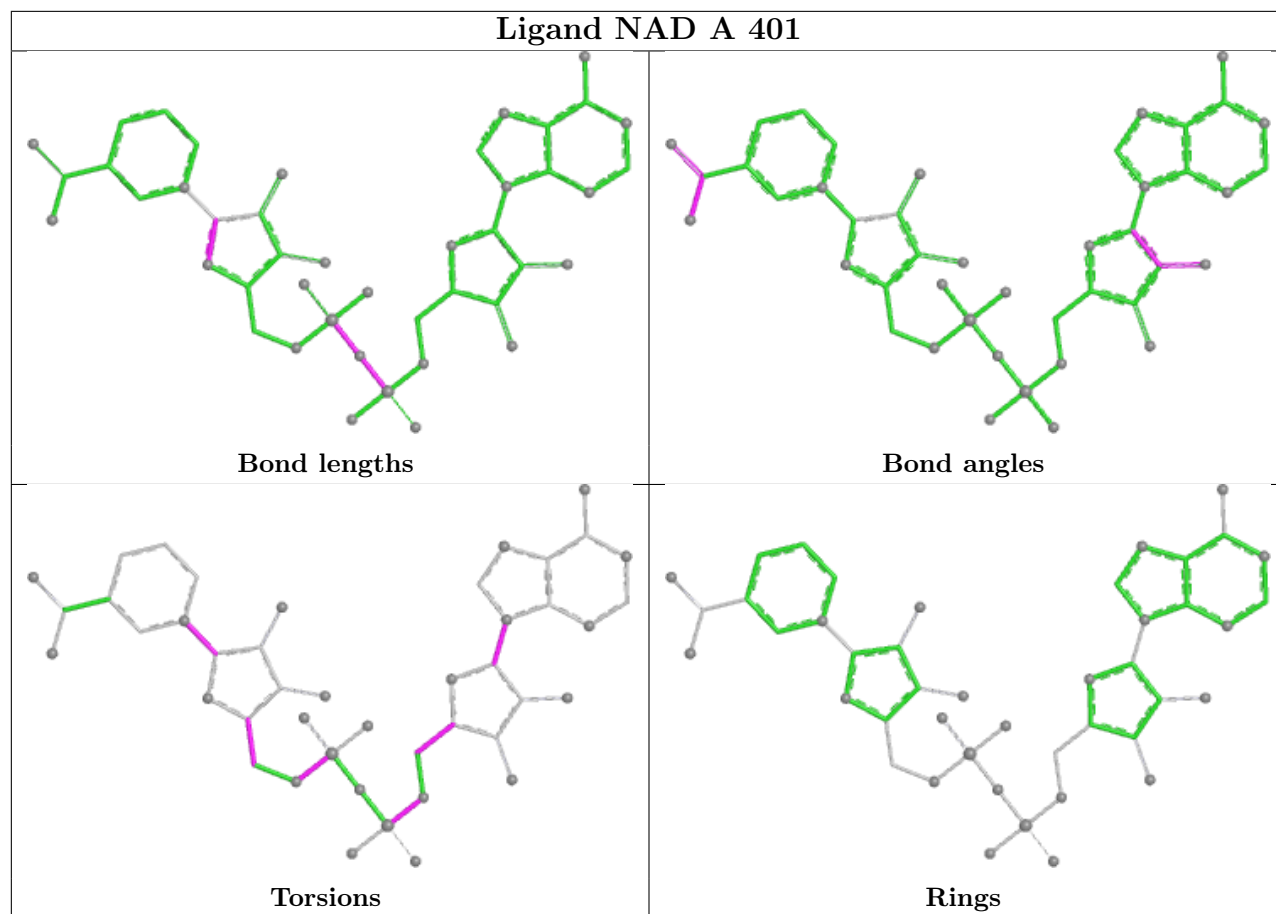
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	401	NAD	2	0
2	T	401	NAD	1	0
2	E	401	NAD	1	0
2	L	401	NAD	1	0
2	J	401	NAD	1	0
2	H	401	NAD	1	0

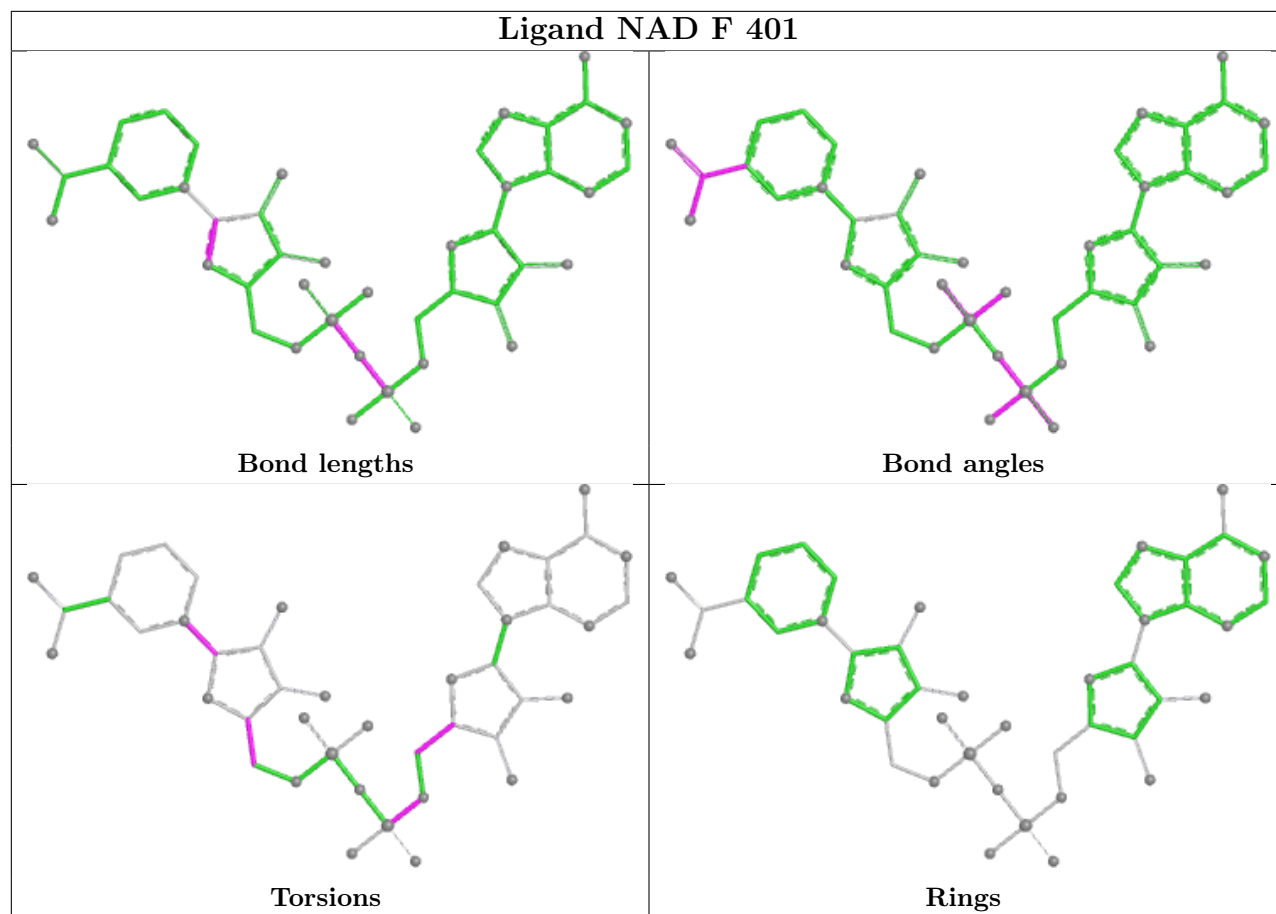
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

