



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 03:28 PM EDT

PDB ID : 6O4E / pdb\_00006o4e  
Title : Structure of ALDH7A1 mutant N167S complexed with NAD  
Authors : Tanner, J.J.; Korasick, D.A.; Laciak, A.R.  
Deposited on : 2019-02-28  
Resolution : 1.75 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
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

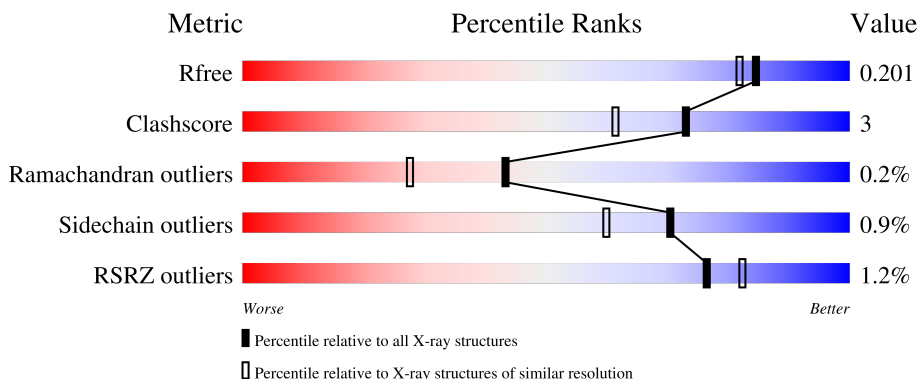
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 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.



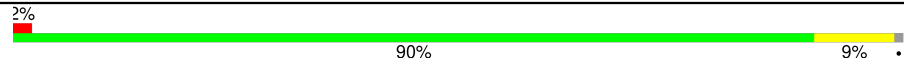
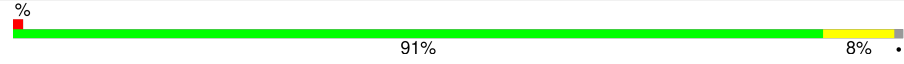
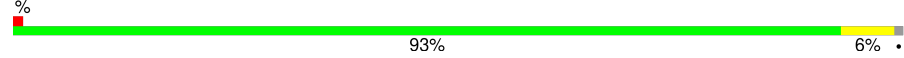
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	513	
1	B	513	
1	C	513	
1	D	513	
1	E	513	

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Mol	Chain	Length	Quality of chain
1	F	513	 2% 90% 9%
1	G	513	 % 91% 8%
1	H	513	 % 93% 6%

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 33404 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 Alpha-aminoadipic semialdehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	508	3858	2456	665	719	18	0	3	0
1	B	508	3867	2460	671	719	17	0	3	0
1	C	508	3857	2455	666	718	18	0	3	0
1	D	509	3868	2459	673	718	18	0	3	0
1	E	508	3850	2451	663	718	18	0	3	0
1	F	509	3853	2449	666	721	17	0	0	0
1	G	508	3849	2445	668	719	17	0	0	0
1	H	509	3875	2469	668	720	18	0	4	0

There are 24 discrepancies between the modelled and reference sequences:

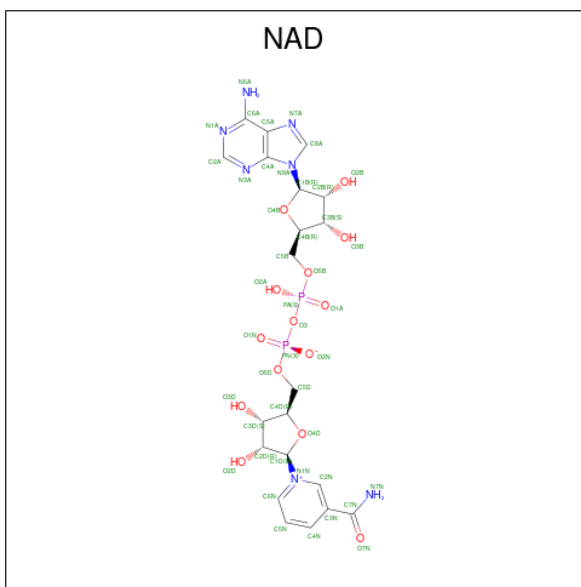
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P49419
A	0	HIS	-	expression tag	UNP P49419
A	167	SER	ASN	engineered mutation	UNP P49419
B	-1	GLY	-	expression tag	UNP P49419
B	0	HIS	-	expression tag	UNP P49419
B	167	SER	ASN	engineered mutation	UNP P49419
C	-1	GLY	-	expression tag	UNP P49419
C	0	HIS	-	expression tag	UNP P49419
C	167	SER	ASN	engineered mutation	UNP P49419
D	-1	GLY	-	expression tag	UNP P49419
D	0	HIS	-	expression tag	UNP P49419
D	167	SER	ASN	engineered mutation	UNP P49419
E	-1	GLY	-	expression tag	UNP P49419

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Chain	Residue	Modelled	Actual	Comment	Reference
E	0	HIS	-	expression tag	UNP P49419
E	167	SER	ASN	engineered mutation	UNP P49419
F	-1	GLY	-	expression tag	UNP P49419
F	0	HIS	-	expression tag	UNP P49419
F	167	SER	ASN	engineered mutation	UNP P49419
G	-1	GLY	-	expression tag	UNP P49419
G	0	HIS	-	expression tag	UNP P49419
G	167	SER	ASN	engineered mutation	UNP P49419
H	-1	GLY	-	expression tag	UNP P49419
H	0	HIS	-	expression tag	UNP P49419
H	167	SER	ASN	engineered mutation	UNP P49419

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula:  $C_{21}H_{27}N_7O_{14}P_2$ ) (labeled as "Ligand of Interest" by depositor).



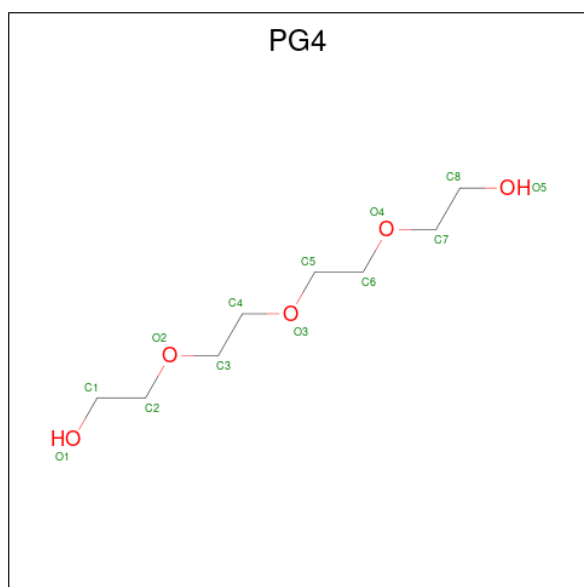
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
			Total	C	N	O			P	
2	A	1	Total	44	21	7	14	2	0	0
2	B	1	Total	44	21	7	14	2	0	0
2	C	1	Total	44	21	7	14	2	0	0
2	D	1	Total	44	21	7	14	2	0	0
2	E	1	Total	44	21	7	14	2	0	0

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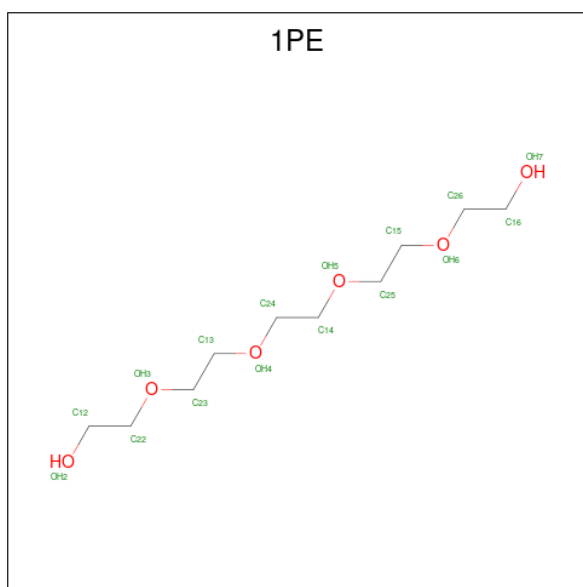
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	Total	C	O	0	0
			13	8	5		
3	D	1	Total	C	O	0	0
			13	8	5		
3	E	1	Total	C	O	0	0
			13	8	5		

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: C<sub>10</sub>H<sub>22</sub>O<sub>6</sub>).

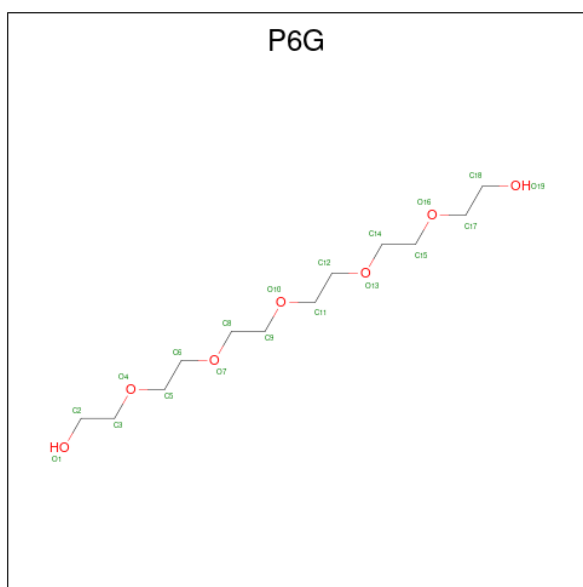


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	C O	0	0
			16	10 6		
4	C	1	Total	C O	0	0
			16	10 6		
4	G	1	Total	C O	0	0
			13	8 5		
4	H	1	Total	C O	0	0
			16	10 6		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		
5	D	1	Total	Mg	0	0
			1	1		
5	F	1	Total	Mg	0	0
			1	1		
5	G	1	Total	Mg	0	0
			1	1		
5	H	1	Total	Mg	0	0
			1	1		

- Molecule 6 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: C<sub>12</sub>H<sub>26</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	C O	0	0
			19	12 7		

