



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:11 AM UTC

PDB ID : 7V1R / pdb_00007v1r
Title : Leifsonia Alcohol Dehydrogenases LnADH
Authors : Song, Y.; Qu, X.
Deposited on : 2021-08-05
Resolution : 2.81 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ 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

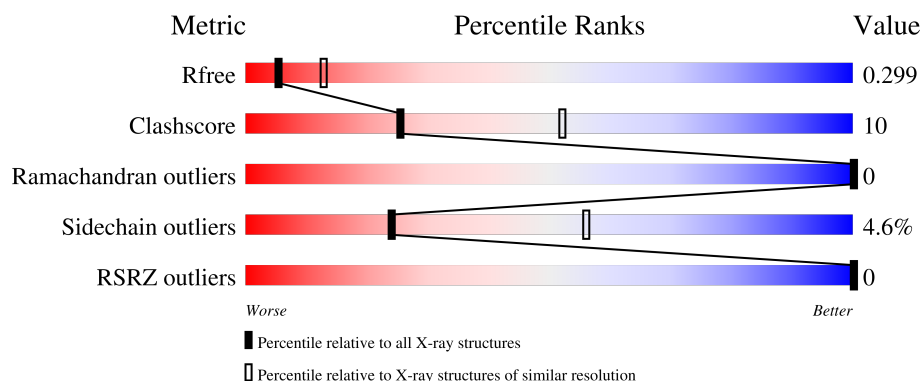
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 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	4591 (2.84-2.80)
Clashscore	190562	5010 (2.84-2.80)
Ramachandran outliers	187476	4916 (2.84-2.80)
Sidechain outliers	187428	4918 (2.84-2.80)
RSRZ outliers	180081	4594 (2.84-2.80)

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	251	 82% 18% .
1	B	251	 80% 19% .
1	C	251	 84% 15% .
1	D	251	 83% 14% .
1	E	251	 80% 18% .

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Mol	Chain	Length	Quality of chain
1	F	251	
1	G	251	
1	H	251	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IPA	F	301	-	-	X	-
2	IPA	G	301	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14432 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 Alcohol Dehydrogenases.

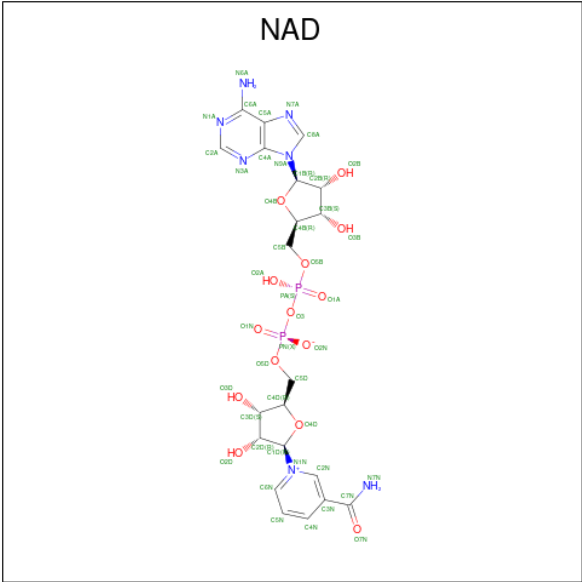
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	1	0
			1752	1105	302	342	3			
1	B	251	Total	C	N	O	S	0	1	0
			1751	1103	302	343	3			
1	C	251	Total	C	N	O	S	0	1	0
			1754	1106	303	342	3			
1	D	251	Total	C	N	O	S	0	1	0
			1749	1103	301	342	3			
1	E	251	Total	C	N	O	S	0	1	0
			1746	1102	300	341	3			
1	F	250	Total	C	N	O	S	0	1	0
			1747	1102	301	341	3			
1	G	251	Total	C	N	O	S	0	1	0
			1752	1105	301	343	3			
1	H	251	Total	C	N	O	S	0	1	0
			1748	1103	301	341	3			

- Molecule 2 is ISOPROPYL ALCOHOL (CCD ID: IPA) (formula: C₃H₈O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	3	1		
2	B	1	Total	C	O	0	0
			4	3	1		
2	C	1	Total	C	O	0	0
			4	3	1		
2	D	1	Total	C	O	0	0
			4	3	1		
2	E	1	Total	C	O	0	0
			4	3	1		
2	F	1	Total	C	O	0	0
			4	3	1		
2	G	1	Total	C	O	0	0
			4	3	1		
2	H	1	Total	C	O	0	0
			4	3	1		

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



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

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Zn	0	0
			4	4		
4	B	4	Total	Zn	0	0
			4	4		
4	C	4	Total	Zn	0	0
			4	4		
4	D	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	1	Total 1	Zn 1	0	0
4	F	2	Total 2	Zn 2	0	0
4	G	1	Total 1	Zn 1	0	0
4	H	1	Total 1	Zn 1	0	0

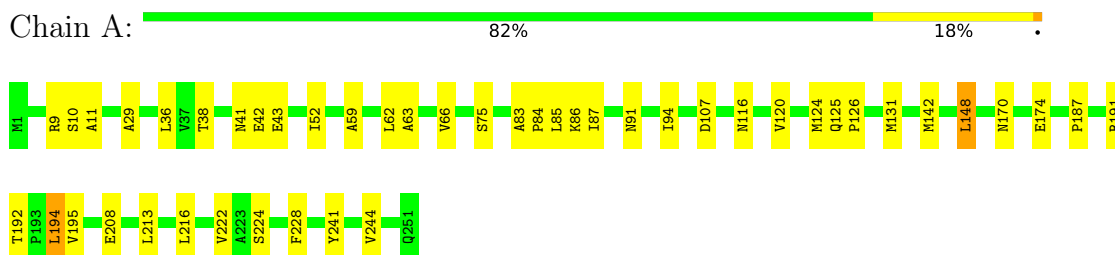
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total 3	O 3	0	0
5	B	1	Total 1	O 1	0	0
5	C	6	Total 6	O 6	0	0
5	D	4	Total 4	O 4	0	0
5	E	2	Total 2	O 2	0	0
5	F	9	Total 9	O 9	0	0
5	G	3	Total 3	O 3	0	0
5	H	3	Total 3	O 3	0	0

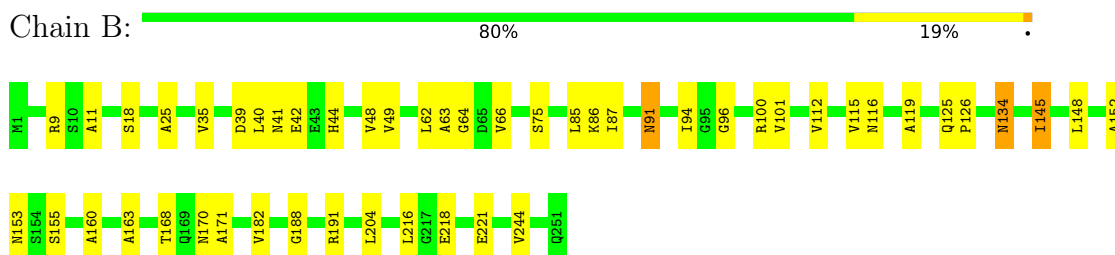
3 Residue-property plots

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.