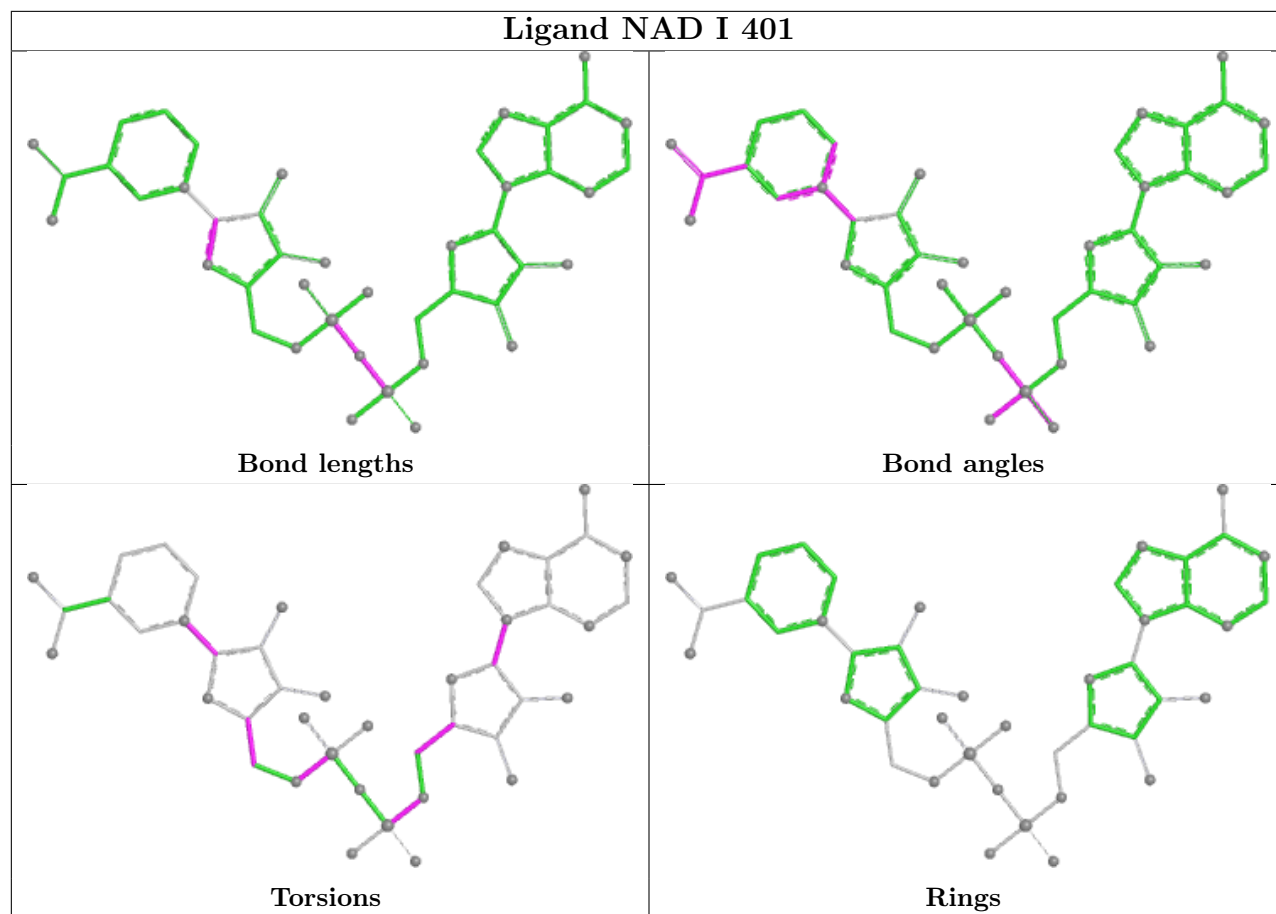


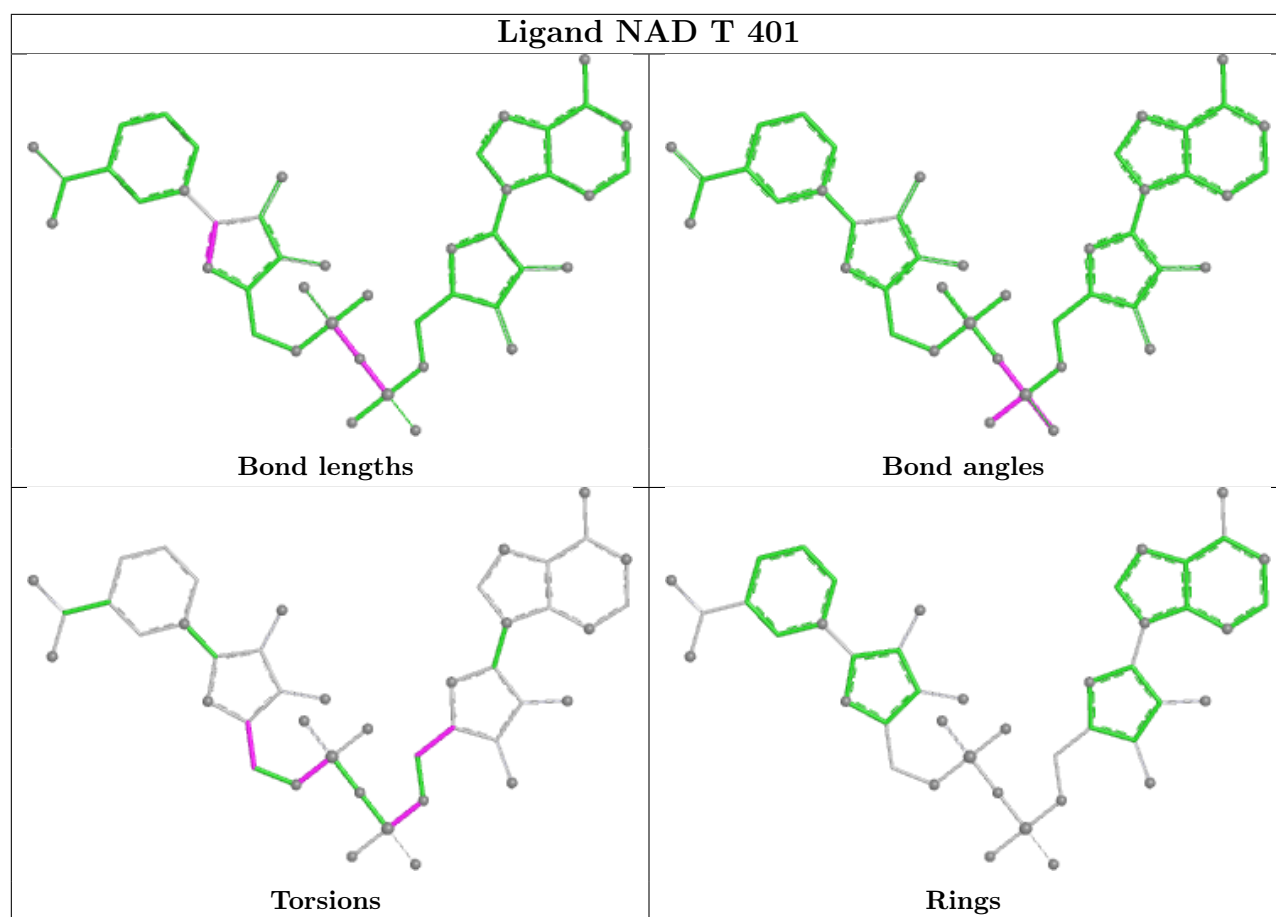


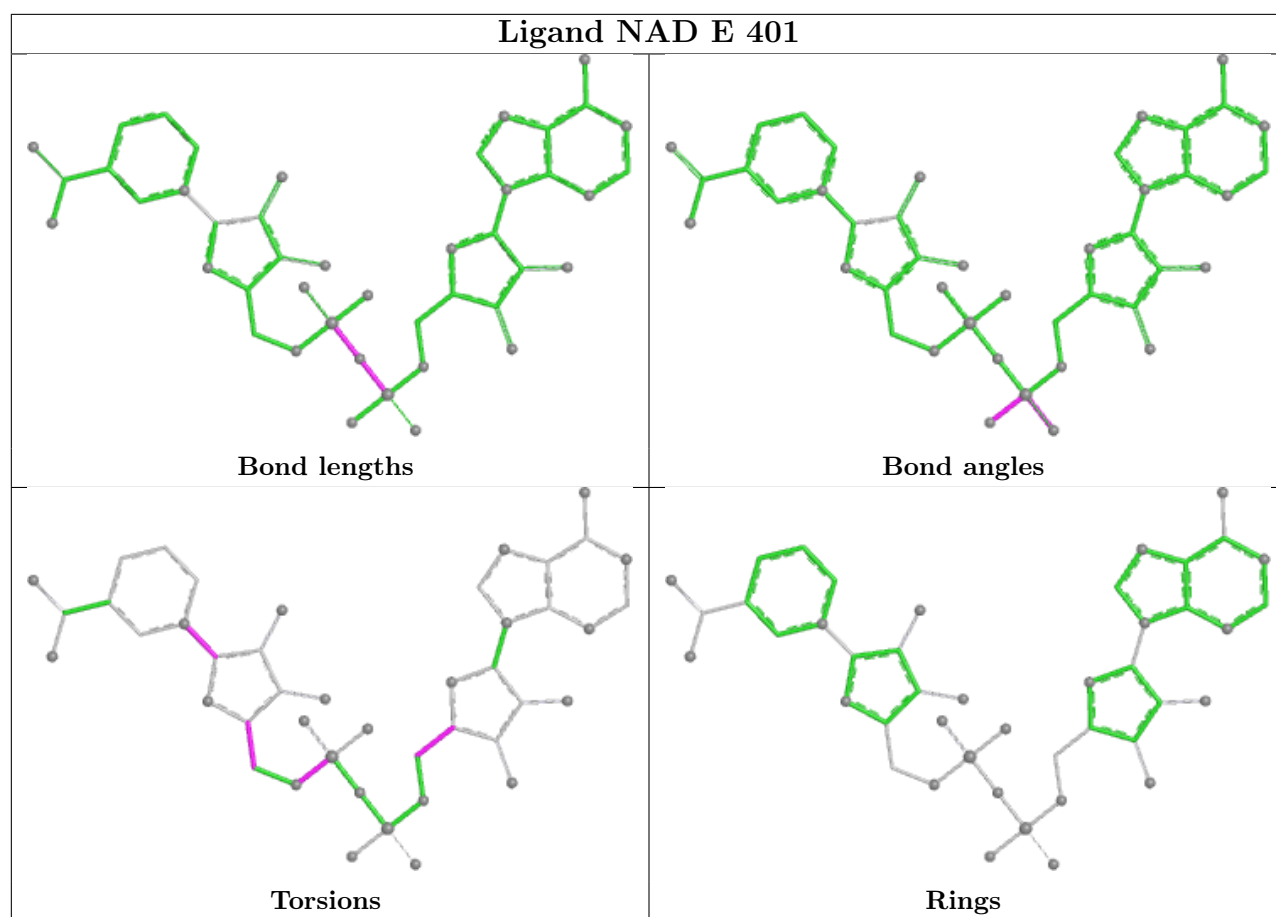


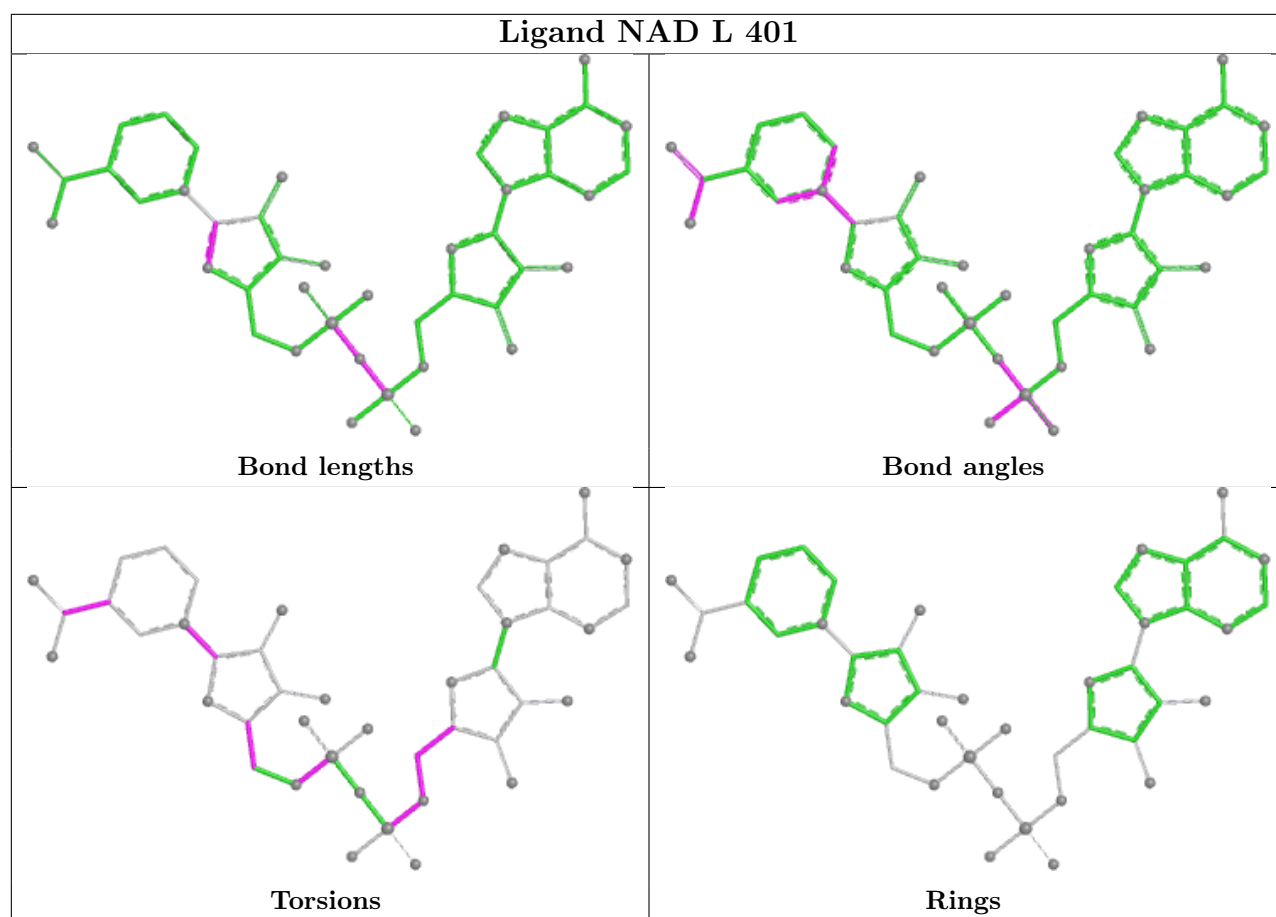


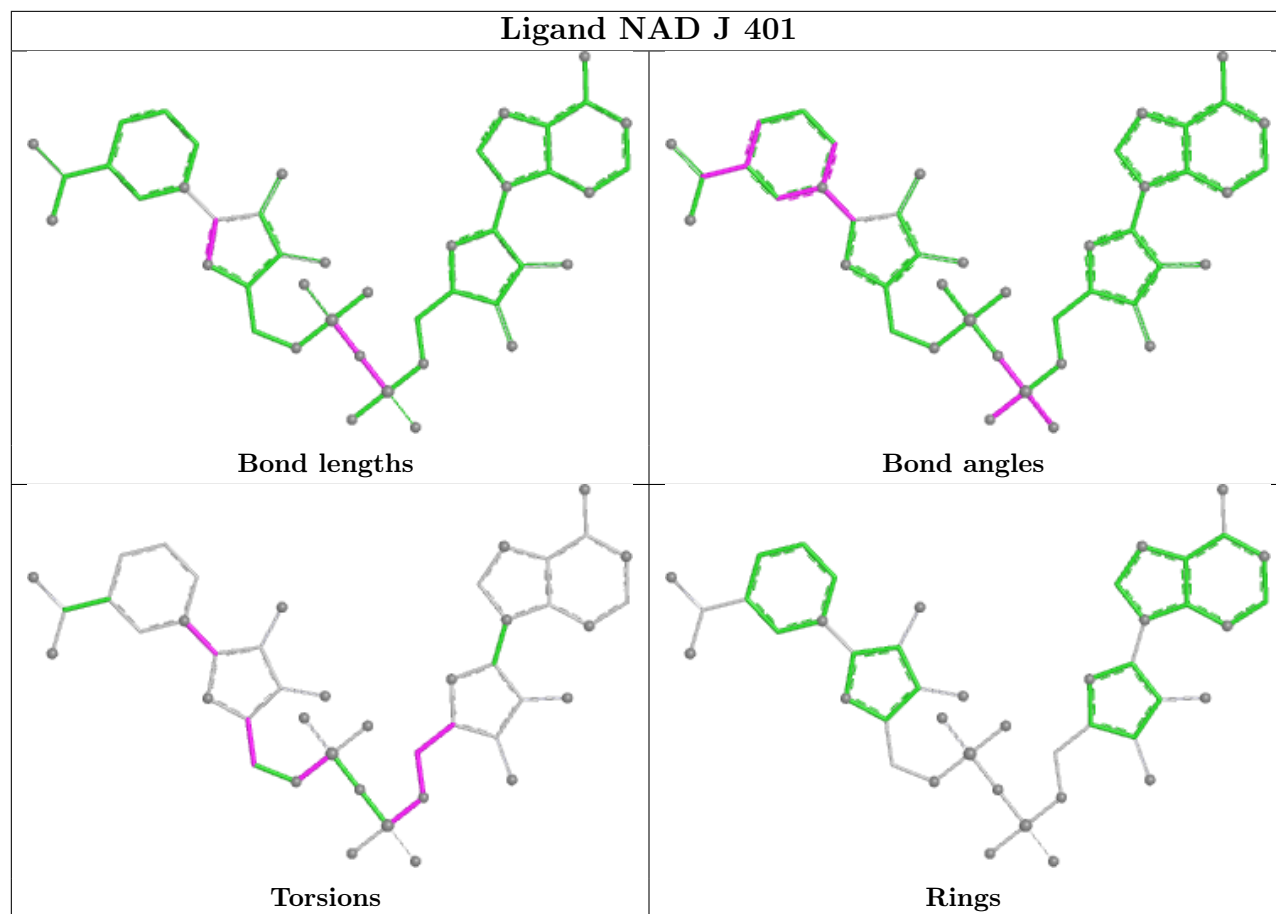


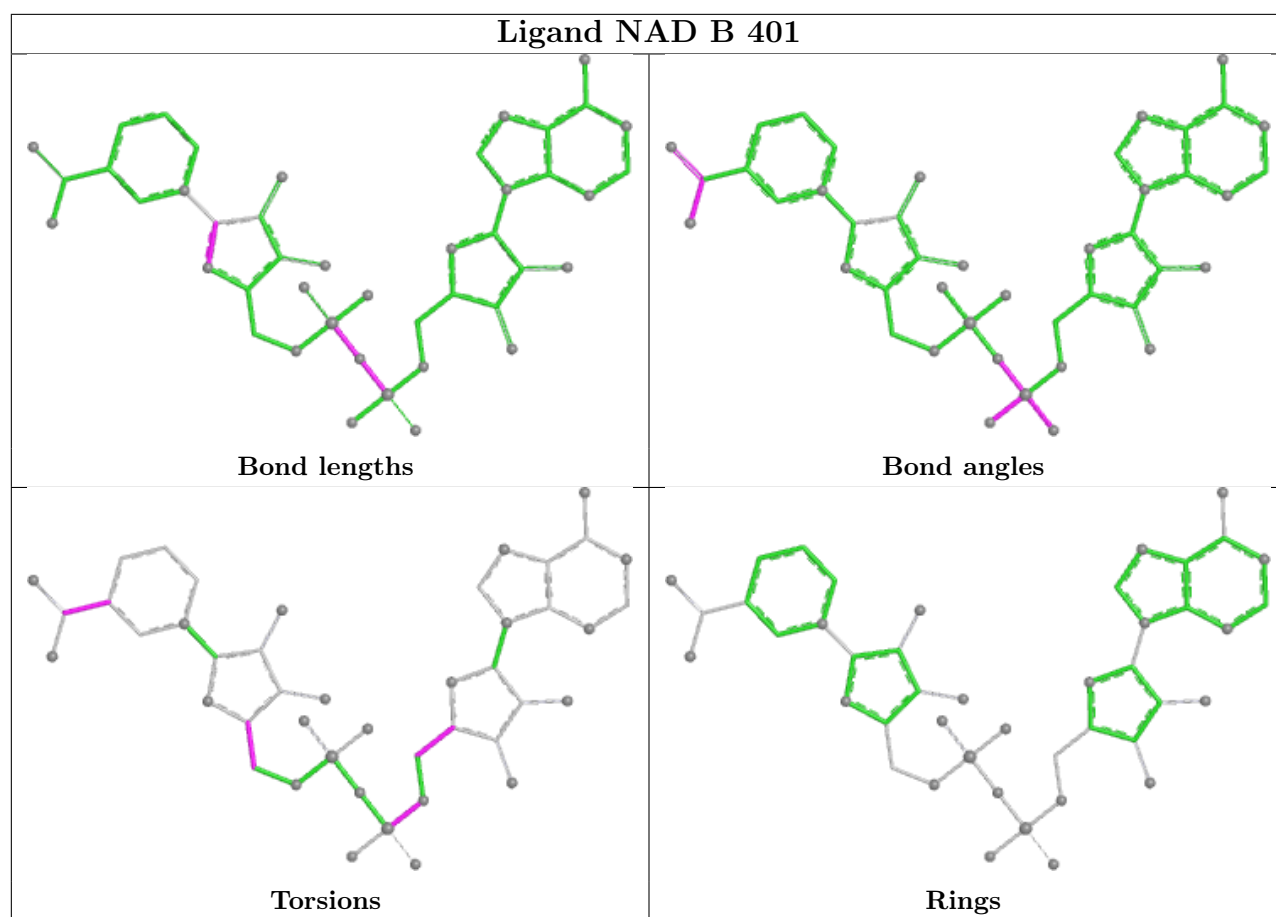


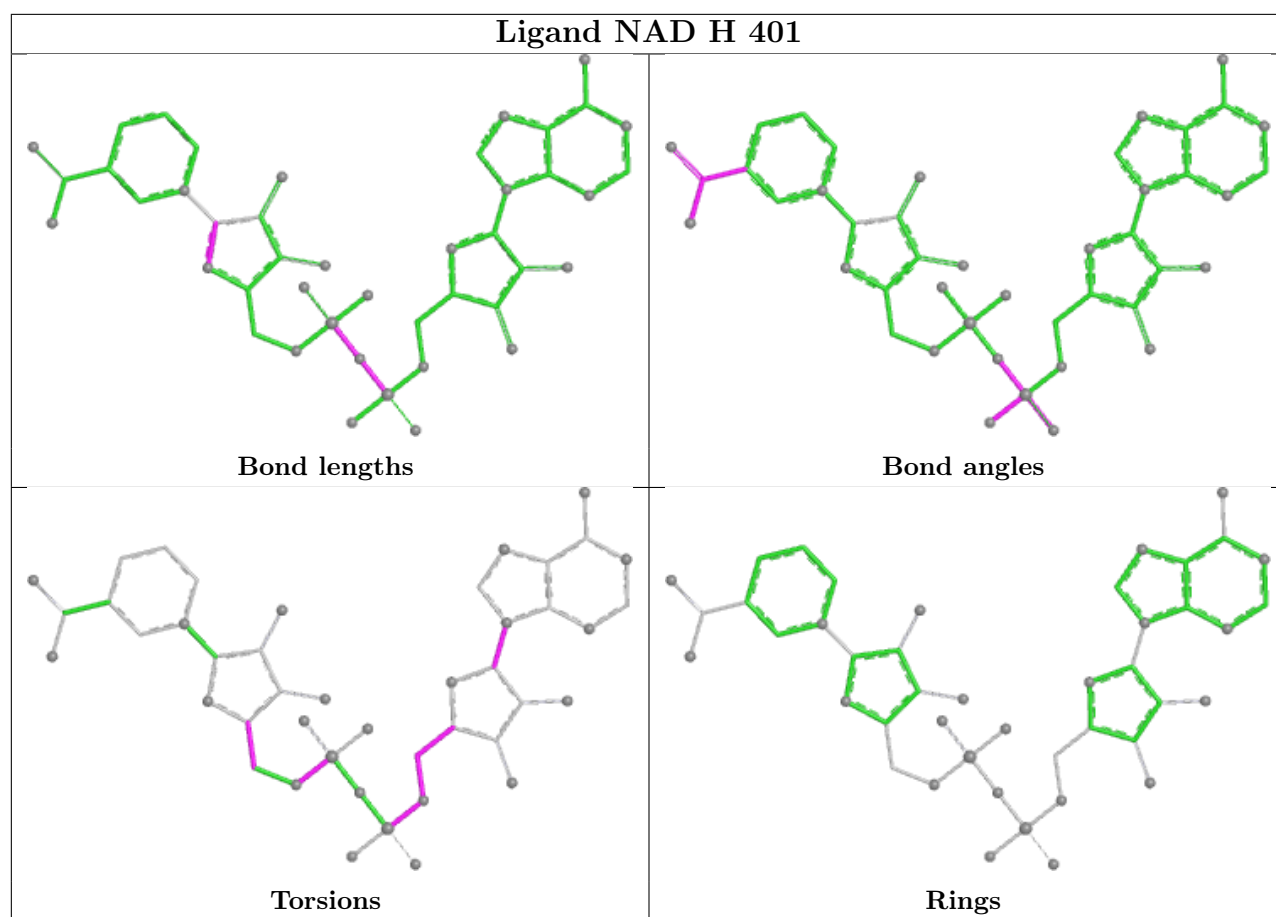


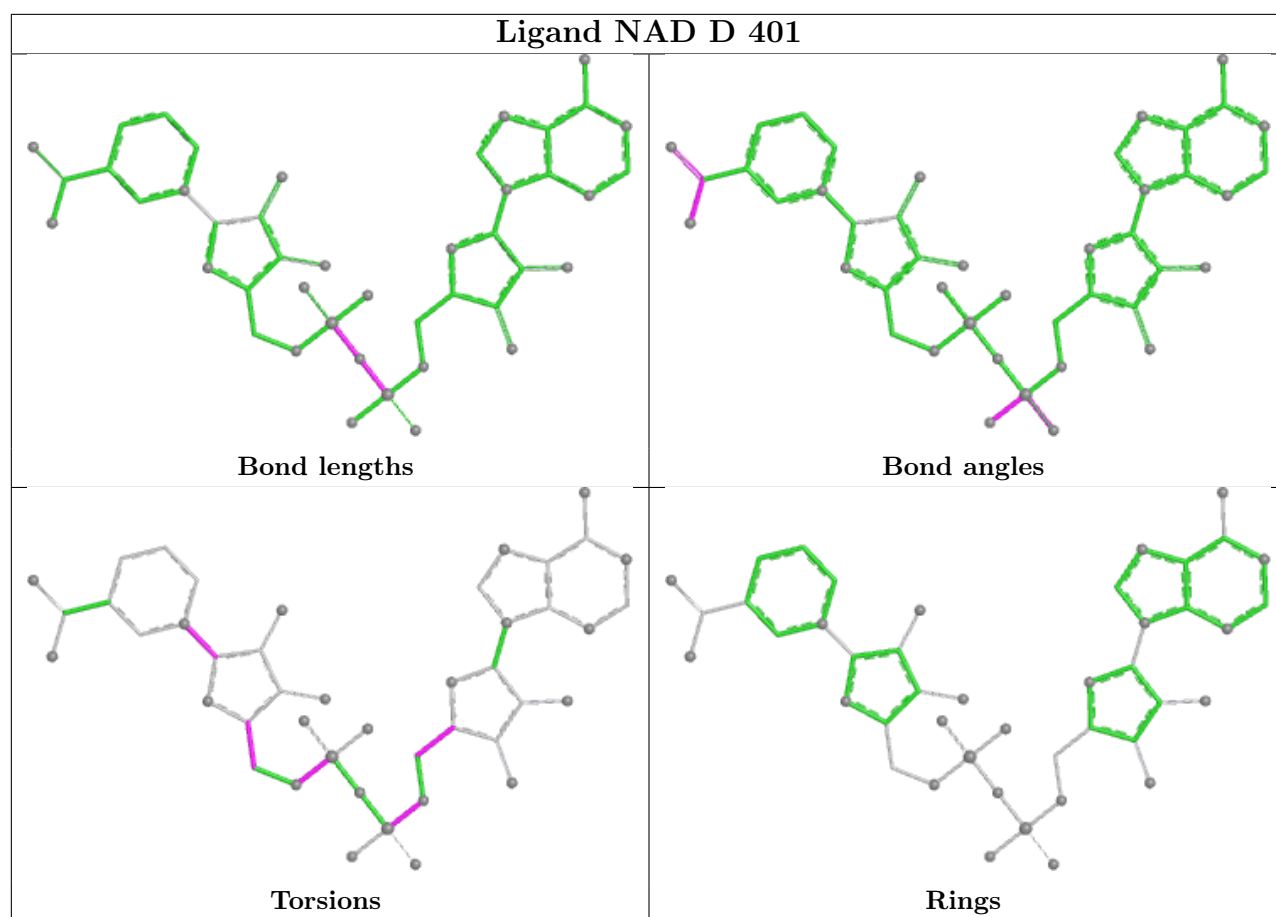












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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, 