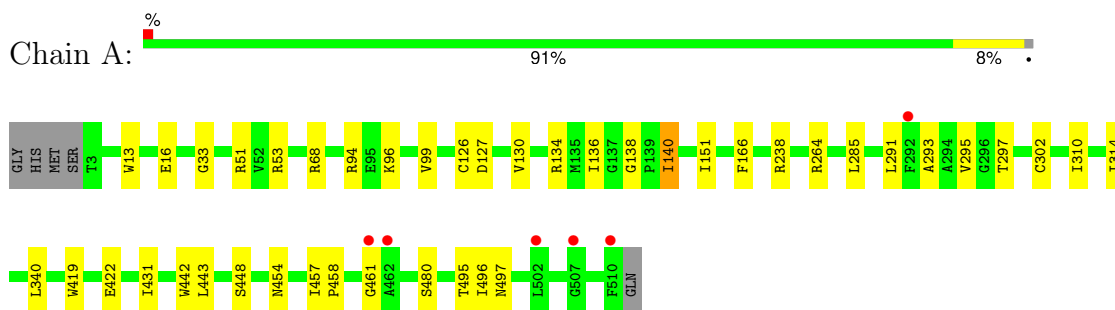
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	255	Total	O	0	0
			255	255		
7	B	252	Total	O	0	1
			253	253		
7	C	257	Total	O	0	0
			257	257		
7	D	228	Total	O	0	2
			230	230		
7	E	248	Total	O	0	0
			248	248		
7	F	247	Total	O	0	0
			247	247		
7	G	275	Total	O	0	0
			275	275		
7	H	284	Total	O	0	1
			285	285		

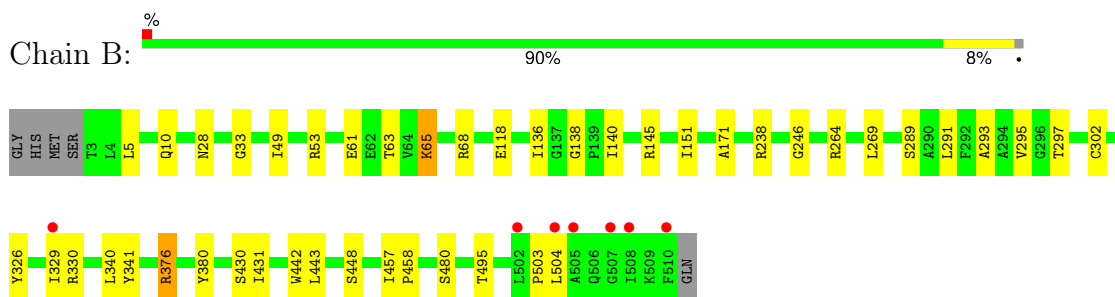
### 3 Residue-property plots [i](#)

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.

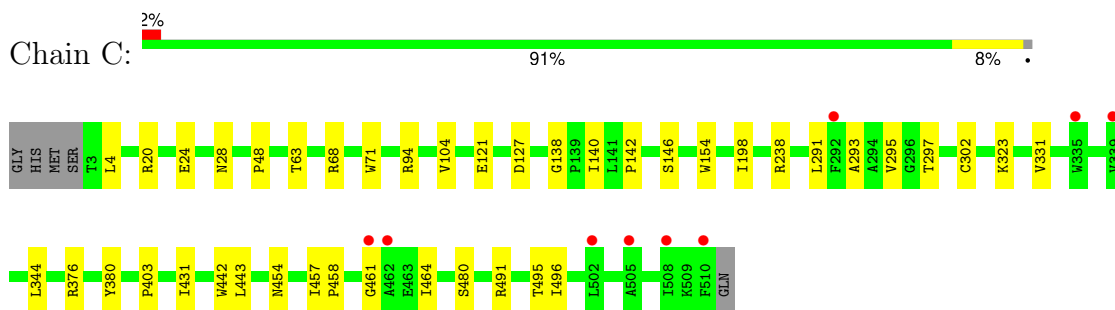
- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase



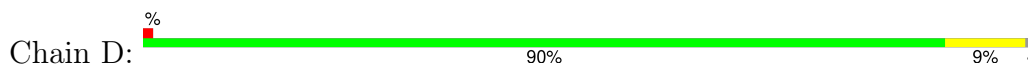
- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase

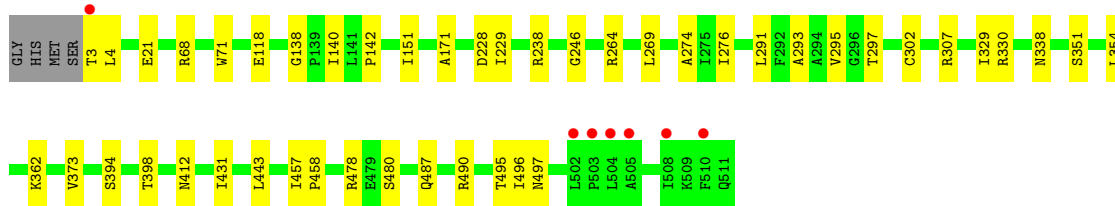


- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase



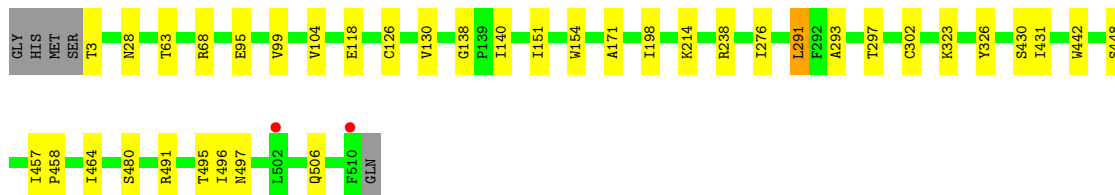
- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase





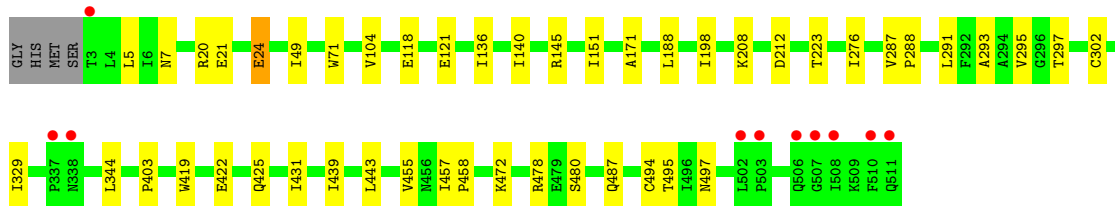
- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase

Chain E: 92% 7%



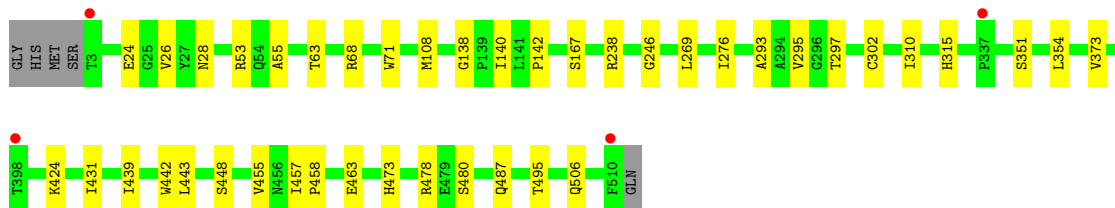
- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase

Chain F: 2% 90% 9%



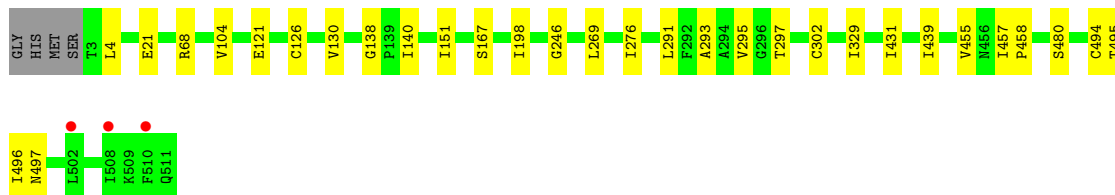
- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase

Chain G: 91% 8%



- Molecule 1: Alpha-aminoadipic semialdehyde dehydrogenase

Chain H: 93% 6%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	154.92Å 161.73Å 158.41Å 90.00° 94.65° 90.00°	Depositor
Resolution (Å)	53.09 – 1.75 53.09 – 1.75	Depositor EDS
% Data completeness (in resolution range)	90.0 (53.09-1.75) 94.1 (53.09-1.75)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.32 (at 1.75Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.168 , 0.202 0.166 , 0.201	Depositor DCC
$R_{free}$ test set	18372 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.4	Xtrriage
Anisotropy	0.424	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 36.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	33404	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.39% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: PG4, NAD, 1PE, P6G, MG

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	0.27	0/3946	0.46	0/5355
1	B	0.26	0/3955	0.46	0/5366
1	C	0.26	0/3945	0.48	0/5355
1	D	0.25	0/3956	0.45	0/5367
1	E	0.27	0/3938	0.48	0/5345
1	F	0.26	0/3932	0.47	0/5336
1	G	0.27	0/3928	0.46	0/5331
1	H	0.27	0/3966	0.47	0/5381
All	All	0.26	0/31566	0.47	0/42836