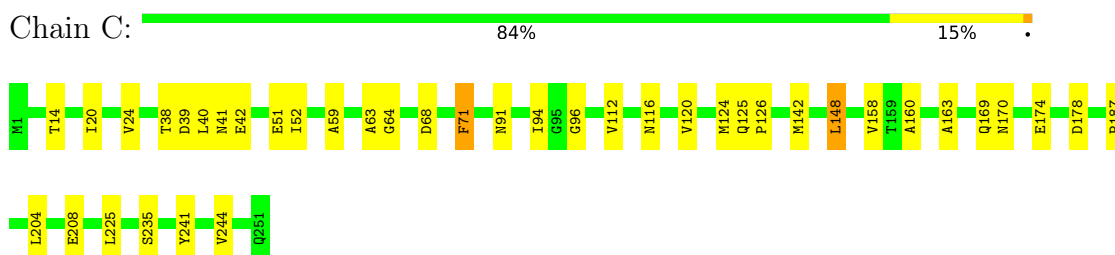
• Molecule 1: Alcohol Dehydrogenases



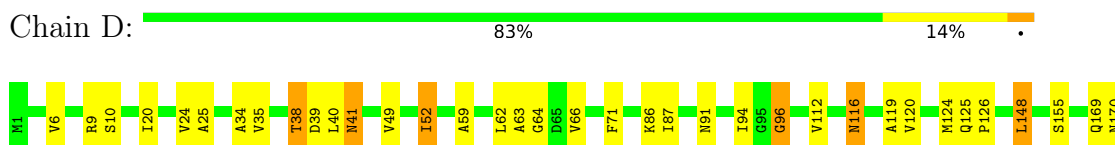
• Molecule 1: Alcohol Dehydrogenases



• Molecule 1: Alcohol Dehydrogenases



• Molecule 1: Alcohol Dehydrogenases





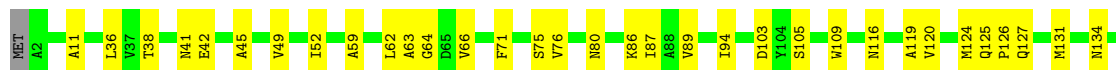
- Molecule 1: Alcohol Dehydrogenases

Chain E: 80% 18% .



- Molecule 1: Alcohol Dehydrogenases

Chain F: 76% 24%



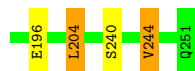
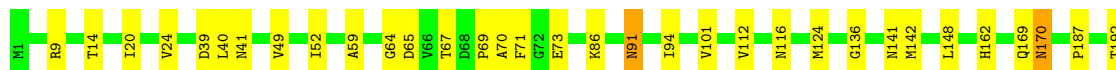
- Molecule 1: Alcohol Dehydrogenases

Chain G: 76% 22% .



- Molecule 1: Alcohol Dehydrogenases

Chain H: 85% 13% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.94Å 237.49Å 68.78Å 90.00° 113.03° 90.00°	Depositor
Resolution (Å)	49.49 – 2.81 49.49 – 2.81	Depositor EDS
% Data completeness (in resolution range)	98.5 (49.49-2.81) 98.8 (49.49-2.81)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.70 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.246 , 0.295 0.249 , 0.299	Depositor DCC
R_{free} test set	1921 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.387	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 11.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.448 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14432	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.32 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2920e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ZN, IPA, NAD

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	1.09	0/1776	1.49	0/2421
1	B	1.08	0/1775	1.49	0/2421
1	C	1.10	0/1778	1.48	2/2423 (0.1%)
1	D	1.10	0/1773	1.48	3/2418 (0.1%)
1	E	1.11	0/1769	1.54	0/2412
1	F	1.12	1/1771 (0.1%)	1.53	0/2414
1	G	1.05	0/1776	1.46	2/2422 (0.1%)
1	H	1.08	0/1772	1.54	1/2417 (0.0%)
All	All	1.09	1/14190 (0.0%)	1.50	8/19348 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	89	VAL	C-O	-6.00	1.17	1.24

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	40	LEU	O-C-N	5.60	128.07	122.08
1	H	136	GLY	CA-C-O	-5.43	118.54	122.45
1	D	52	ILE	CB-CA-C	-5.15	105.38	111.97
1	G	122	TYR	CA-C-N	5.14	125.69	119.98
1	G	122	TYR	C-N-CA	5.14	125.69	119.98
1	D	96	GLY	CA-C-O	-5.07	117.32	122.59
1	C	71	PHE	CA-C-N	5.04	125.57	119.98
1	C	71	PHE	C-N-CA	5.04	125.57	119.98

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	1752	0	1725	33	0
1	B	1751	0	1718	30	0
1	C	1754	0	1732	32	0
1	D	1749	0	1716	26	0
1	E	1746	0	1717	31	0
1	F	1747	0	1720	50	0
1	G	1752	0	1717	53	0
1	H	1748	0	1713	26	0
2	A	4	0	8	2	0
2	B	4	0	8	1	0
2	C	4	0	8	1	0
2	D	4	0	8	0	0
2	E	4	0	8	0	0
2	F	4	0	8	6	0
2	G	4	0	8	10	0
2	H	4	0	8	1	0
3	A	44	0	26	4	0
3	B	44	0	26	2	0
3	C	44	0	26	2	0
3	D	44	0	26	1	0
3	E	44	0	26	2	0
3	F	44	0	26	1	0
3	G	44	0	26	5	0
3	H	44	0	26	3	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	2	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	3	0	0	0	0
5	B	1	0	0	0	0
5	C	6	0	0	2	0
5	D	4	0	0	0	0
5	E	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	9	0	0	2	0
5	G	3	0	0	0	0
5	H	3	0	0	0	0
All	All	14432	0	14030	274	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 10.