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	A	333/342 (97%)	-0.55	1 (0%) 90 80	50, 85, 127, 159	0
1	B	334/342 (97%)	-0.57	0 100 100	49, 87, 140, 159	0
1	C	332/342 (97%)	-0.61	0 100 100	50, 75, 109, 132	0
1	D	334/342 (97%)	-0.54	0 100 100	56, 81, 122, 158	0
1	E	334/342 (97%)	-0.61	0 100 100	50, 83, 121, 177	0
1	F	334/342 (97%)	-0.58	0 100 100	59, 90, 128, 167	0
1	G	333/342 (97%)	-0.60	0 100 100	53, 80, 114, 162	0
1	H	333/342 (97%)	-0.42	0 100 100	58, 103, 175, 223	0
1	I	332/342 (97%)	-0.46	0 100 100	66, 101, 151, 186	0
1	J	334/342 (97%)	-0.55	0 100 100	60, 87, 124, 157	0
1	K	333/342 (97%)	-0.48	0 100 100	53, 98, 144, 172	0
1	L	333/342 (97%)	-0.53	0 100 100	59, 102, 160, 190	0
1	M	324/342 (94%)	-0.23	0 100 100	76, 136, 187, 215	0
1	N	333/342 (97%)	-0.43	1 (0%) 90 80	76, 114, 146, 165	0
1	O	329/342 (96%)	-0.33	0 100 100	76, 114, 162, 215	0
1	P	328/342 (95%)	-0.00	2 (0%) 85 70	96, 151, 189, 219	0
1	Q	333/342 (97%)	-0.38	1 (0%) 90 80	92, 126, 163, 205	0
1	R	333/342 (97%)	-0.37	0 100 100	104, 127, 155, 183	0
1	S	333/342 (97%)	-0.40	0 100 100	97, 127, 160, 195	0
1	T	334/342 (97%)	-0.35	2 (0%) 85 70	101, 135, 169, 220	0
All	All	6646/6840 (97%)	-0.45	7 (0%) 92 86	49, 106, 162, 223	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	T	210	SER	3.0
1	Q	244	GLU	2.5
1	A	204	LEU	2.3
1	P	133	GLY	2.2
1	N	62	ASP	2.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