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 [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	3858	0	3846	32	0
1	B	3867	0	3871	33	0
1	C	3857	0	3846	30	0
1	D	3868	0	3864	31	0
1	E	3850	0	3839	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3853	0	3835	33	0
1	G	3849	0	3833	29	0
1	H	3875	0	3882	25	0
2	A	44	0	24	1	0
2	B	44	0	24	2	0
2	C	44	0	25	1	0
2	D	44	0	24	1	0
2	E	44	0	24	1	0
2	F	44	0	24	1	0
2	G	44	0	24	1	0
2	H	44	0	25	2	0
3	A	13	0	18	1	0
3	D	13	0	18	2	0
3	E	13	0	18	2	0
4	B	16	0	22	0	0
4	C	16	0	22	1	0
4	G	13	0	17	3	0
4	H	16	0	22	4	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
6	F	19	0	26	1	0
7	A	255	0	0	2	0
7	B	253	0	0	3	0
7	C	257	0	0	0	0
7	D	230	0	0	2	0
7	E	248	0	0	2	0
7	F	247	0	0	1	0
7	G	275	0	0	0	0
7	H	285	0	0	0	0
All	All	33404	0	31173	201	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 201 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:F:291:LEU:HD11	1:F:329:ILE:HD11	1.66	0.78
1:A:461:GLY:O	1:B:145:ARG:NH1	2.24	0.70
1:D:291:LEU:HD11	1:D:329:ILE:HD11	1.72	0.69
1:D:4:LEU:HD12	1:D:21:GLU:HG2	1.78	0.66
1:A:140[A]:ILE:HG22	1:A:151:ILE:HG12	1.76	0.65

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	509/513 (99%)	495 (97%)	13 (3%)	1 (0%)	43	27
1	B	509/513 (99%)	494 (97%)	14 (3%)	1 (0%)	43	27
1	C	509/513 (99%)	493 (97%)	15 (3%)	1 (0%)	43	27
1	D	510/513 (99%)	495 (97%)	14 (3%)	1 (0%)	43	27
1	E	509/513 (99%)	493 (97%)	15 (3%)	1 (0%)	43	27
1	F	507/513 (99%)	491 (97%)	15 (3%)	1 (0%)	43	27
1	G	506/513 (99%)	493 (97%)	12 (2%)	1 (0%)	43	27
1	H	511/513 (100%)	494 (97%)	16 (3%)	1 (0%)	43	27
All	All	4070/4104 (99%)	3948 (97%)	114 (3%)	8 (0%)	43	27

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	480	SER
1	B	480	SER
1	C	480	SER
1	D	480	SER
1	E	480	SER

### 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	400/410 (98%)	396 (99%)	4 (1%)	68	56
1	B	403/410 (98%)	397 (98%)	6 (2%)	57	41
1	C	400/410 (98%)	394 (98%)	6 (2%)	57	41
1	D	402/410 (98%)	399 (99%)	3 (1%)	76	67
1	E	400/410 (98%)	394 (98%)	6 (2%)	57	41
1	F	400/410 (98%)	398 (100%)	2 (0%)	81	75
1	G	400/410 (98%)	396 (99%)	4 (1%)	68	56
1	H	404/410 (98%)	403 (100%)	1 (0%)	87	84
All	All	3209/3280 (98%)	3177 (99%)	32 (1%)	70	56

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	297	THR
1	G	351	SER
1	C	146	SER
1	C	121[B]	GLU
1	G	463	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	155	ASN
1	H	155	ASN
1	F	177	ASN
1	G	338	ASN
1	F	155	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 6 are monoatomic - leaving 16 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
6	P6G	F	602	-	18,18,18	0.55	0	17,17,17	0.40	0
4	1PE	G	602	-	12,12,15	0.55	0	11,11,14	0.33	0
3	PG4	D	602	-	12,12,12	0.64	0	11,11,11	0.30	0
3	PG4	A	602	-	12,12,12	0.65	0	11,11,11	0.44	0
2	NAD	B	601	5	46,48,48	3.61	14 (30%)	64,73,73	1.77	12 (18%)
2	NAD	H	601	5	46,48,48	3.56	15 (32%)	64,73,73	1.70	12 (18%)
2	NAD	F	601	5	46,48,48	3.55	17 (36%)	64,73,73	1.75	12 (18%)
2	NAD	D	601	5	46,48,48	3.64	16 (34%)	64,73,73	1.68	11 (17%)
2	NAD	G	601	5	46,48,48	3.55	15 (32%)	64,73,73	1.64	10 (15%)
4	1PE	H	602	-	15,15,15	0.54	0	14,14,14	0.44	0
2	NAD	A	601	-	46,48,48	3.58	15 (32%)	64,73,73	1.68	12 (18%)
4	1PE	C	602	-	15,15,15	0.52	0	14,14,14	0.24	0
3	PG4	E	602	-	12,12,12	0.68	0	11,11,11	0.35	0
2	NAD	C	601	5	46,48,48	3.59	15 (32%)	64,73,73	1.73	13 (20%)
4	1PE	B	602	-	15,15,15	0.55	0	14,14,14	0.41	0
2	NAD	E	601	-	46,48,48	3.59	16 (34%)	64,73,73	1.71	12 (18%)

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
6	P6G	F	602	-	-	4/16/16/16	-
4	1PE	G	602	-	-	5/10/10/13	-
3	PG4	D	602	-	-	6/10/10/10	-
3	PG4	A	602	-	-	6/10/10/10	-
2	NAD	B	601	5	-	6/30/62/62	0/5/5/5
2	NAD	H	601	5	-	6/30/62/62	0/5/5/5
2	NAD	F	601	5	-	6/30/62/62	0/5/5/5
2	NAD	D	601	5	-	6/30/62/62	0/5/5/5
2	NAD	G	601	5	-	6/30/62/62	0/5/5/5
4	1PE	H	602	-	-	6/13/13/13	-
2	NAD	A	601	-	-	6/30/62/62	0/5/5/5
4	1PE	C	602	-	-	2/13/13/13	-
3	PG4	E	602	-	-	5/10/10/10	-
2	NAD	C	601	5	-	6/30/62/62	0/5/5/5
4	1PE	B	602	-	-	4/13/13/13	-
2	NAD	E	601	-	-	6/30/62/62	0/5/5/5

The worst 5 of 123 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	NAD	O4D-C1D	15.93	1.61	1.40
2	D	601	NAD	O4D-C1D	15.83	1.61	1.40
2	B	601	NAD	O4D-C1D	15.79	1.61	1.40
2	A	601	NAD	O4D-C1D	15.61	1.61	1.40
2	E	601	NAD	O4D-C1D	15.58	1.61	1.40

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	601	NAD	N3A-C2A-N1A	-6.03	119.46	128.58
2	C	601	NAD	N3A-C2A-N1A	-5.97	119.55	128.58
2	D	601	NAD	N3A-C2A-N1A	-5.85	119.72	128.58
2	F	601	NAD	N3A-C2A-N1A	-5.58	120.14	128.58
2	H	601	NAD	N3A-C2A-N1A	-5.54	120.19	128.58

There are no chirality outliers.

5 of 86 torsion outliers are listed below:

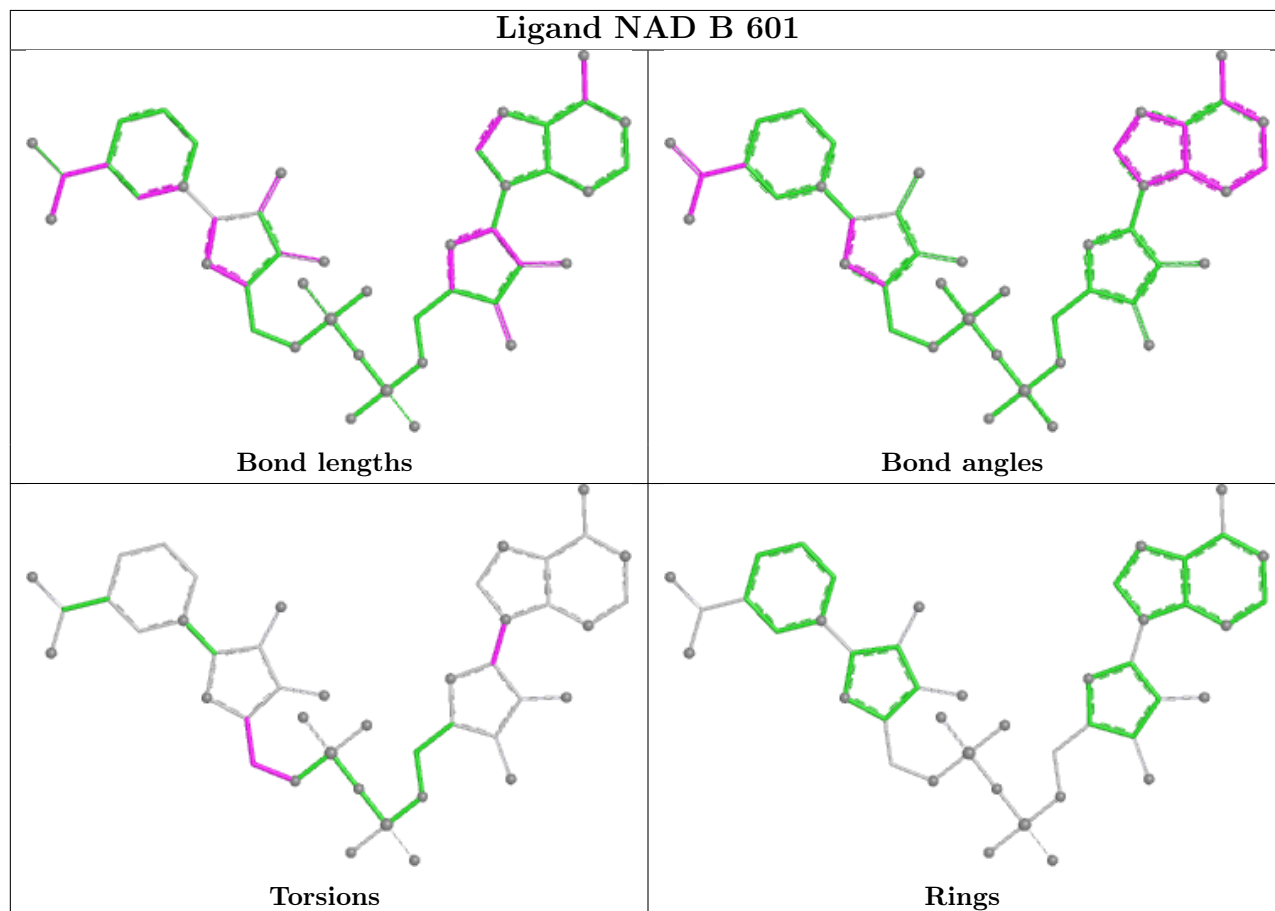
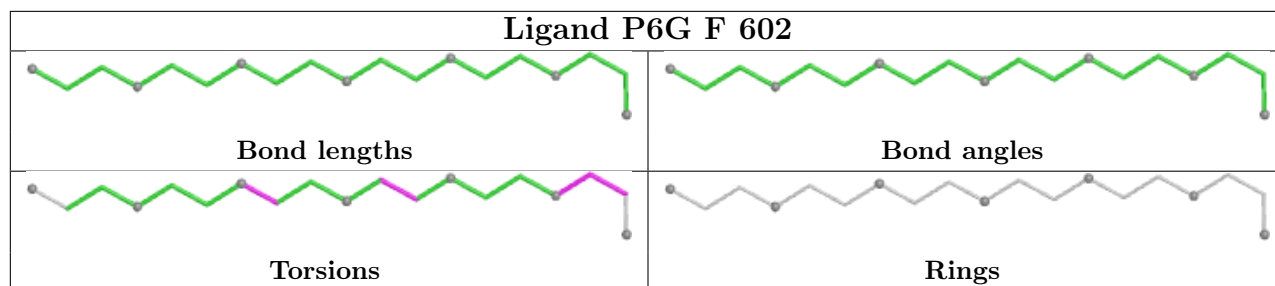
Mol	Chain	Res	Type	Atoms
2	G	601	NAD	C3D-C4D-C5D-O5D
3	A	602	PG4	O2-C3-C4-O3
2	B	601	NAD	O4D-C4D-C5D-O5D
2	B	601	NAD	C3D-C4D-C5D-O5D
2	C	601	NAD	C3D-C4D-C5D-O5D