All (274) 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:B:42:GLU:HA	1:B:63:ALA:HB2	1.45	0.98
1:G:157:TYR:OH	2:G:301:IPA:H11	1.73	0.87
1:C:148:LEU:HD13	1:C:241:TYR:CE2	2.12	0.83
1:A:142:MET:CE	1:A:187:PRO:HG2	2.09	0.82
1:F:142:MET:CE	1:F:187:PRO:HG2	2.12	0.80
1:G:42:GLU:HA	1:G:63:ALA:HB2	1.63	0.79
1:F:142:MET:CE	1:F:187:PRO:CG	2.61	0.78
1:F:148:LEU:HD12	1:F:149:VAL:HG13	1.66	0.78
1:G:142:MET:HE1	1:G:187:PRO:HG2	1.69	0.75
1:G:157:TYR:CE2	2:G:301:IPA:C1	2.71	0.74
1:A:148:LEU:HD13	1:A:241:TYR:CE2	2.25	0.72
1:E:52:ILE:HG21	1:E:59:ALA:HB2	1.72	0.72
1:C:40:LEU:HB2	5:C:403:HOH:O	1.88	0.71
1:F:142:MET:HE2	1:F:187:PRO:HG2	1.73	0.69
1:G:91:ASN:O	3:G:302:NAD:H4D	1.92	0.69
1:A:142:MET:CE	1:A:187:PRO:CG	2.70	0.68
1:C:94:ILE:H	1:C:116:ASN:HD21	1.40	0.67
1:G:157:TYR:CE2	2:G:301:IPA:H13	2.30	0.67
1:E:194:LEU:O	1:E:198:ASN:ND2	2.27	0.67
1:D:94:ILE:H	1:D:116:ASN:HD21	1.43	0.67
1:H:124:MET:CE	1:H:141:ASN:HD21	2.08	0.67
1:F:148:LEU:HD12	1:F:148:LEU:C	2.20	0.66
1:G:191:ARG:HG3	1:G:216:LEU:HB2	1.77	0.66
1:G:9:ARG:HB2	1:G:86:LYS:HB2	1.78	0.66
1:F:157:TYR:CE2	2:F:301:IPA:H13	2.31	0.66
1:G:157:TYR:CZ	2:G:301:IPA:C1	2.80	0.65
1:F:157:TYR:HE2	2:F:301:IPA:H13	1.62	0.64
1:F:148:LEU:HD23	1:F:241:TYR:HE2	1.62	0.64
1:H:52:ILE:HG21	1:H:59:ALA:HB2	1.80	0.64
1:B:145:ILE:HG12	1:B:188:GLY:HA2	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:175:TYR:CZ	1:E:100:ARG:NH1	2.66	0.64
1:C:42:GLU:HB2	1:C:63:ALA:HB2	1.79	0.64
1:G:120:VAL:O	1:G:124:MET:HG3	1.96	0.64
1:C:120:VAL:O	1:C:124:MET:HG3	1.98	0.63
1:F:52:ILE:HG21	1:F:59:ALA:HB2	1.80	0.63
1:G:94:ILE:H	1:G:116:ASN:HD21	1.45	0.63
2:A:301:IPA:H32	3:A:302:NAD:N7N	2.13	0.62
1:B:191:ARG:HG3	1:B:216:LEU:HB2	1.81	0.62
1:H:94:ILE:H	1:H:116:ASN:HD21	1.47	0.62
1:E:9:ARG:HD3	1:E:86:LYS:HB2	1.82	0.62
1:B:91:ASN:O	3:B:302:NAD:H4D	1.99	0.61
1:B:42:GLU:CA	1:B:63:ALA:HB2	2.25	0.61
1:A:9:ARG:HB2	1:A:86:LYS:HB2	1.83	0.61
1:G:157:TYR:CZ	2:G:301:IPA:H11	2.35	0.61
1:D:41:ASN:C	1:D:41:ASN:HD22	2.09	0.60
1:H:91:ASN:HA	1:H:142:MET:HB2	1.84	0.60
1:C:40:LEU:CB	5:C:403:HOH:O	2.46	0.60
1:B:94:ILE:H	1:B:116:ASN:HD21	1.50	0.60
1:G:49:VAL:HG21	1:G:61:ALA:N	2.17	0.60
1:C:91:ASN:O	3:C:302:NAD:H4D	2.02	0.59
1:G:157:TYR:OH	2:G:301:IPA:C1	2.49	0.59
1:F:11:ALA:HA	1:F:87:ILE:O	2.02	0.58
1:C:158:VAL:HG21	1:H:170:ASN:OD1	2.04	0.58
1:F:142:MET:HE1	1:F:187:PRO:CG	2.33	0.58
1:F:94:ILE:H	1:F:116:ASN:HD21	1.52	0.57
2:F:301:IPA:H2	3:F:302:NAD:C4N	2.35	0.57
1:G:52:ILE:HG21	1:G:59:ALA:HB2	1.87	0.57
1:C:41:ASN:C	1:C:41:ASN:HD22	2.13	0.57
1:G:42:GLU:HA	1:G:63:ALA:CB	2.33	0.57
1:A:192:THR:O	1:A:195:VAL:N	2.39	0.56
1:E:234:ALA:HB1	1:E:237:ILE:HD12	1.88	0.56
1:E:127:GLN:O	1:E:131:MET:HG3	2.05	0.56
1:H:124:MET:HE3	1:H:141:ASN:HD21	1.70	0.56
1:G:65:ASP:OD1	3:G:302:NAD:N6A	2.38	0.55
1:F:228:PHE:O	1:F:231:SER:OG	2.23	0.55
2:C:301:IPA:H2	3:C:302:NAD:C4N	2.35	0.55
1:C:52:ILE:HD13	1:C:59:ALA:HB2	1.87	0.55
1:F:142:MET:HE3	1:F:187:PRO:CD	2.37	0.55
1:D:6:VAL:HG12	1:D:87:ILE:HD11	1.88	0.55
1:A:94:ILE:H	1:A:116:ASN:HD21	1.53	0.55
1:D:20:ILE:O	1:D:24:VAL:HG23	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:204:LEU:HD13	1:H:204:LEU:C	2.32	0.55
1:E:94:ILE:H	1:E:116:ASN:HD21	1.55	0.54
1:G:116:ASN:N	1:G:116:ASN:HD22	2.04	0.54
1:F:189:PHE:CE2	2:F:301:IPA:H31	2.43	0.54
1:A:142:MET:HE1	1:A:187:PRO:CG	2.38	0.54
1:G:11:ALA:HA	1:G:87:ILE:O	2.08	0.54
1:G:41:ASN:OD1	1:G:44:HIS:CD2	2.61	0.54
1:G:40:LEU:HA	1:G:64:GLY:O	2.07	0.53
1:F:148:LEU:CD1	1:F:149:VAL:HG13	2.36	0.53
1:G:218:GLU:N	1:G:221:GLU:OE1	2.39	0.53
1:A:38:THR:HA	1:A:62:LEU:O	2.08	0.53
1:F:49:VAL:HG13	1:F:59:ALA:O	2.09	0.53
1:C:39:ASP:O	1:C:63:ALA:HA	2.09	0.53
1:E:94:ILE:HD11	1:E:112:VAL:HA	1.90	0.53
1:F:142:MET:HE1	1:F:187:PRO:HG3	1.91	0.53
1:E:14:THR:O	1:E:91:ASN:HB3	2.09	0.52
1:F:36:LEU:CD1	5:F:402:HOH:O	2.57	0.52
1:H:91:ASN:O	3:H:302:NAD:H4D	2.08	0.52
1:C:169:GLN:OE1	1:H:162:HIS:NE2	2.42	0.52
1:E:16:GLY:HA3	1:E:37:VAL:HG13	1.90	0.52
1:E:91:ASN:O	3:E:302:NAD:H4D	2.09	0.52
1:E:187:PRO:HA	1:E:244:VAL:HG13	1.92	0.52
1:D:91:ASN:O	3:D:302:NAD:H4D	2.09	0.52
1:H:124:MET:HE1	1:H:141:ASN:HD21	1.74	0.52
1:C:42:GLU:HB2	1:C:63:ALA:CB	2.39	0.52
1:E:39:ASP:O	1:E:63:ALA:HA	2.10	0.52
1:E:64:GLY:HA3	1:E:71:PHE:CE1	2.45	0.52
1:G:39:ASP:O	1:G:63:ALA:HA	2.10	0.51
1:A:191:ARG:NH1	1:A:208:GLU:OE2	2.43	0.51
1:A:107:ASP:HB3	1:G:97:GLU:OE1	2.10	0.51
1:F:189:PHE:CE2	2:F:301:IPA:C3	2.93	0.51
1:G:250:ALA:HA	1:H:169:GLN:HE21	1.76	0.51
1:D:204:LEU:HD13	1:D:204:LEU:C	2.36	0.51
1:A:142:MET:HE3	1:A:187:PRO:CD	2.41	0.51
1:F:86:LYS:NZ	1:F:134:ASN:O	2.43	0.50
1:E:100:ARG:HH11	1:E:100:ARG:HB3	1.75	0.50
1:E:65:ASP:OD1	3:E:302:NAD:N6A	2.42	0.50
1:G:157:TYR:HE2	2:G:301:IPA:H13	1.76	0.50
1:F:42:GLU:HA	1:F:63:ALA:HB2	1.92	0.50
1:E:116:ASN:HD22	1:E:116:ASN:N	2.07	0.50
1:E:192:THR:HG22	1:E:219:PRO:HG3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:91:ASN:HA	1:G:142:MET:HB2	1.93	0.50
1:E:66:VAL:HG23	1:E:119:ALA:HB1	1.94	0.50
1:G:191:ARG:HG3	1:G:216:LEU:CB	2.41	0.50
1:G:84:PRO:HB3	1:G:134:ASN:OD1	2.12	0.50
1:B:168:THR:HG23	1:B:182:VAL:HG12	1.94	0.49
1:D:120:VAL:O	1:D:124:MET:HG3	2.13	0.49
1:G:41:ASN:C	1:G:41:ASN:HD22	2.20	0.49
1:G:160:ALA:O	1:G:163:ALA:HB3	2.13	0.49
1:A:187:PRO:HA	1:A:244:VAL:HG13	1.96	0.48
1:E:204:LEU:C	1:E:204:LEU:HD13	2.38	0.48
1:C:235:SER:OG	1:F:221:GLU:OE2	2.25	0.48
1:E:20:ILE:O	1:E:24:VAL:HG23	2.12	0.48
1:F:145:ILE:HD12	1:F:248:TYR:CE1	2.48	0.48
1:G:41:ASN:OD1	1:G:44:HIS:NE2	2.46	0.48
1:C:52:ILE:HG21	1:C:59:ALA:HB2	1.96	0.47
1:H:187:PRO:HA	1:H:244:VAL:HG13	1.96	0.47
1:A:142:MET:HE3	1:A:187:PRO:CG	2.43	0.47
1:D:96:GLY:HA3	1:D:112:VAL:HG21	1.96	0.47
1:F:76:VAL:O	1:F:80:ASN:HB2	2.14	0.47
1:B:9:ARG:HB2	1:B:86:LYS:HB2	1.95	0.47
1:B:39:ASP:O	1:B:63:ALA:HA	2.14	0.47
1:F:127:GLN:O	1:F:131:MET:HG3	2.14	0.47
1:G:66:VAL:HG23	1:G:119:ALA:HB1	1.97	0.47
1:E:115:VAL:O	1:E:119:ALA:HB3	2.14	0.47
1:F:52:ILE:HG21	1:F:59:ALA:CB	2.44	0.47
2:B:301:IPA:H2	3:B:302:NAD:C4N	2.44	0.47
1:A:11:ALA:HA	1:A:87:ILE:O	2.14	0.47
1:G:168:THR:HG23	1:G:182:VAL:HG12	1.96	0.47
1:B:125:GLN:HB2	1:B:126:PRO:HD3	1.97	0.47
1:A:52:ILE:HG21	1:A:59:ALA:HB2	1.97	0.46
1:B:96:GLY:HA3	1:B:112:VAL:HG21	1.97	0.46
1:C:20:ILE:O	1:C:24:VAL:HG23	2.15	0.46
1:H:64:GLY:HA3	1:H:71:PHE:CE1	2.49	0.46
1:B:160:ALA:O	1:B:163:ALA:HB3	2.14	0.46
1:G:86:LYS:O	1:G:87:ILE:HG13	2.15	0.46