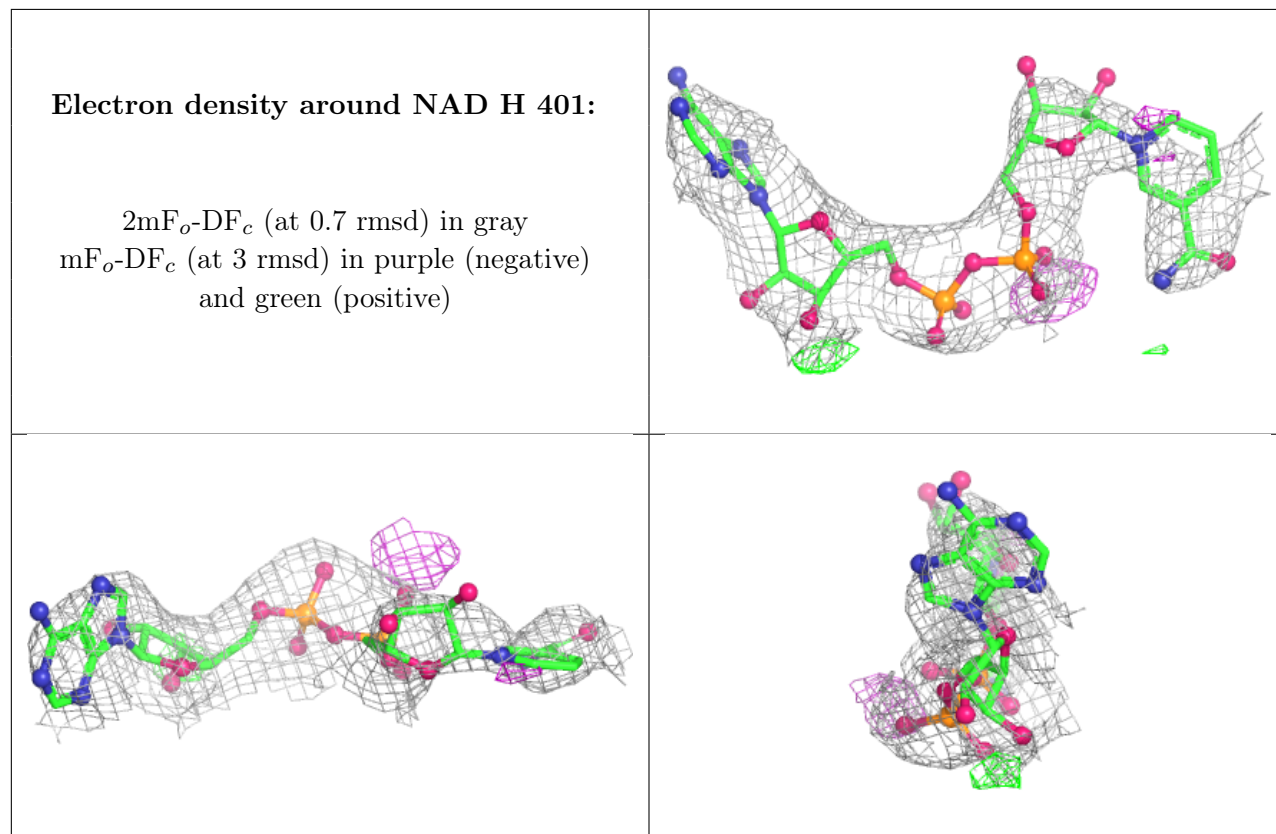
6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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($\text{\AA}^2$)	Q<0.9
2	NAD	H	401	44/44	0.85	0.11	83,120,137,141	44
2	NAD	L	401	44/44	0.90	0.08	90,115,136,144	0
3	NA	A	402	1/1	0.90	0.06	103,103,103,103	0
3	NA	O	401	1/1	0.90	0.08	76,76,76,76	0
2	NAD	I	401	44/44	0.92	0.07	88,111,125,134	0
2	NAD	T	401	44/44	0.92	0.07	92,121,131,135	0
2	NAD	Q	401	44/44	0.93	0.07	109,123,129,134	0
3	NA	C	401	1/1	0.93	0.09	73,73,73,73	0
2	NAD	N	401	44/44	0.93	0.07	81,111,119,126	0
2	NAD	K	401	44/44	0.94	0.08	80,99,110,115	0
2	NAD	D	401	44/44	0.94	0.07	65,88,110,118	0
2	NAD	F	401	44/44	0.95	0.07	66,87,102,108	0
2	NAD	B	401	44/44	0.95	0.07	67,87,97,107	0
2	NAD	E	401	44/44	0.95	0.07	69,80,90,98	0
2	NAD	J	401	44/44	0.95	0.07	66,85,99,101	0
2	NAD	A	401	44/44	0.96	0.06	58,74,88,92	0
3	NA	G	401	1/1	0.97	0.12	76,76,76,76	0

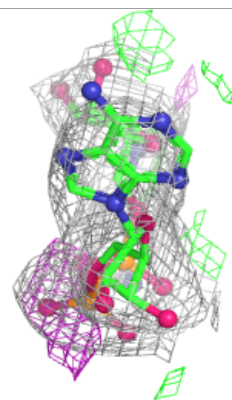
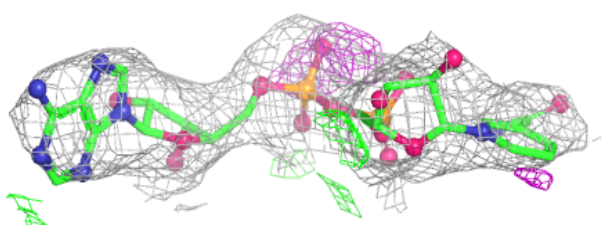
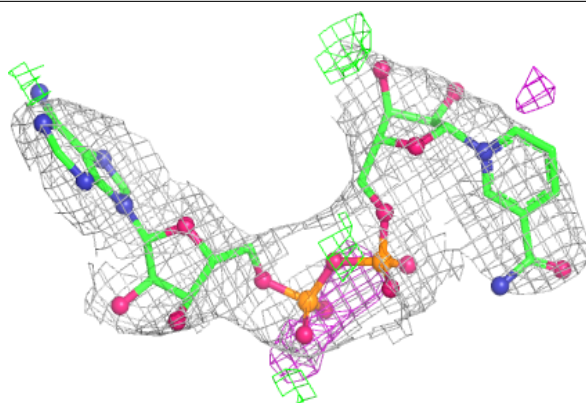
The following is a graphical depiction of the model fit to experimental electron density of all

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.