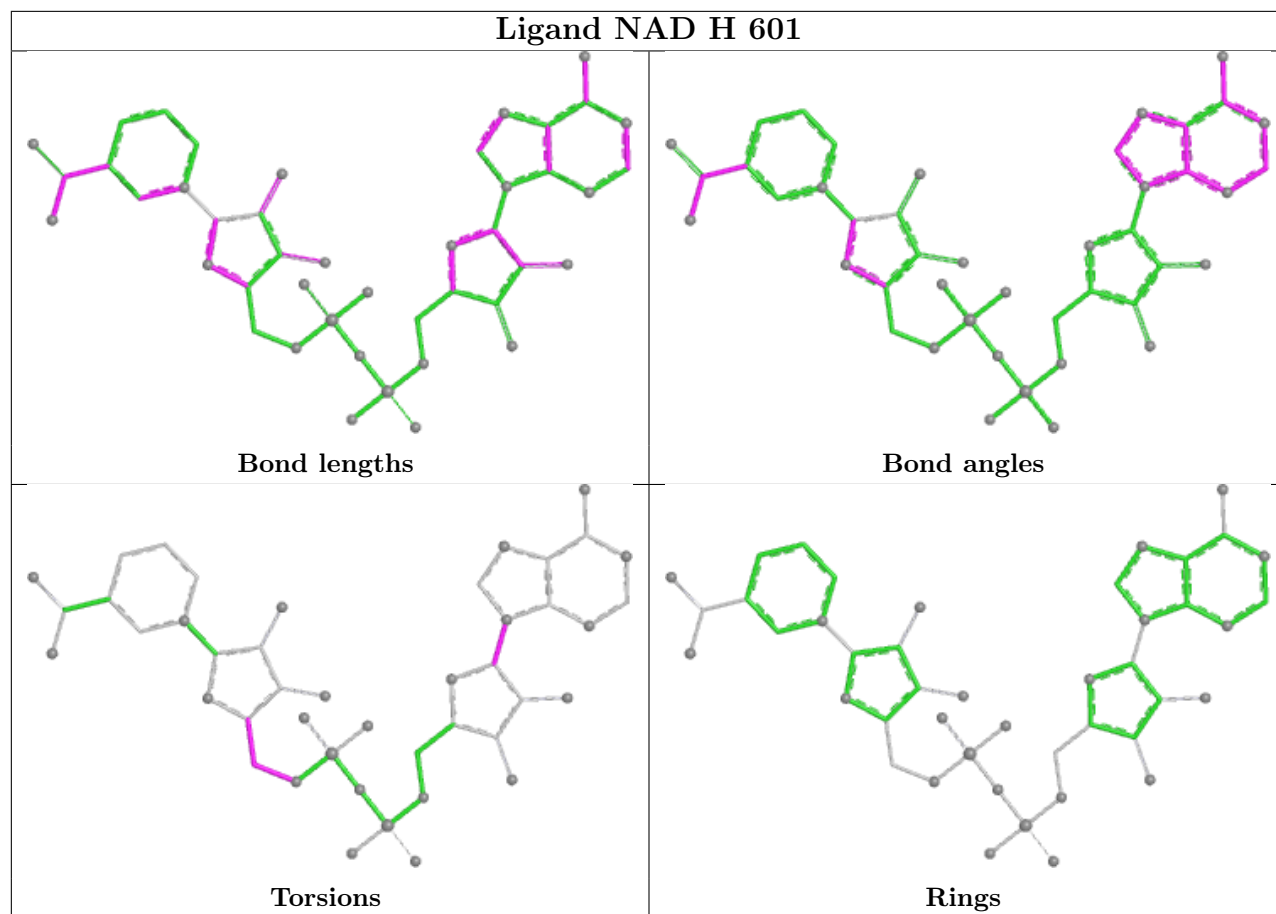
There are no ring outliers.

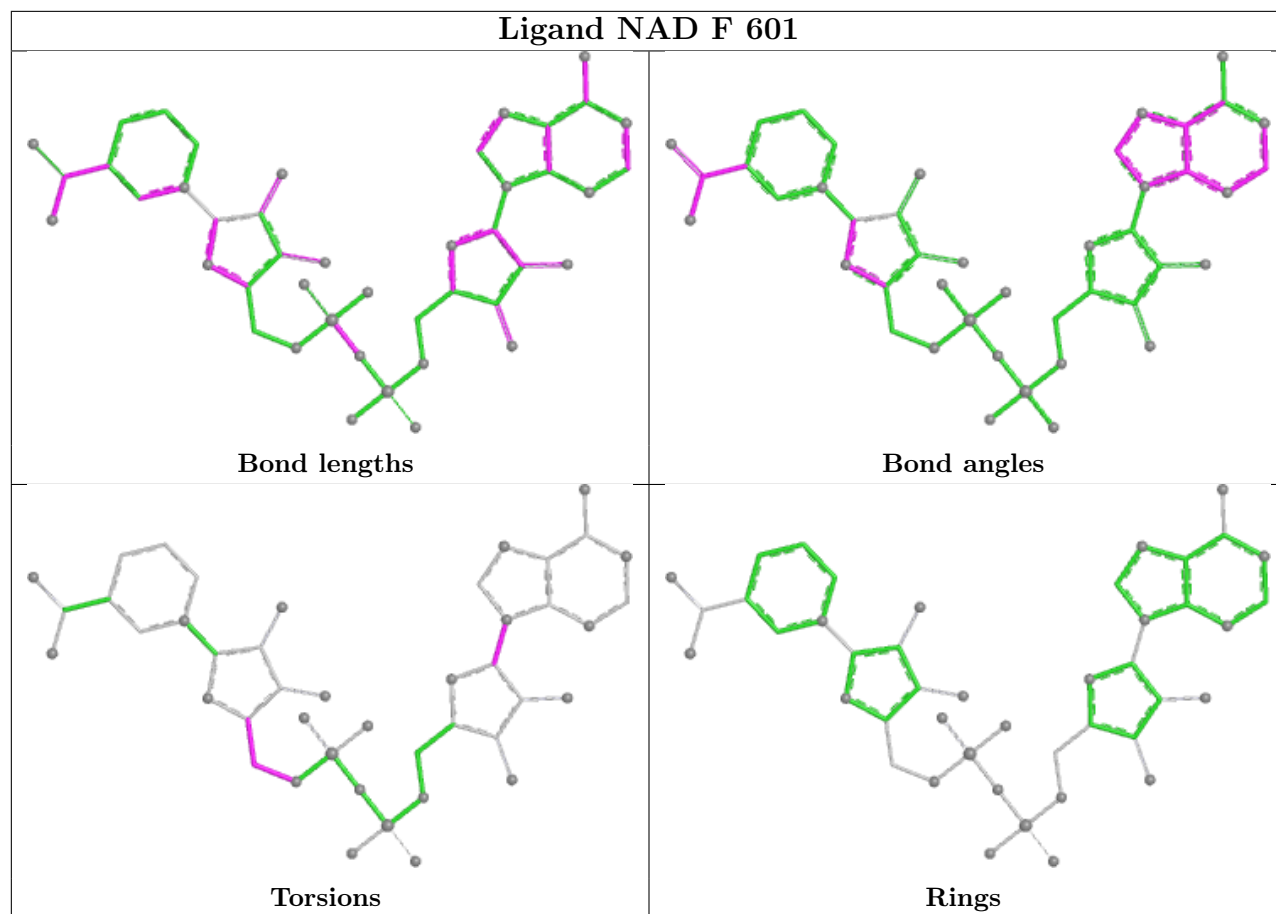
15 monomers are involved in 24 short contacts:

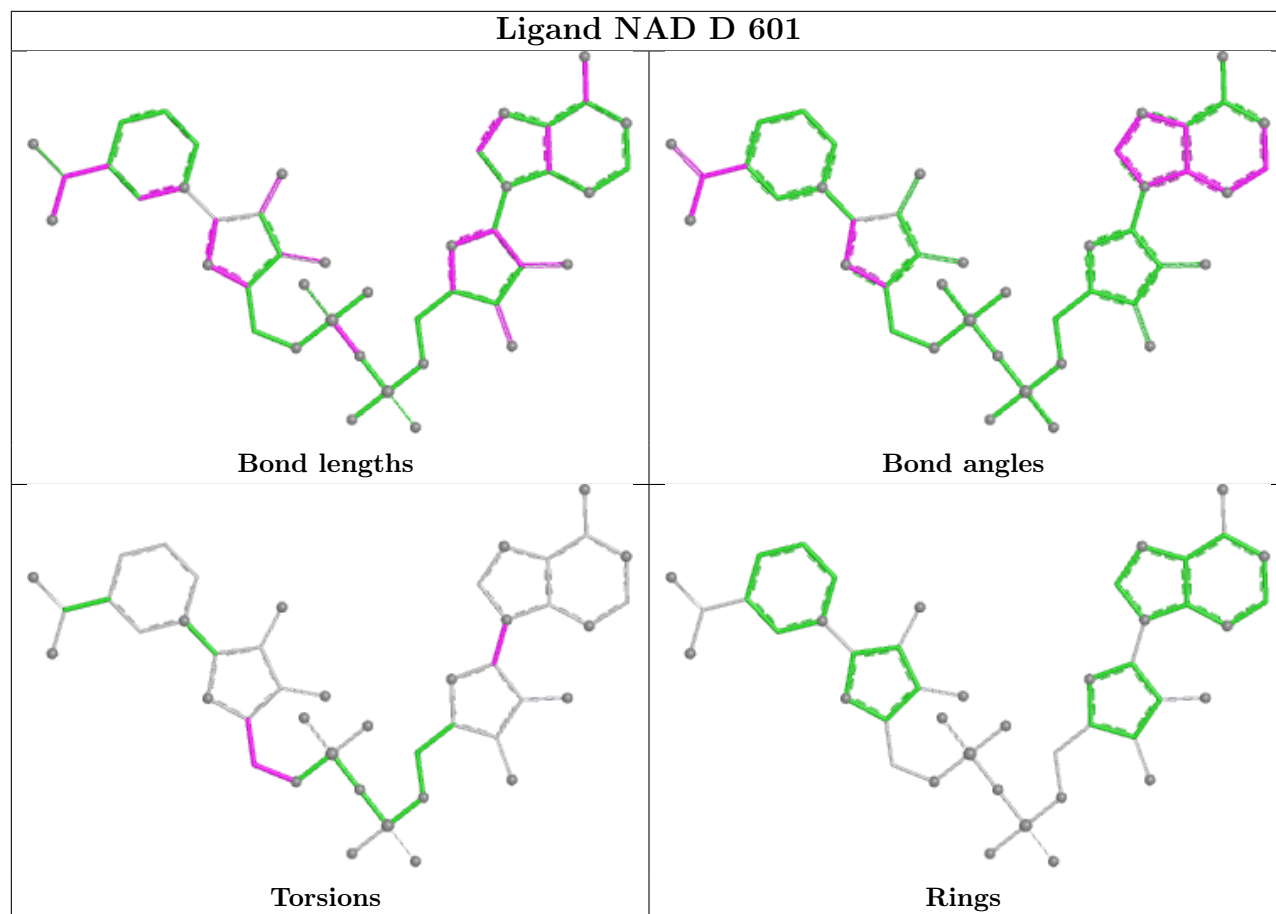
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	602	P6G	1	0
4	G	602	1PE	3	0
3	D	602	PG4	2	0
3	A	602	PG4	1	0
2	B	601	NAD	2	0
2	H	601	NAD	2	0
2	F	601	NAD	1	0
2	D	601	NAD	1	0
2	G	601	NAD	1	0
4	H	602	1PE	4	0
2	A	601	NAD	1	0
4	C	602	1PE	1	0
3	E	602	PG4	2	0
2	C	601	NAD	1	0
2	E	601	NAD	1	0

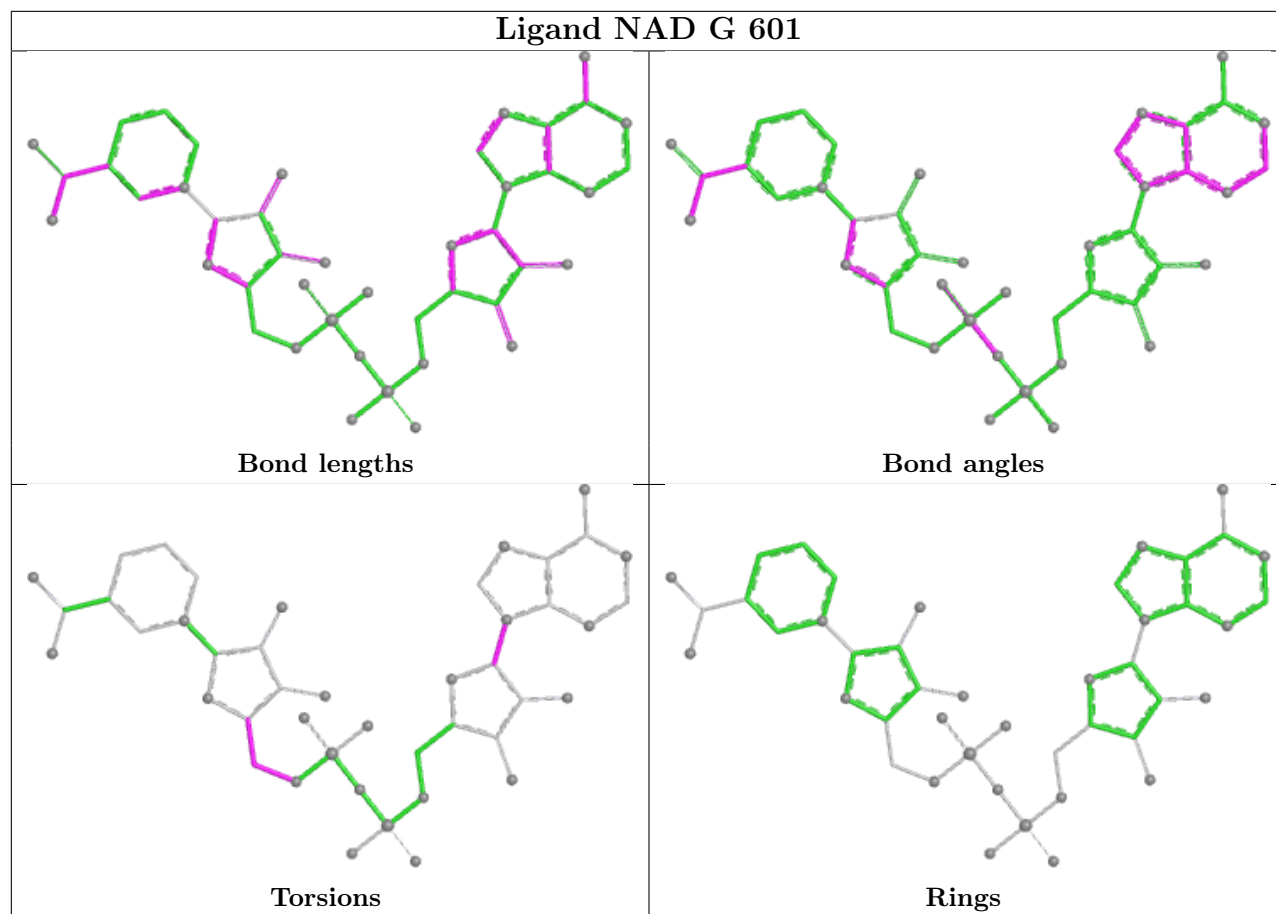
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