1:B:116:ASN:N	1:B:116:ASN:HD22	2.12	0.46
1:F:86:LYS:O	1:F:87:ILE:HG13	2.15	0.46
1:B:41:ASN:HB3	1:B:44:HIS:HB2	1.97	0.46
1:A:10:SER:OG	1:A:85:LEU:HA	2.16	0.46
1:C:64:GLY:HA3	1:C:71:PHE:CE1	2.51	0.46
1:E:49:VAL:HG13	1:E:59:ALA:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:64:GLY:HA3	1:F:71:PHE:CE1	2.51	0.46
1:E:108:SER:O	1:E:112:VAL:HG23	2.16	0.46
1:G:10:SER:OG	1:G:85:LEU:HA	2.16	0.46
1:F:87:ILE:HA	1:F:138:ALA:O	2.16	0.45
1:H:9:ARG:HD3	1:H:86:LYS:HB2	1.98	0.45
1:B:62:LEU:HD23	1:B:75:SER:HA	1.98	0.45
1:E:79:ALA:HB1	1:E:85:LEU:HD13	1.97	0.45
1:D:38:THR:HA	1:D:62:LEU:O	2.16	0.45
1:F:36:LEU:HD22	1:F:75:SER:O	2.17	0.45
1:F:191:ARG:O	1:F:191:ARG:HG2	2.15	0.45
1:G:83:ALA:O	1:G:84:PRO:C	2.57	0.45
1:G:157:TYR:CE2	2:G:301:IPA:H11	2.50	0.45
1:A:228:PHE:CZ	1:D:225:LEU:HA	2.50	0.45
1:E:22:ARG:HG3	1:E:48:VAL:HG22	1.99	0.45
1:F:207:LEU:O	1:F:210:LYS:N	2.47	0.45
1:G:96:GLY:HA3	1:G:112:VAL:CG2	2.46	0.45
1:C:187:PRO:HA	1:C:244:VAL:HG13	1.98	0.45
1:C:204:LEU:HD13	1:C:204:LEU:C	2.42	0.45
1:A:43:GLU:HG2	1:G:43:GLU:HB3	1.98	0.45
1:A:36:LEU:HD22	1:A:75:SER:O	2.17	0.45
1:E:211:HIS:HD2	1:E:245:ASP:O	2.00	0.45
1:F:145:ILE:HD12	1:F:248:TYR:CD1	2.52	0.45
1:G:195:VAL:HG13	1:G:199:LEU:HD11	1.99	0.45
1:H:41:ASN:C	1:H:41:ASN:HD22	2.25	0.45
1:B:66:VAL:HG23	1:B:119:ALA:HB1	1.99	0.45
1:C:174:GLU:OE1	1:H:101:VAL:HG23	2.17	0.45
1:F:174:GLU:OE1	1:G:101:VAL:HG23	2.17	0.45
1:G:13:VAL:HG12	1:G:13:VAL:O	2.16	0.45
1:A:142:MET:HE1	1:A:222:VAL:HG11	1.99	0.45
1:H:67:THR:O	1:H:69:PRO:HD3	2.17	0.45
1:B:218:GLU:N	1:B:221:GLU:OE1	2.47	0.44
1:D:52:ILE:HD12	1:D:59:ALA:CB	2.47	0.44
1:D:66:VAL:HG23	1:D:119:ALA:HB1	2.00	0.44
1:E:170:ASN:O	1:E:171:ALA:C	2.61	0.44
1:B:96:GLY:HA3	1:B:112:VAL:CG2	2.47	0.44
1:D:64:GLY:HA3	1:D:71:PHE:CE1	2.53	0.44
1:H:39:ASP:OD1	1:H:40:LEU:N	2.49	0.44
1:H:70:ALA:O	1:H:73:GLU:HB2	2.17	0.44
1:D:9:ARG:HD3	1:D:86:LYS:HB2	1.99	0.44
1:G:39:ASP:OD1	1:G:40:LEU:N	2.50	0.44
1:D:112:VAL:O	1:D:116:ASN:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:193:PRO:HA	1:E:196:GLU:HG3	1.99	0.44
1:G:187:PRO:HA	1:G:244:VAL:HG13	2.00	0.44
1:F:178:ASP:OD2	1:G:100:ARG:NH2	2.47	0.44
1:A:85:LEU:HG	1:A:131:MET:HE2	2.00	0.44
1:F:36:LEU:HD12	5:F:402:HOH:O	2.16	0.44
1:F:120:VAL:O	1:F:124:MET:HG3	2.17	0.44
1:A:86:LYS:O	1:A:87:ILE:HG13	2.18	0.43
1:C:42:GLU:CB	1:C:63:ALA:HB2	2.48	0.43
1:F:45:ALA:O	1:F:49:VAL:HG23	2.18	0.43
1:B:152:ALA:O	1:B:153:ASN:HB2	2.18	0.43
1:D:39:ASP:O	1:D:63:ALA:HA	2.18	0.43
1:D:148:LEU:HG	1:D:241:TYR:HE2	1.83	0.43
3:G:302:NAD:O7N	3:G:302:NAD:O1N	2.36	0.43
1:A:29:ALA:HB1	1:A:52:ILE:HG23	1.99	0.43
1:B:191:ARG:HG3	1:B:216:LEU:CB	2.47	0.43
1:C:96:GLY:HA3	1:C:112:VAL:HG21	2.01	0.43
1:G:114:GLU:OE1	1:G:122:TYR:OH	2.29	0.43
1:A:120:VAL:O	1:A:124:MET:HG3	2.18	0.43
1:B:85:LEU:O	1:B:134:ASN:OD1	2.37	0.43
2:H:301:IPA:H32	3:H:302:NAD:H71N	1.83	0.43
1:B:48:VAL:O	1:B:49:VAL:C	2.62	0.43
1:B:171:ALA:HB1	1:B:182:VAL:HG21	2.00	0.43
1:G:41:ASN:CG	1:G:44:HIS:CG	2.96	0.43
1:H:192:THR:O	1:H:196:GLU:HG3	2.18	0.43
1:C:14:THR:HA	1:C:38:THR:OG1	2.19	0.43
1:C:125:GLN:HB2	1:C:126:PRO:CD	2.48	0.43
1:A:83:ALA:O	1:A:84:PRO:C	2.62	0.42
2:G:301:IPA:H2	3:G:302:NAD:C4N	2.48	0.42
1:F:66:VAL:HG23	1:F:119:ALA:HB1	2.01	0.42
1:H:14:THR:O	1:H:91:ASN:HB3	2.19	0.42
1:C:91:ASN:HA	1:C:142:MET:CB	2.49	0.42
1:B:25:ALA:HB1	1:B:35:VAL:HG11	2.02	0.42
1:D:49:VAL:O	1:D:49:VAL:HG12	2.19	0.42
1:D:187:PRO:HA	1:D:244:VAL:HG13	1.99	0.42
1:F:125:GLN:HB2	1:F:126:PRO:HD3	2.01	0.42
1:H:116:ASN:N	1:H:116:ASN:HD22	2.17	0.42
1:A:142:MET:HE3	1:A:187:PRO:HG2	1.96	0.42
1:F:189:PHE:CD2	2:F:301:IPA:H31	2.54	0.42
1:F:142:MET:CE	1:F:187:PRO:CD	2.97	0.42
1:G:129:LYS:O	1:G:133:ALA:HB2	2.19	0.42
1:H:49:VAL:O	1:H:52:ILE:HB	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:301:IPA:H32	3:A:302:NAD:C7N	2.49	0.42
1:H:20:ILE:O	1:H:24:VAL:HG23	2.20	0.42
1:A:66:VAL:HG22	3:A:302:NAD:N1A	2.35	0.42
1:B:41:ASN:OD1	1:B:44:HIS:CD2	2.73	0.42
1:B:42:GLU:CA	1:B:63:ALA:CB	2.96	0.42
1:C:160:ALA:O	1:C:163:ALA:HB3	2.20	0.42
1:F:38:THR:HA	1:F:62:LEU:O	2.20	0.42
1:A:42:GLU:HA	1:A:63:ALA:HB2	2.02	0.41
1:C:116:ASN:HD22	1:C:116:ASN:N	2.18	0.41
1:F:142:MET:HE3	1:F:187:PRO:HD3	2.01	0.41
1:G:91:ASN:O	3:G:302:NAD:C4D	2.66	0.41
1:C:178:ASP:N	1:C:178:ASP:OD1	2.53	0.41
1:D:125:GLN:HB2	1:D:126:PRO:CD	2.49	0.41
1:D:10:SER:HA	1:D:34:ALA:O	2.20	0.41
1:F:148:LEU:HD12	1:F:148:LEU:O	2.20	0.41
1:A:213:LEU:HA	1:D:176:ALA:HB1	2.02	0.41
1:D:169:GLN:OE1	1:E:162:HIS:NE2	2.51	0.41
1:B:11:ALA:HA	1:B:87:ILE:O	2.20	0.41
1:B:40:LEU:HA	1:B:64:GLY:O	2.20	0.41
1:B:115:VAL:O	1:B:119:ALA:HB3	2.20	0.41
1:F:143:ALA:N	1:F:185:VAL:O	2.46	0.41
1:G:169:GLN:O	1:G:173:LEU:HG	2.20	0.41
1:A:91:ASN:O	3:A:302:NAD:H4D	2.20	0.41
1:A:174:GLU:OE1	1:B:101:VAL:HG23	2.19	0.41
1:C:68:ASP:OD1	1:C:68:ASP:C	2.64	0.41
1:C:225:LEU:HA	1:F:228:PHE:CZ	2.56	0.41
1:E:79:ALA:CB	1:E:85:LEU:HD13	2.51	0.41
1:G:144:SER:OG	2:G:301:IPA:O2	2.34	0.41
1:D:148:LEU:HG	1:D:241:TYR:CE2	2.56	0.41
1:F:109:TRP:CE3	1:F:156:ALA:HB2	2.56	0.41
1:C:148:LEU:CD1	1:C:241:TYR:CE2	2.93	0.40
1:G:96:GLY:HA3	1:G:112:VAL:HG21	2.02	0.40
1:A:125:GLN:HB2	1:A:126:PRO:HD3	2.03	0.40
1:A:192:THR:O	1:A:194:LEU:N	2.53	0.40
1:D:25:ALA:HB1	1:D:35:VAL:HG11	2.03	0.40
1:F:168:THR:HG23	1:F:182:VAL:HG12	2.03	0.40
1:H:65:ASP:OD1	3:H:302:NAD:N6A	2.50	0.40
1:H:112:VAL:O	1:H:116:ASN:HB2	2.22	0.40
1:C:204:LEU:O	1:C:208:GLU:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	249/251 (99%)	232 (93%)	17 (7%)	0	100	100
1	B	249/251 (99%)	226 (91%)	23 (9%)	0	100	100
1	C	249/251 (99%)	239 (96%)	10 (4%)	0	100	100
1	D	249/251 (99%)	234 (94%)	15 (6%)	0	100	100
1	E	249/251 (99%)	233 (94%)	16 (6%)	0	100	100
1	F	248/251 (99%)	230 (93%)	18 (7%)	0	100	100
1	G	249/251 (99%)	230 (92%)	19 (8%)	0	100	100
1	H	249/251 (99%)	233 (94%)	16 (6%)	0	100	100
All	All	1991/2008 (99%)	1857 (93%)	134 (7%)	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	160/167 (96%)	154 (96%)	6 (4%)	29	62
1	B	160/167 (96%)	150 (94%)	10 (6%)	16	43
1	C	161/167 (96%)	158 (98%)	3 (2%)	50	79
1	D	159/167 (95%)	152 (96%)	7 (4%)	25	58
1	E	158/167 (95%)	149 (94%)	9 (6%)	18	47
1	F	160/167 (96%)	152 (95%)	8 (5%)	22	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	159/167 (95%)	150 (94%)	9 (6%)	18	47
1	H	158/167 (95%)	152 (96%)	6 (4%)	29	62
All	All	1275/1336 (95%)	1217 (96%)	58 (4%)	24	57