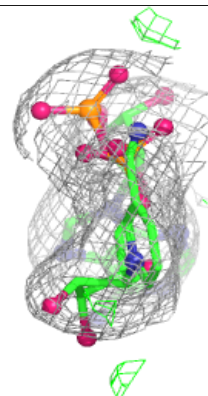
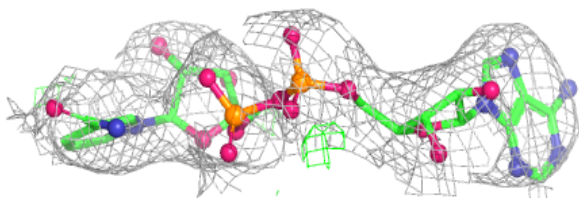
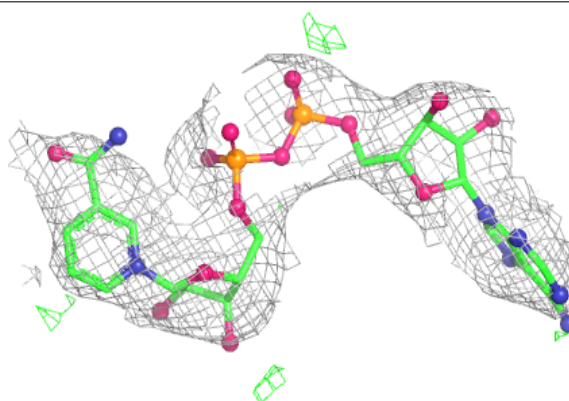


Electron density around NAD L 401:

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

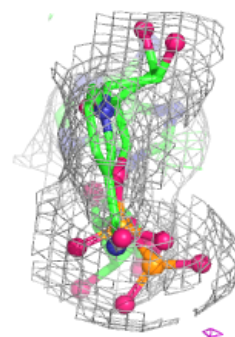
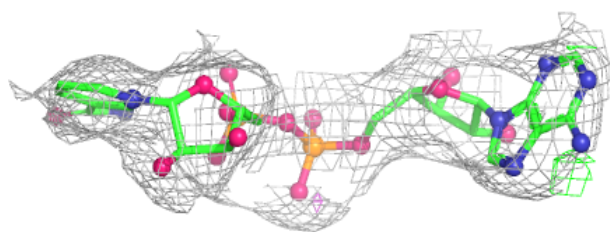
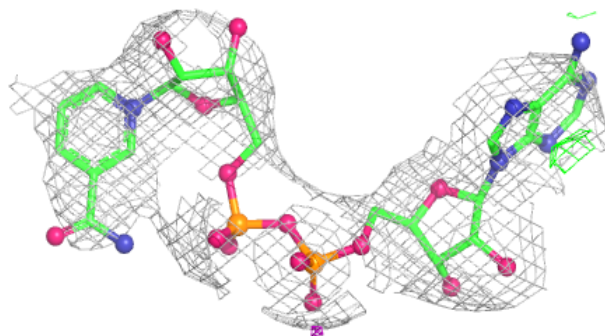
**Electron density around NAD I 401:**

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

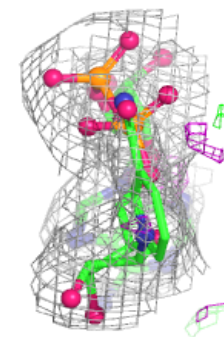
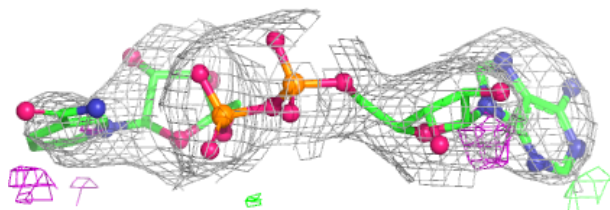
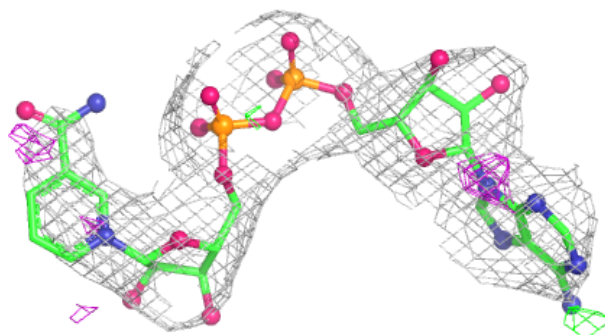


Electron density around NAD T 401:

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

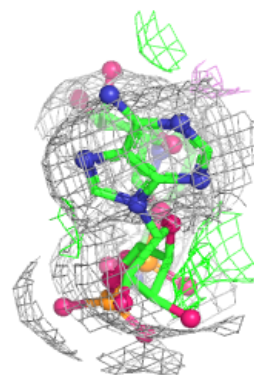
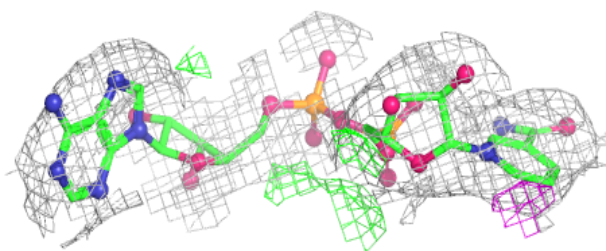
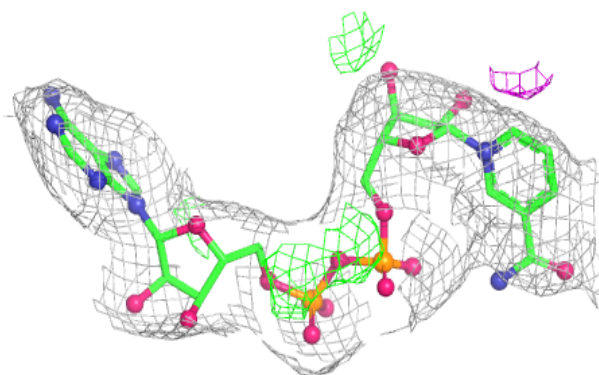
**Electron density around NAD Q 401:**

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

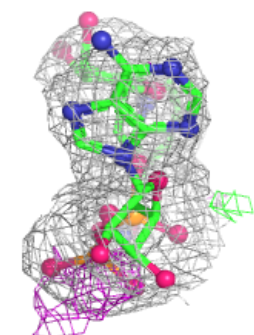
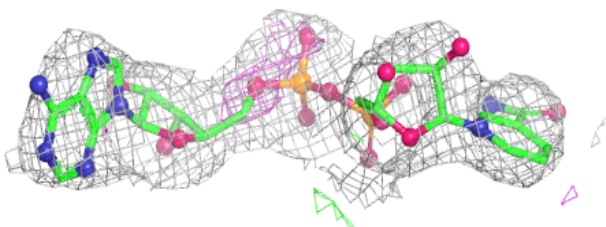
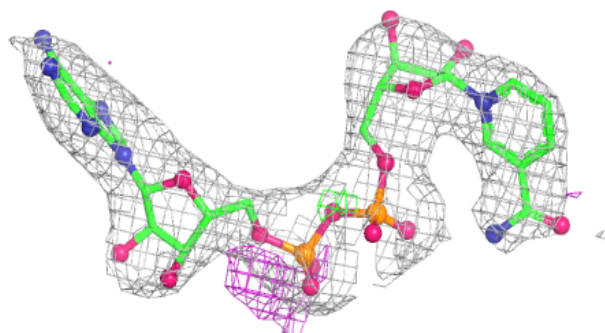


Electron density around NAD N 401:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

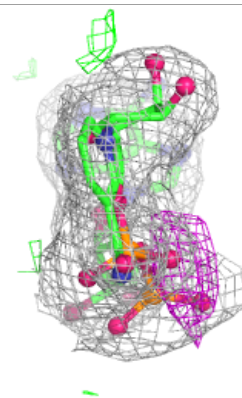
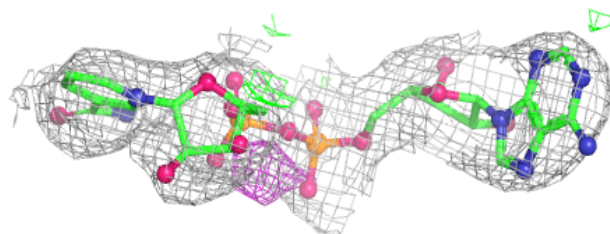
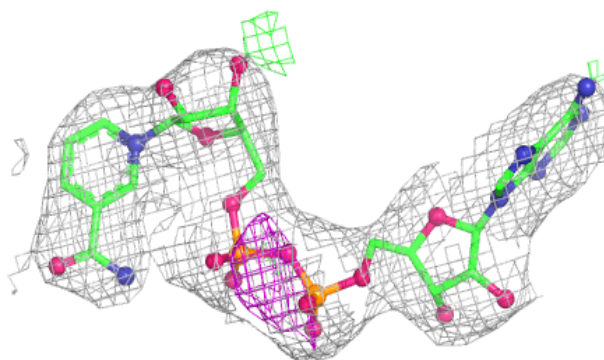
**Electron density around NAD K 401:**