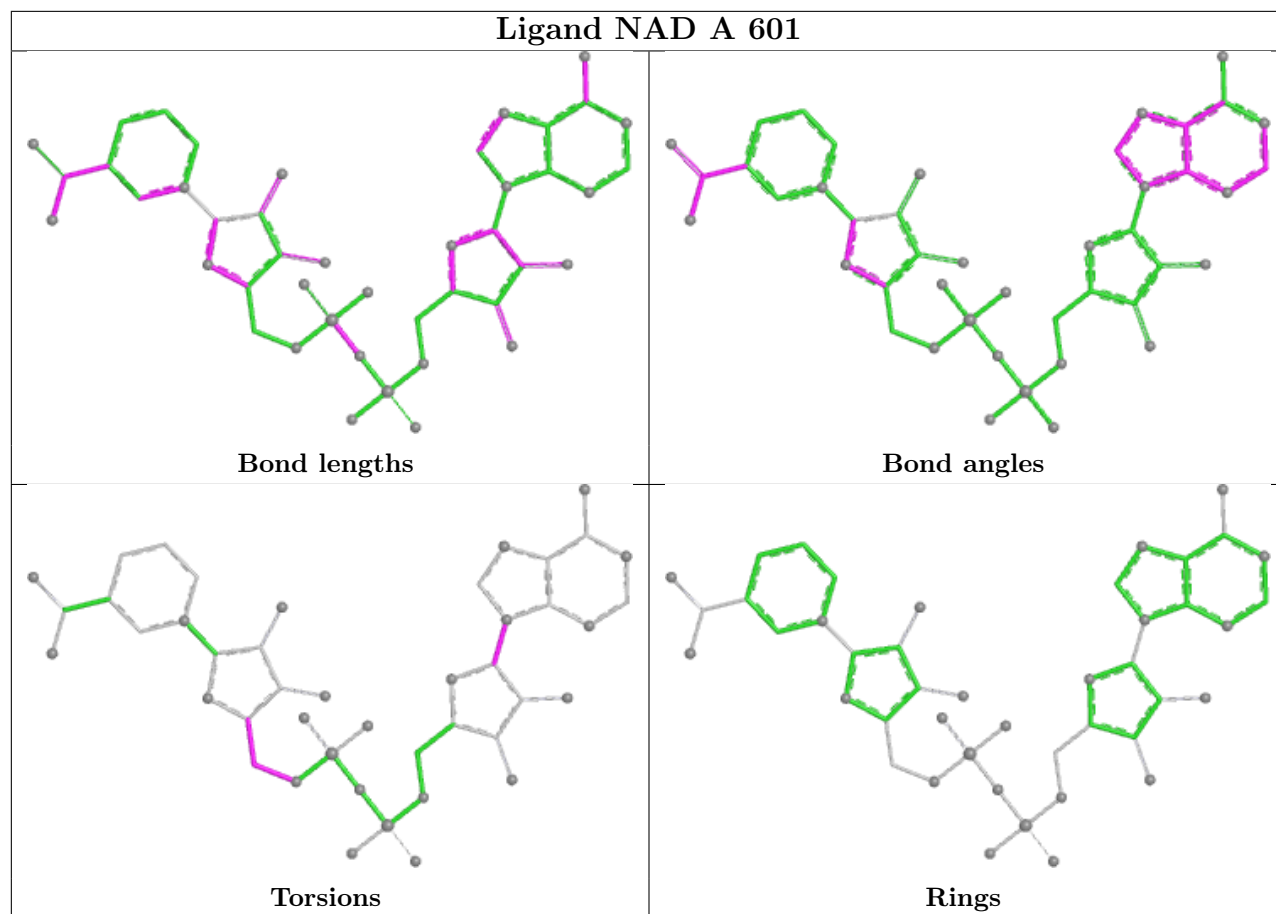


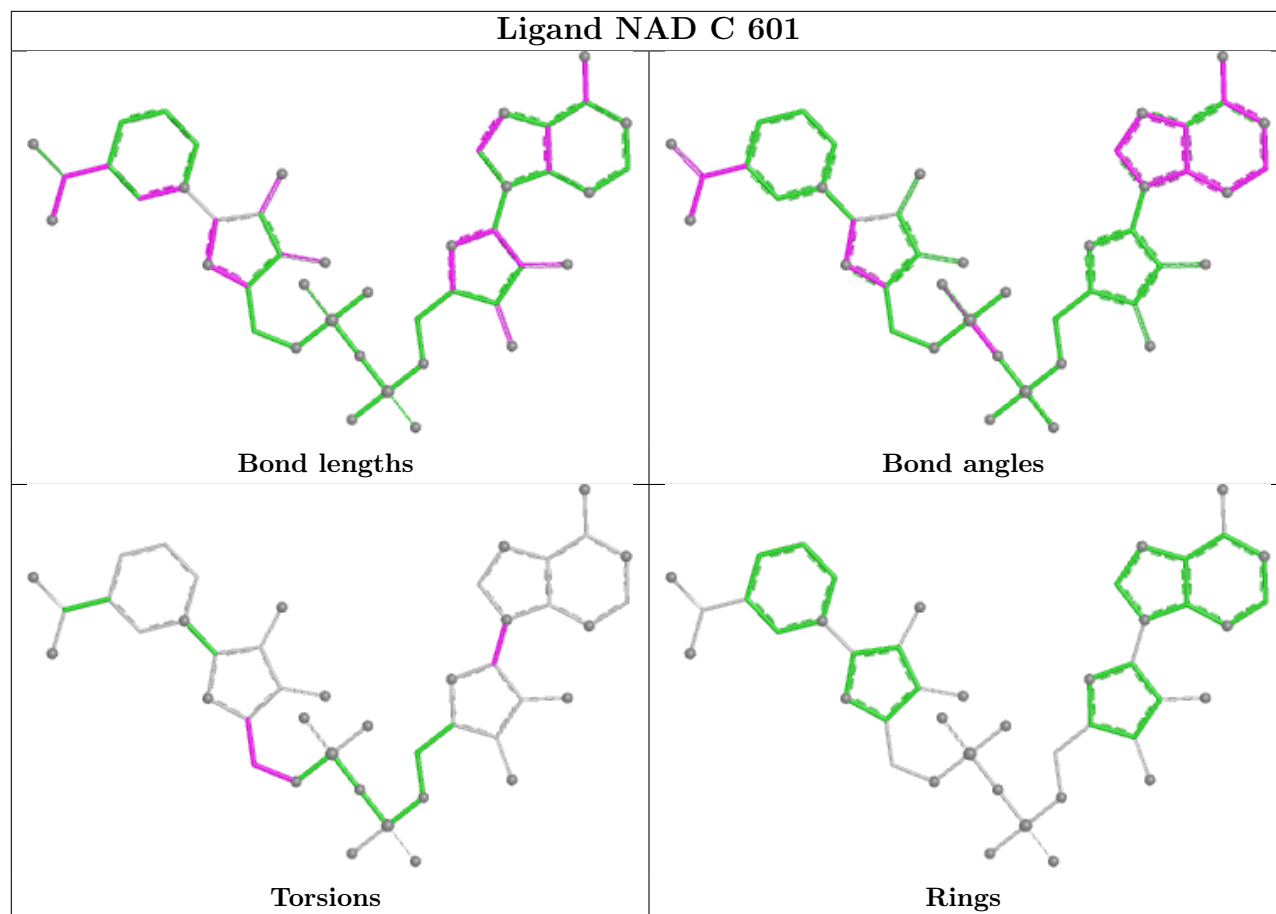


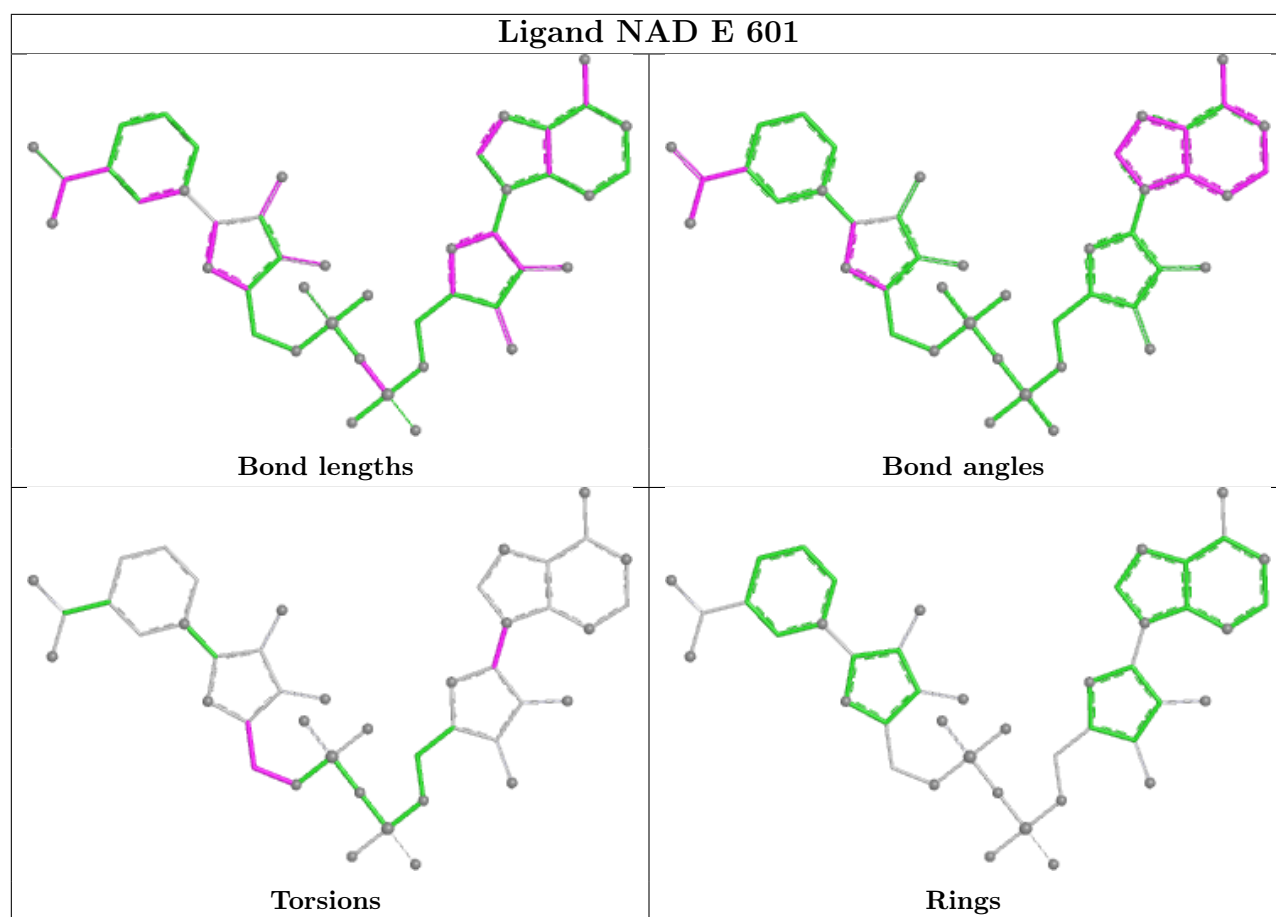












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	508/513 (99%)	-0.23	6 (1%) 76 82	12, 27, 43, 58	3 (0%)
1	B	508/513 (99%)	-0.23	7 (1%) 73 80	14, 27, 44, 70	3 (0%)
1	C	508/513 (99%)	-0.17	9 (1%) 67 74	13, 27, 49, 69	3 (0%)
1	D	509/513 (99%)	-0.17	7 (1%) 73 80	13, 29, 50, 71	3 (0%)
1	E	508/513 (99%)	-0.29	2 (0%) 88 91	13, 27, 41, 54	3 (0%)
1	F	509/513 (99%)	-0.19	10 (1%) 65 71	20, 27, 43, 56	0
1	G	508/513 (99%)	-0.26	4 (0%) 82 86	19, 27, 41, 64	0
1	H	509/513 (99%)	-0.27	3 (0%) 85 89	12, 27, 43, 64	4 (0%)
All	All	4067/4104 (99%)	-0.22	48 (1%) 76 82	12, 27, 45, 71	19 (0%)

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	338	ASN	4.6
1	C	335	TRP	4.2
1	E	510	PHE	3.9
1	B	504	LEU	3.7
1	G	337	PRO	3.6