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	148	LEU
1	A	170	ASN
1	A	194	LEU
1	A	216	LEU
1	A	224	SER
1	B	18	SER
1	B	91	ASN
1	B	100	ARG
1	B	134	ASN
1	B	145	ILE
1	B	148	LEU
1	B	155	SER
1	B	170	ASN
1	B	204	LEU
1	B	244	VAL
1	C	51	GLU
1	C	148	LEU
1	C	170	ASN
1	D	38	THR
1	D	41	ASN
1	D	116	ASN
1	D	148	LEU
1	D	155	SER
1	D	170	ASN
1	D	244	VAL
1	E	38	THR
1	E	41	ASN
1	E	100	ARG
1	E	170	ASN
1	E	193	PRO
1	E	204	LEU
1	E	224	SER
1	E	240	SER

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Mol	Chain	Res	Type
1	E	244	VAL
1	F	41	ASN
1	F	103	ASP
1	F	105	SER
1	F	148	LEU
1	F	155	SER
1	F	170	ASN
1	F	216	LEU
1	F	244	VAL
1	G	18	SER
1	G	41	ASN
1	G	91	ASN
1	G	100	ARG
1	G	170	ASN
1	G	194	LEU
1	G	204	LEU
1	G	216	LEU
1	G	244	VAL
1	H	91	ASN
1	H	148	LEU
1	H	170	ASN
1	H	204	LEU
1	H	240	SER
1	H	244	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	116	ASN
1	B	46	GLN
1	B	91	ASN
1	B	116	ASN
1	C	41	ASN
1	C	90	ASN
1	C	116	ASN
1	C	127	GLN
1	D	44	HIS
1	D	116	ASN
1	E	41	ASN
1	E	116	ASN
1	E	153	ASN