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

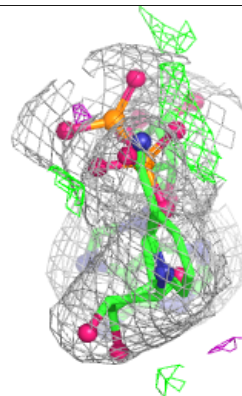
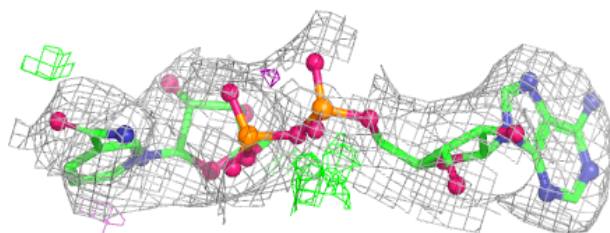
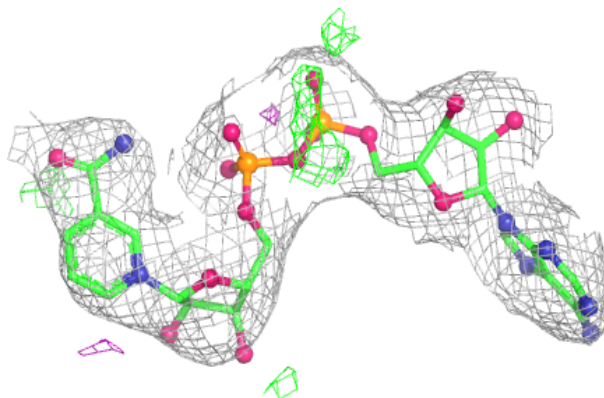


Electron density around NAD D 401:

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

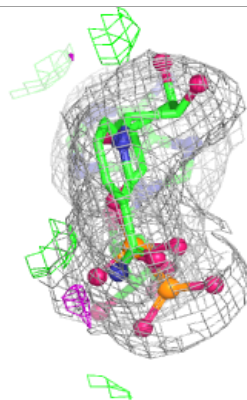
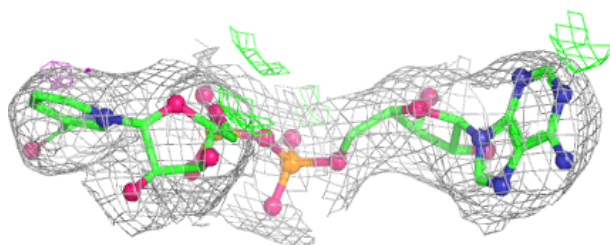
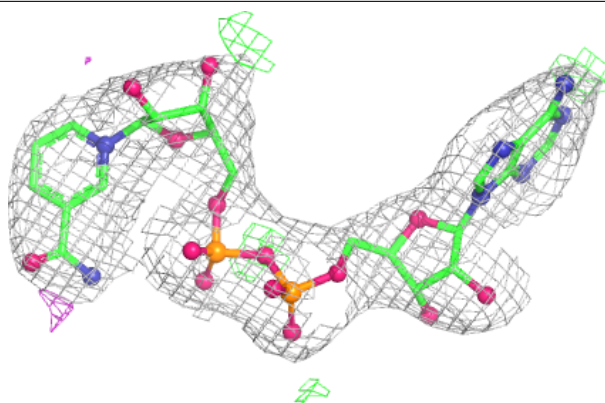
**Electron density around NAD F 401:**

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

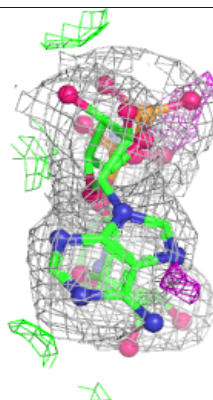
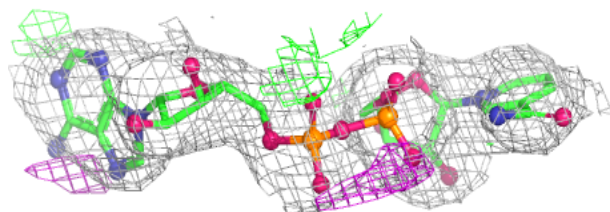
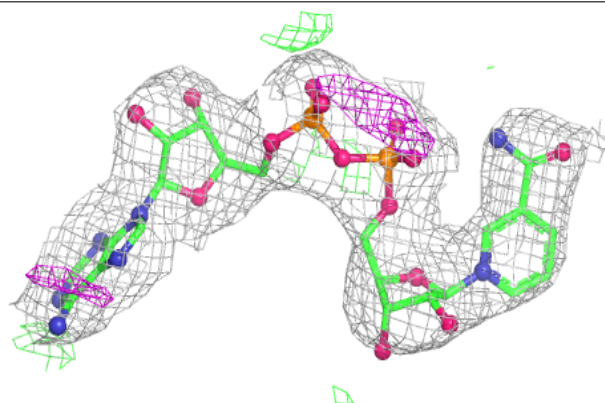


Electron density around NAD B 401:

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

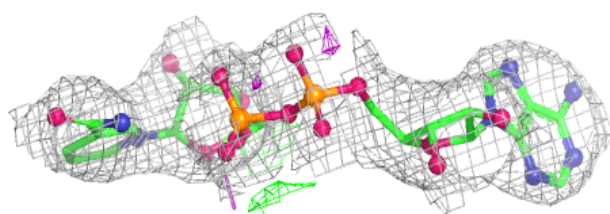
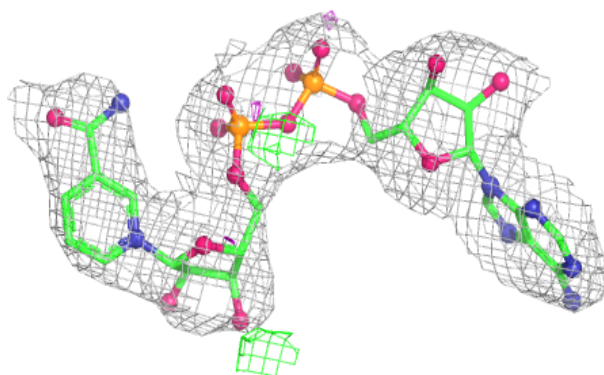
**Electron density around NAD E 401:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

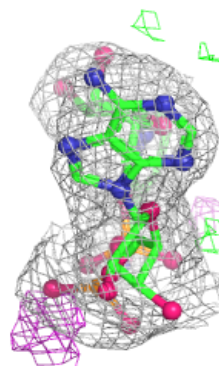
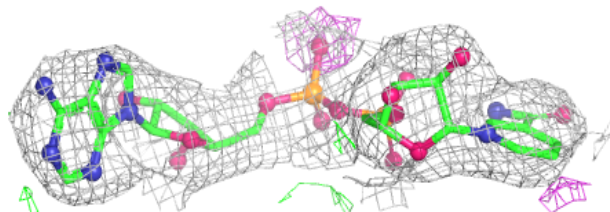
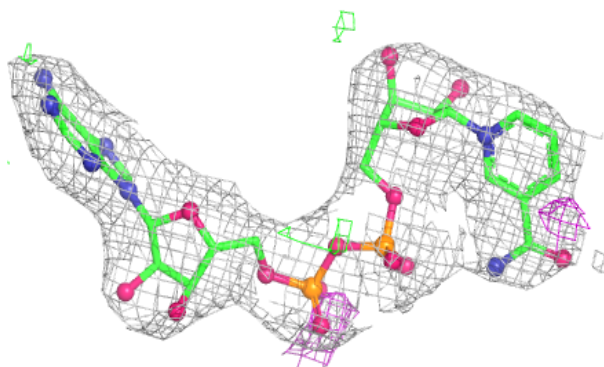


Electron density around NAD J 401:

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

**Electron density around NAD A 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.