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

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

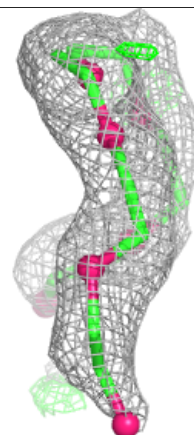
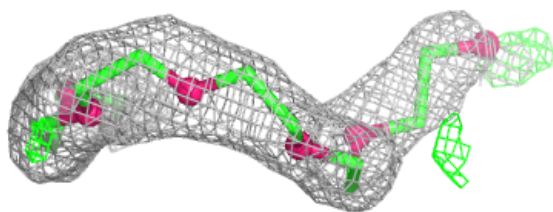
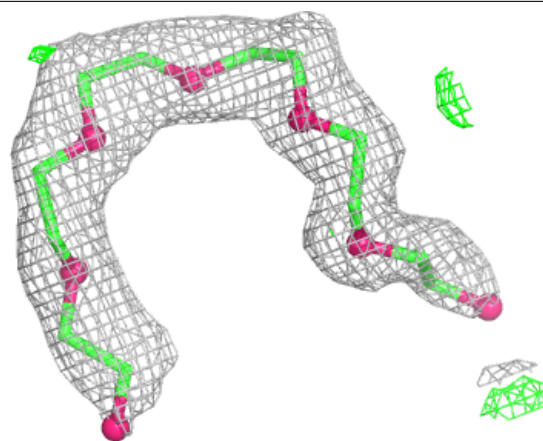
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	MG	C	603	1/1	0.84	0.10	48,48,48,48	0
5	MG	D	603	1/1	0.87	0.07	48,48,48,48	0
4	1PE	H	602	16/16	0.88	0.12	38,46,53,54	0
4	1PE	B	602	16/16	0.90	0.11	41,45,51,56	0
3	PG4	A	602	13/13	0.90	0.12	31,42,55,56	0
6	P6G	F	602	19/19	0.90	0.11	37,46,61,67	0
3	PG4	E	602	13/13	0.91	0.11	35,42,49,50	0
5	MG	H	603	1/1	0.91	0.07	47,47,47,47	0
3	PG4	D	602	13/13	0.91	0.11	36,41,54,55	0
4	1PE	G	602	13/16	0.92	0.11	29,44,55,61	0
4	1PE	C	602	16/16	0.92	0.10	32,39,53,59	0
2	NAD	E	601	44/44	0.94	0.10	18,30,49,56	0
5	MG	F	603	1/1	0.95	0.07	39,39,39,39	0
2	NAD	H	601	44/44	0.95	0.09	16,29,48,60	0
2	NAD	G	601	44/44	0.95	0.09	19,30,55,66	0
5	MG	B	603	1/1	0.96	0.08	43,43,43,43	0
2	NAD	F	601	44/44	0.96	0.08	20,29,53,61	0
2	NAD	B	601	44/44	0.96	0.08	20,29,55,62	0
2	NAD	C	601	44/44	0.96	0.09	20,30,57,64	0
5	MG	G	603	1/1	0.96	0.08	44,44,44,44	0
2	NAD	D	601	44/44	0.96	0.09	22,31,57,62	0
2	NAD	A	601	44/44	0.96	0.09	18,28,51,56	44

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.

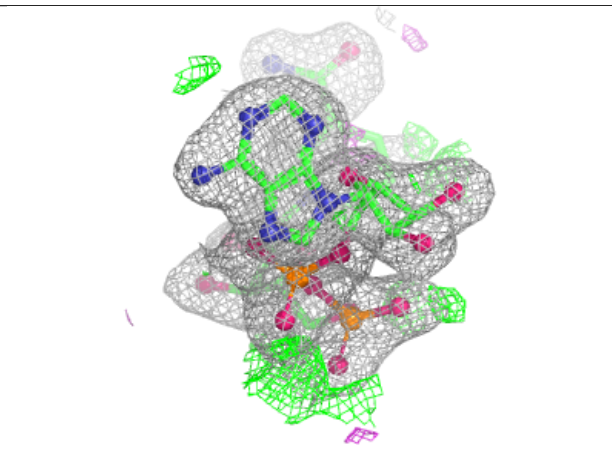
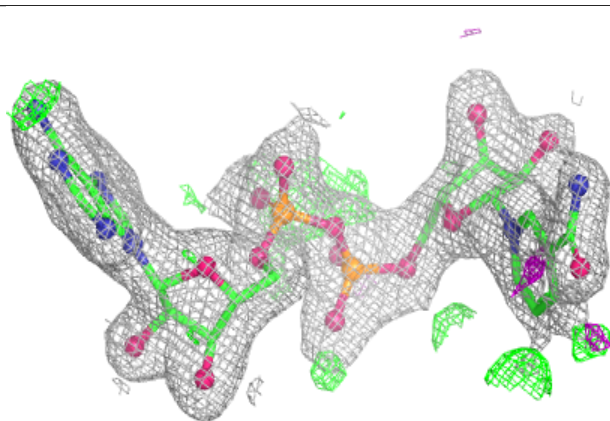
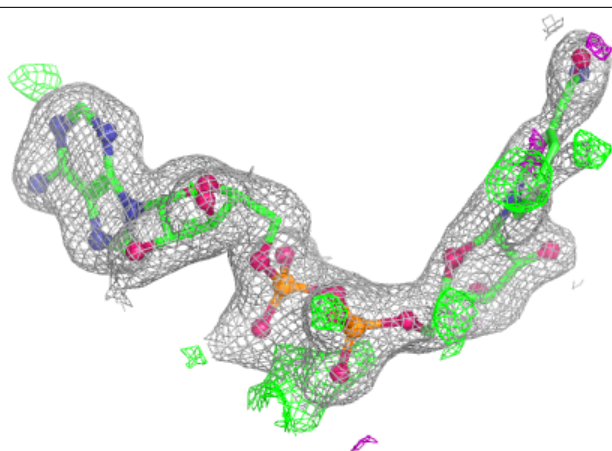
**Electron density around P6G F 602:**

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

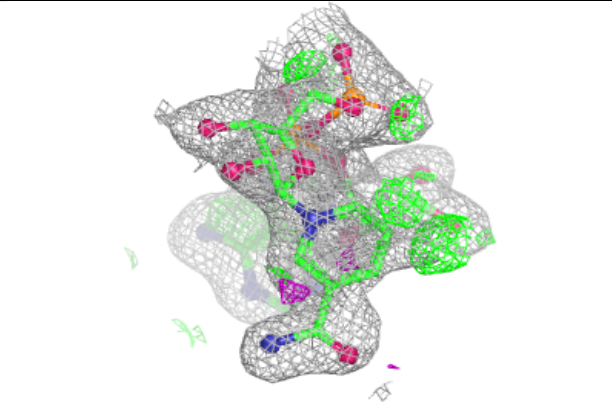
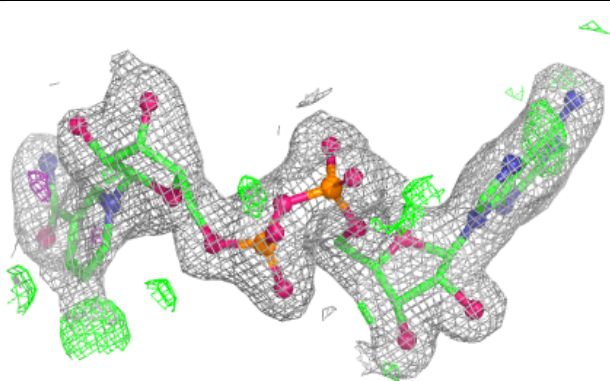
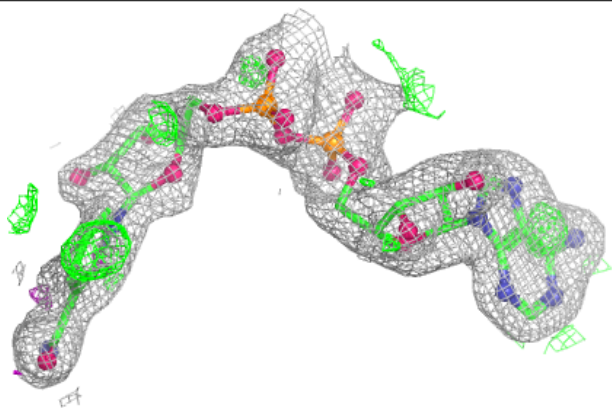


**Electron density around NAD E 601:**

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

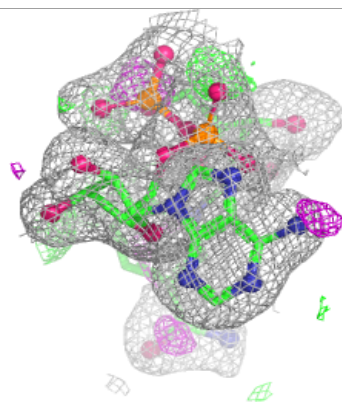
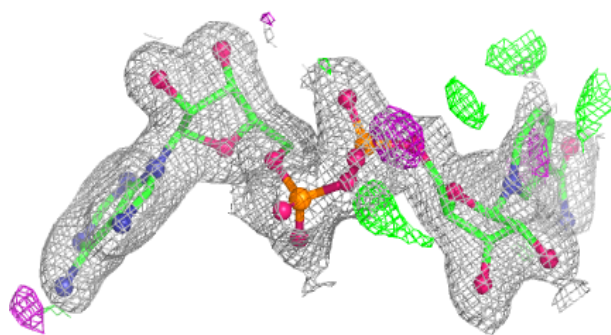
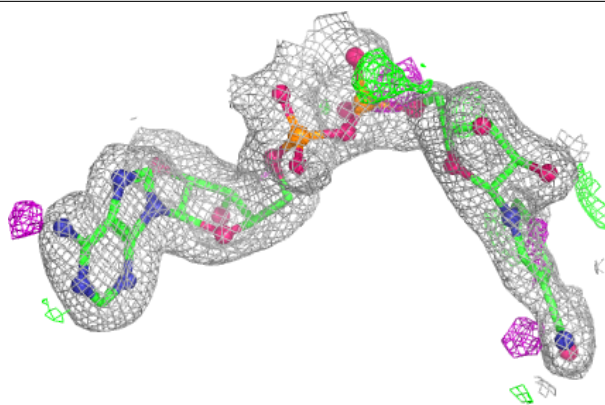
**Electron density around NAD H 601:**