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Mol	Chain	Res	Type
1	F	116	ASN
1	G	91	ASN
1	G	116	ASN
1	H	90	ASN
1	H	116	ASN
1	H	127	GLN
1	H	141	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 34 ligands modelled in this entry, 18 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	$\# Z > 2$
2	IPA	E	301	-	3,3,3	0.25	0	3,3,3	0.10	0
3	NAD	G	302	-	46,48,48	0.81	2 (4%)	64,73,73	0.62	1 (1%)
2	IPA	A	301	-	3,3,3	0.29	0	3,3,3	0.22	0
2	IPA	B	301	-	3,3,3	0.22	0	3,3,3	0.20	0
3	NAD	H	302	-	46,48,48	0.73	1 (2%)	64,73,73	0.77	1 (1%)
2	IPA	F	301	-	3,3,3	0.11	0	3,3,3	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	IPA	C	301	-	3,3,3	0.20	0	3,3,3	0.29	0
2	IPA	D	301	-	3,3,3	0.24	0	3,3,3	0.31	0
2	IPA	G	301	-	3,3,3	0.24	0	3,3,3	0.24	0
2	IPA	H	301	-	3,3,3	0.26	0	3,3,3	0.08	0
3	NAD	A	302	-	46,48,48	0.64	1 (2%)	64,73,73	0.69	1 (1%)
3	NAD	E	302	-	46,48,48	0.66	1 (2%)	64,73,73	0.68	1 (1%)
3	NAD	F	302	-	46,48,48	0.74	1 (2%)	64,73,73	0.69	2 (3%)
3	NAD	C	302	-	46,48,48	0.81	1 (2%)	64,73,73	0.61	1 (1%)
3	NAD	B	302	-	46,48,48	0.77	1 (2%)	64,73,73	0.61	1 (1%)
3	NAD	D	302	-	46,48,48	0.79	2 (4%)	64,73,73	0.71	1 (1%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAD	G	302	-	-	7/30/62/62	0/5/5/5
3	NAD	H	302	-	-	8/30/62/62	0/5/5/5
3	NAD	A	302	-	-	3/30/62/62	0/5/5/5
3	NAD	E	302	-	-	9/30/62/62	0/5/5/5
3	NAD	F	302	-	-	6/30/62/62	0/5/5/5
3	NAD	C	302	-	-	7/30/62/62	0/5/5/5
3	NAD	B	302	-	-	6/30/62/62	0/5/5/5
3	NAD	D	302	-	-	6/30/62/62	0/5/5/5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	302	NAD	C2N-N1N	3.73	1.39	1.35
3	C	302	NAD	C2N-N1N	3.69	1.39	1.35
3	H	302	NAD	C2N-N1N	3.68	1.39	1.35
3	F	302	NAD	C2N-N1N	3.59	1.38	1.35
3	B	302	NAD	C2N-N1N	3.51	1.38	1.35
3	D	302	NAD	C2N-N1N	3.34	1.38	1.35
3	E	302	NAD	C2N-N1N	3.24	1.38	1.35
3	A	302	NAD	C2N-N1N	2.77	1.38	1.35
3	G	302	NAD	PN-O3	2.06	1.61	1.59
3	D	302	NAD	PA-O3	2.04	1.61	1.59

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	302	NAD	C6N-N1N-C2N	-3.40	118.99	121.88
3	G	302	NAD	C6N-N1N-C2N	-2.77	119.52	121.88
3	E	302	NAD	C6N-N1N-C2N	-2.58	119.68	121.88
3	B	302	NAD	C6N-N1N-C2N	-2.41	119.83	121.88
3	C	302	NAD	C6N-N1N-C2N	-2.38	119.85	121.88
3	F	302	NAD	C6N-N1N-C2N	-2.30	119.92	121.88
3	A	302	NAD	C6N-N1N-C2N	-2.26	119.96	121.88
3	D	302	NAD	O4B-C1B-N9A	2.20	112.31	108.09
3	F	302	NAD	O4B-C1B-N9A	2.12	112.17	108.09

There are no chirality outliers.