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

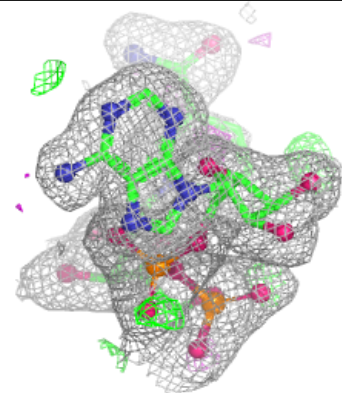
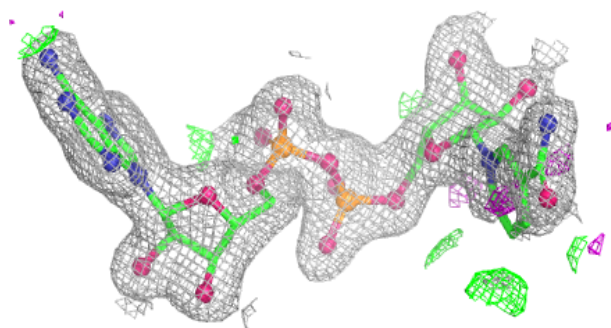
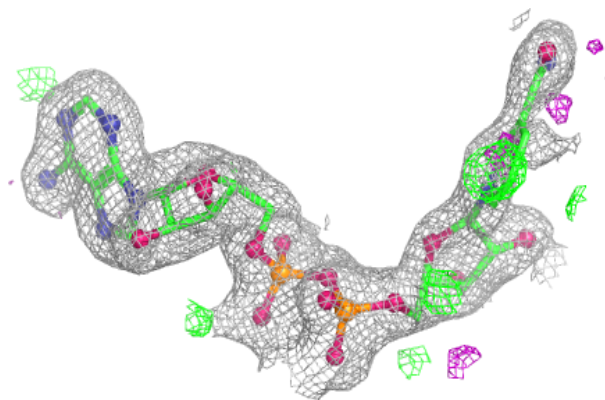


**Electron density around NAD G 601:**

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

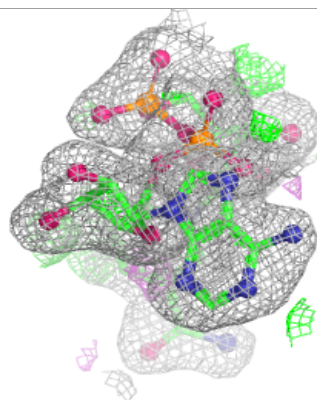
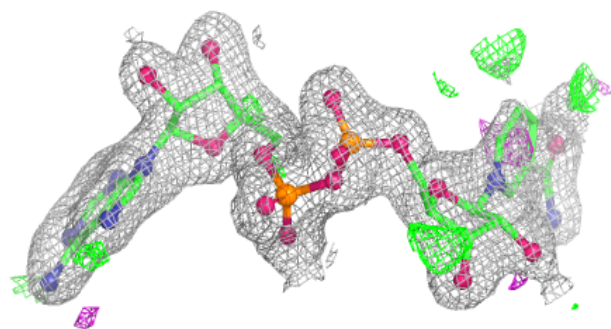
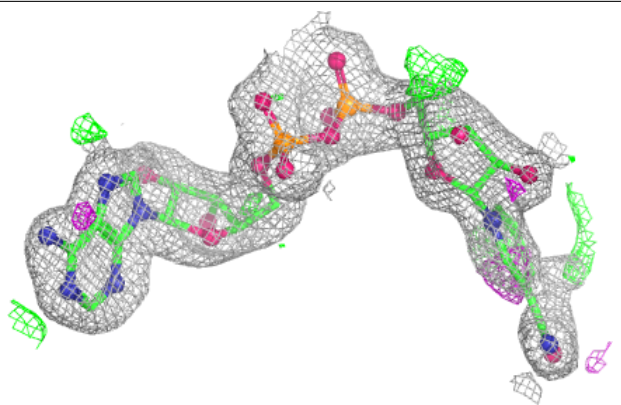
**Electron density around NAD F 601:**

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

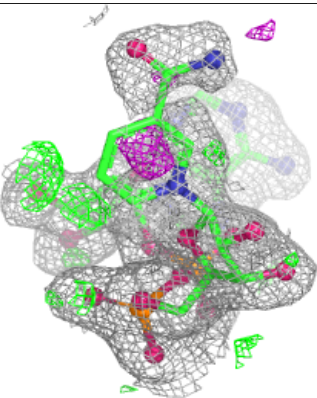
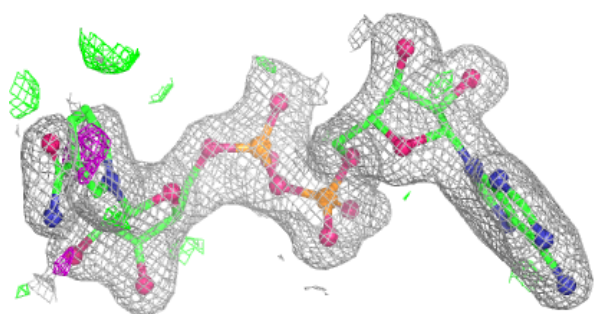
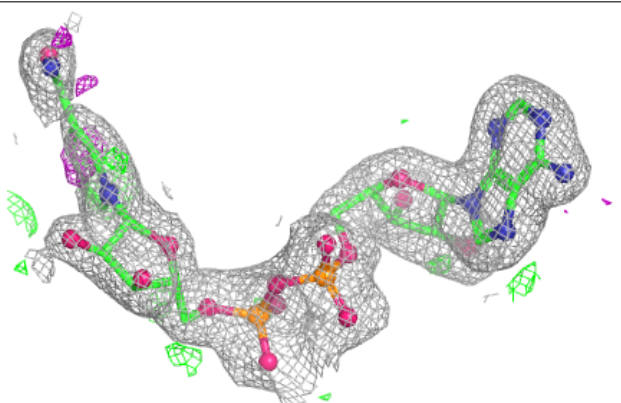


**Electron density around NAD B 601:**

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

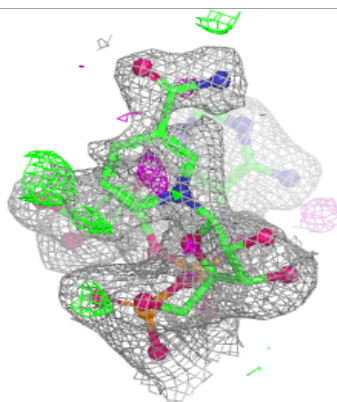
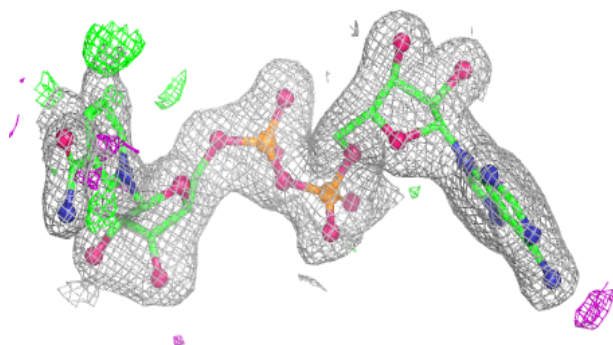
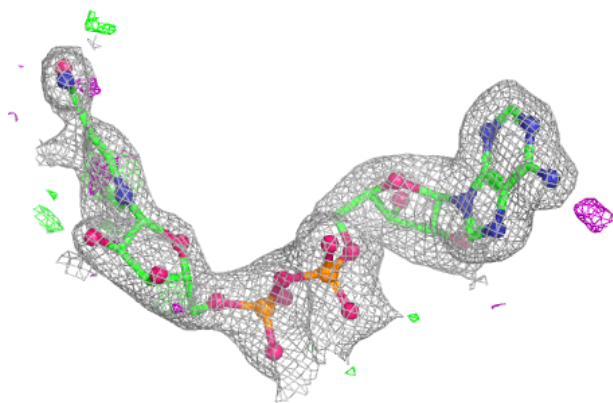
**Electron density around NAD C 601:**

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and green (positive)

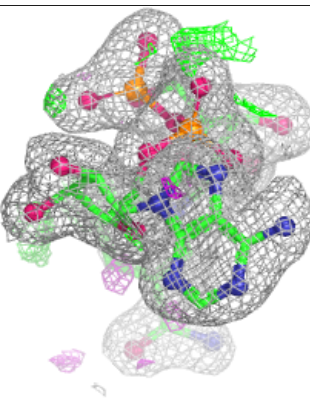
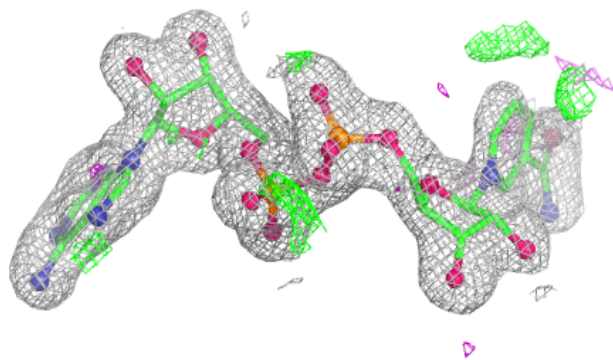
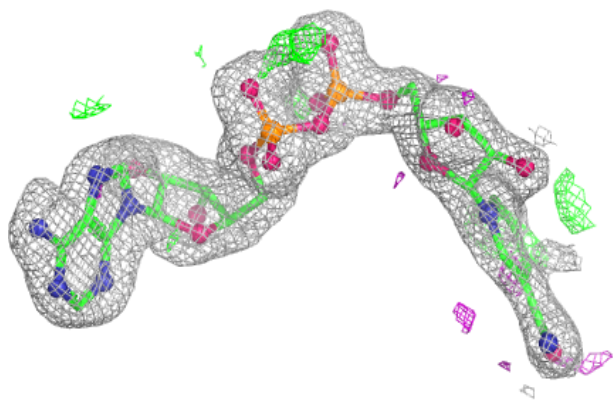


**Electron density around NAD D 601:**

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

**Electron density around NAD A 601:**

$2mF_o-DF_c$  (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.