All (52) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	NAD	O4D-C1D-N1N-C2N
3	B	302	NAD	C5D-O5D-PN-O3
3	B	302	NAD	C5D-O5D-PN-O1N
3	B	302	NAD	C5D-O5D-PN-O2N
3	B	302	NAD	O4D-C1D-N1N-C2N
3	C	302	NAD	C5D-O5D-PN-O3
3	C	302	NAD	C5D-O5D-PN-O1N
3	C	302	NAD	C5D-O5D-PN-O2N
3	C	302	NAD	O4D-C1D-N1N-C2N
3	C	302	NAD	O4D-C1D-N1N-C6N
3	D	302	NAD	C5D-O5D-PN-O3
3	D	302	NAD	C5D-O5D-PN-O2N
3	D	302	NAD	O4D-C1D-N1N-C2N
3	E	302	NAD	C5D-O5D-PN-O3
3	E	302	NAD	C5D-O5D-PN-O1N
3	E	302	NAD	C5D-O5D-PN-O2N
3	E	302	NAD	O4D-C1D-N1N-C2N
3	E	302	NAD	O4D-C1D-N1N-C6N
3	F	302	NAD	C5D-O5D-PN-O3
3	F	302	NAD	C5D-O5D-PN-O1N
3	F	302	NAD	C5D-O5D-PN-O2N
3	F	302	NAD	O4D-C1D-N1N-C2N
3	G	302	NAD	C5D-O5D-PN-O3
3	G	302	NAD	C5D-O5D-PN-O2N
3	G	302	NAD	O4D-C1D-N1N-C2N
3	H	302	NAD	PN-O3-PA-O5B
3	H	302	NAD	C5D-O5D-PN-O3

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Mol	Chain	Res	Type	Atoms
3	H	302	NAD	C5D-O5D-PN-O1N
3	H	302	NAD	C5D-O5D-PN-O2N
3	H	302	NAD	O4D-C1D-N1N-C2N
3	E	302	NAD	PN-O3-PA-O5B
3	H	302	NAD	PA-O3-PN-O2N
3	D	302	NAD	C5D-O5D-PN-O1N
3	G	302	NAD	C5D-O5D-PN-O1N
3	B	302	NAD	PA-O3-PN-O2N
3	D	302	NAD	PA-O3-PN-O2N
3	E	302	NAD	PA-O3-PN-O2N
3	C	302	NAD	C2D-C1D-N1N-C6N
3	E	302	NAD	C2D-C1D-N1N-C6N
3	A	302	NAD	O4D-C1D-N1N-C6N
3	B	302	NAD	O4D-C1D-N1N-C6N
3	D	302	NAD	O4D-C1D-N1N-C6N
3	F	302	NAD	O4D-C1D-N1N-C6N
3	G	302	NAD	O4D-C1D-N1N-C6N
3	H	302	NAD	O4D-C1D-N1N-C6N
3	C	302	NAD	PA-O3-PN-O2N
3	G	302	NAD	PA-O3-PN-O2N
3	E	302	NAD	O4B-C4B-C5B-O5B
3	F	302	NAD	PA-O3-PN-O2N
3	H	302	NAD	PA-O3-PN-O1N
3	A	302	NAD	PN-O3-PA-O2A
3	G	302	NAD	PA-O3-PN-O1N

There are no ring outliers.

14 monomers are involved in 34 short contacts:

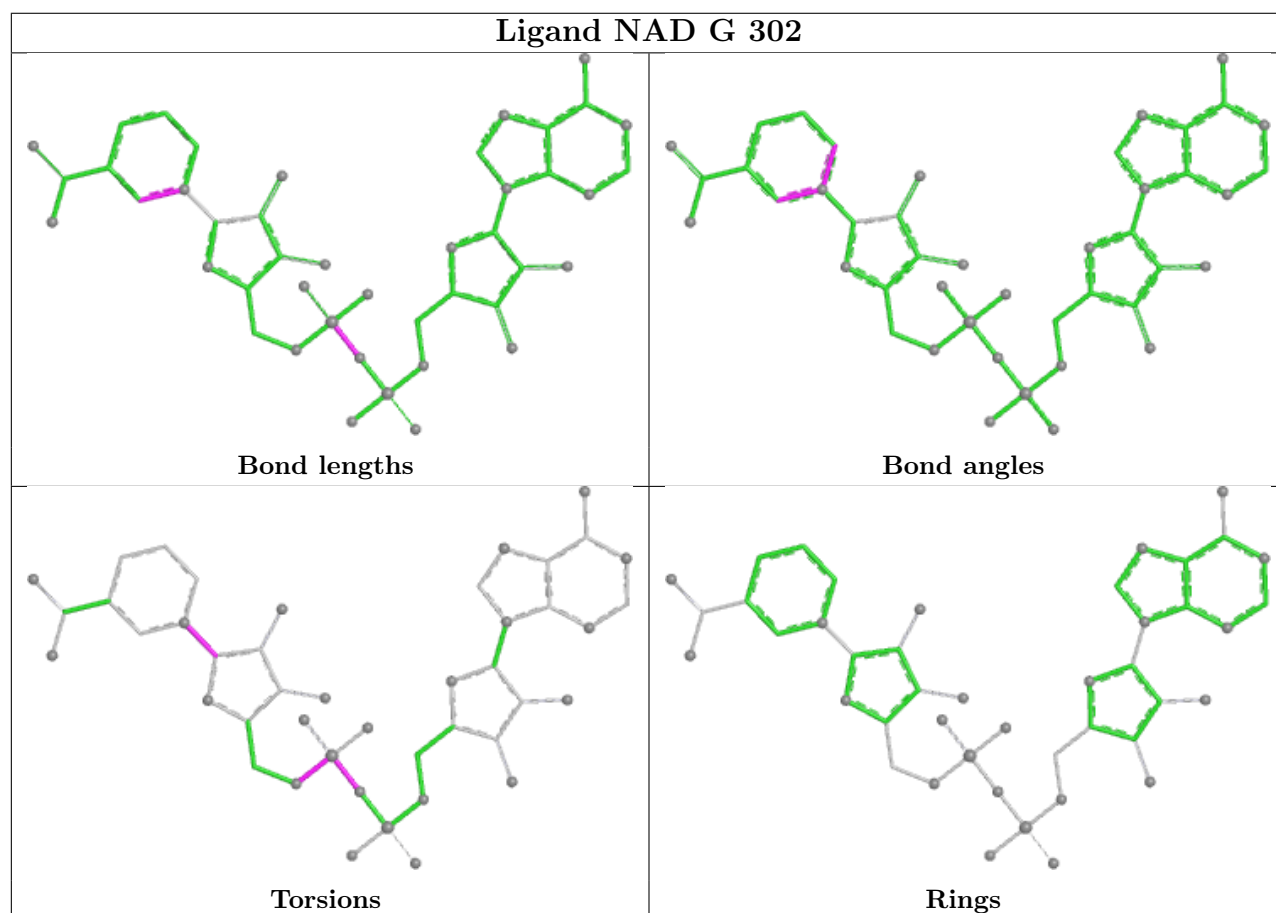
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	302	NAD	5	0
2	A	301	IPA	2	0
2	B	301	IPA	1	0
3	H	302	NAD	3	0
2	F	301	IPA	6	0
2	C	301	IPA	1	0
2	G	301	IPA	10	0
2	H	301	IPA	1	0
3	A	302	NAD	4	0
3	E	302	NAD	2	0
3	F	302	NAD	1	0
3	C	302	NAD	2	0

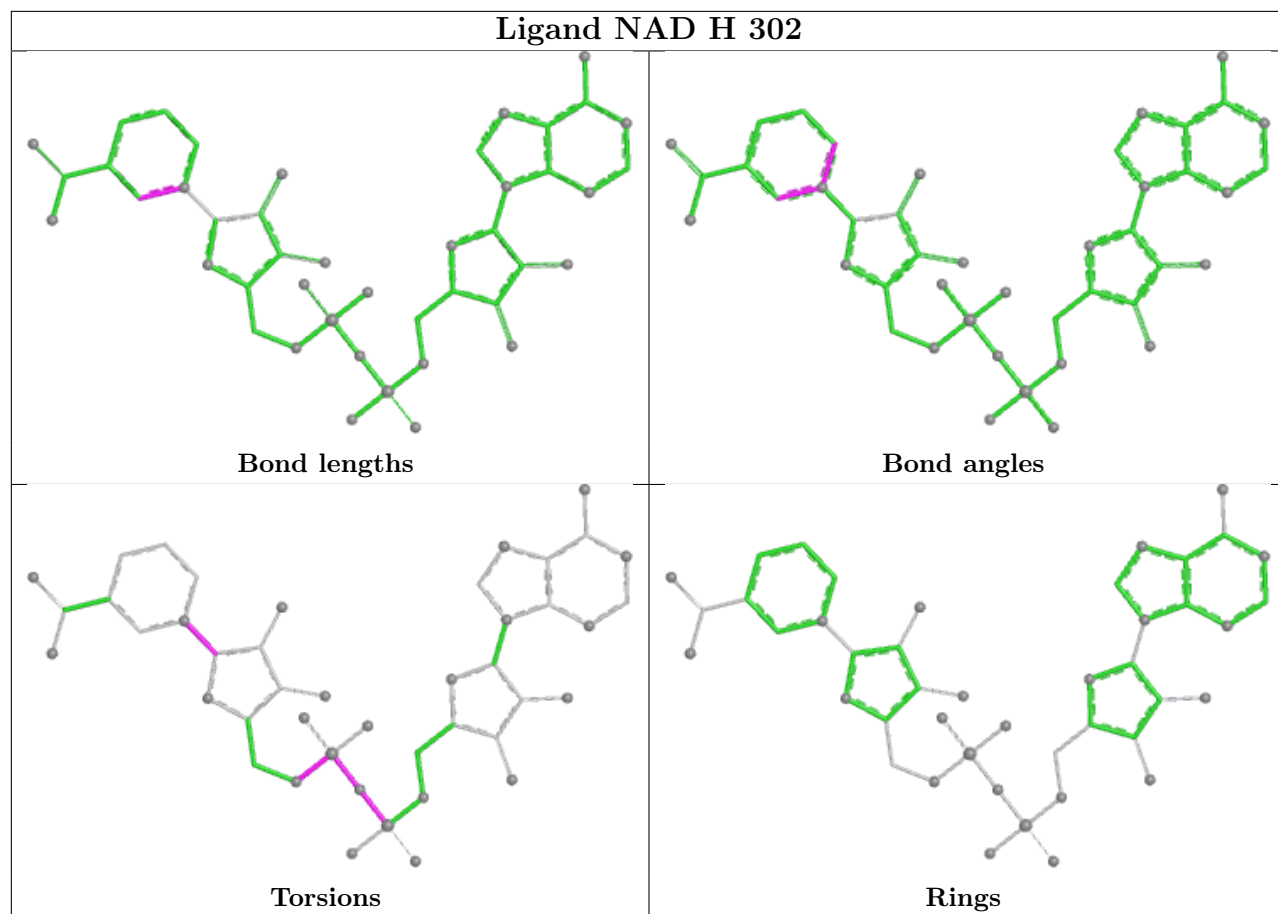
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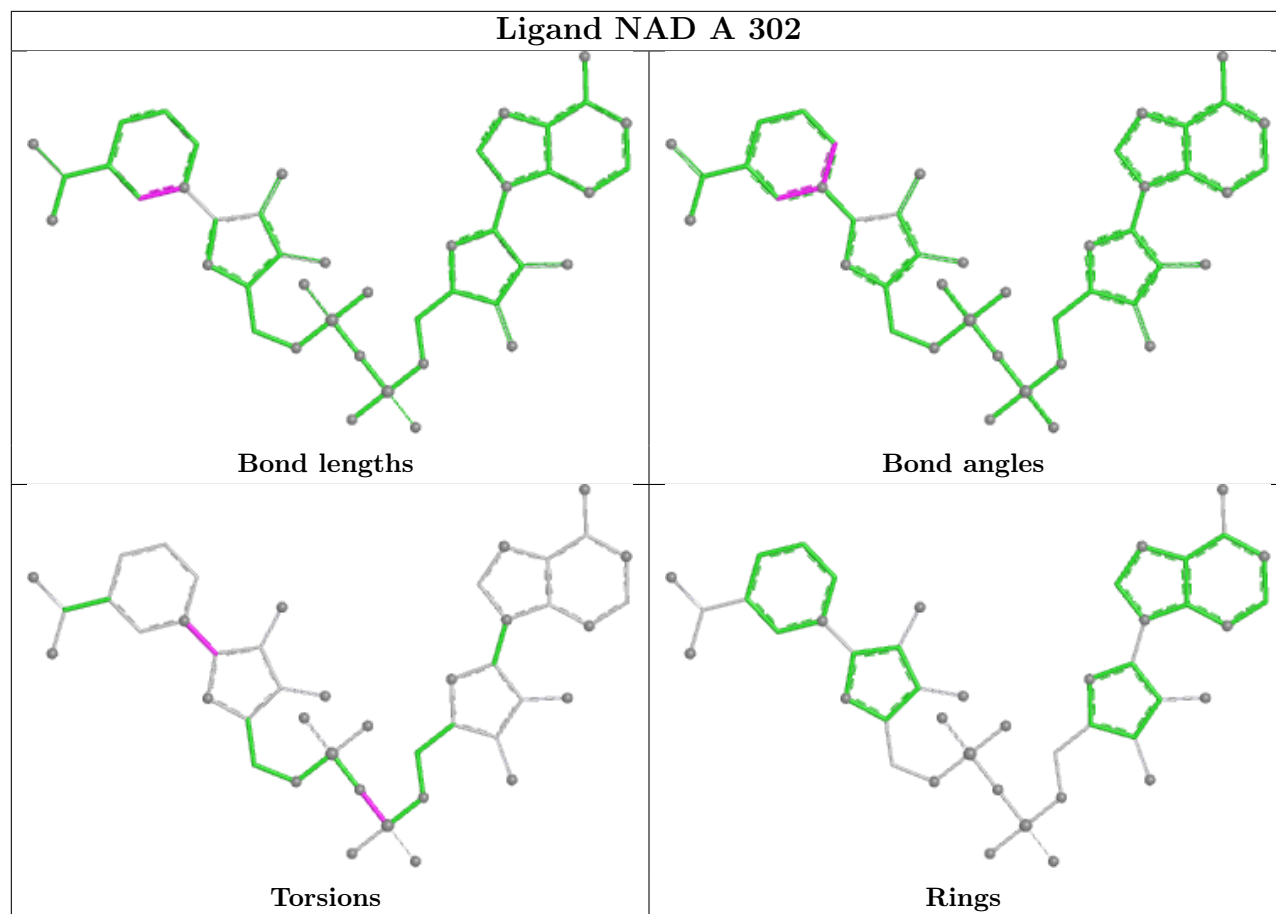
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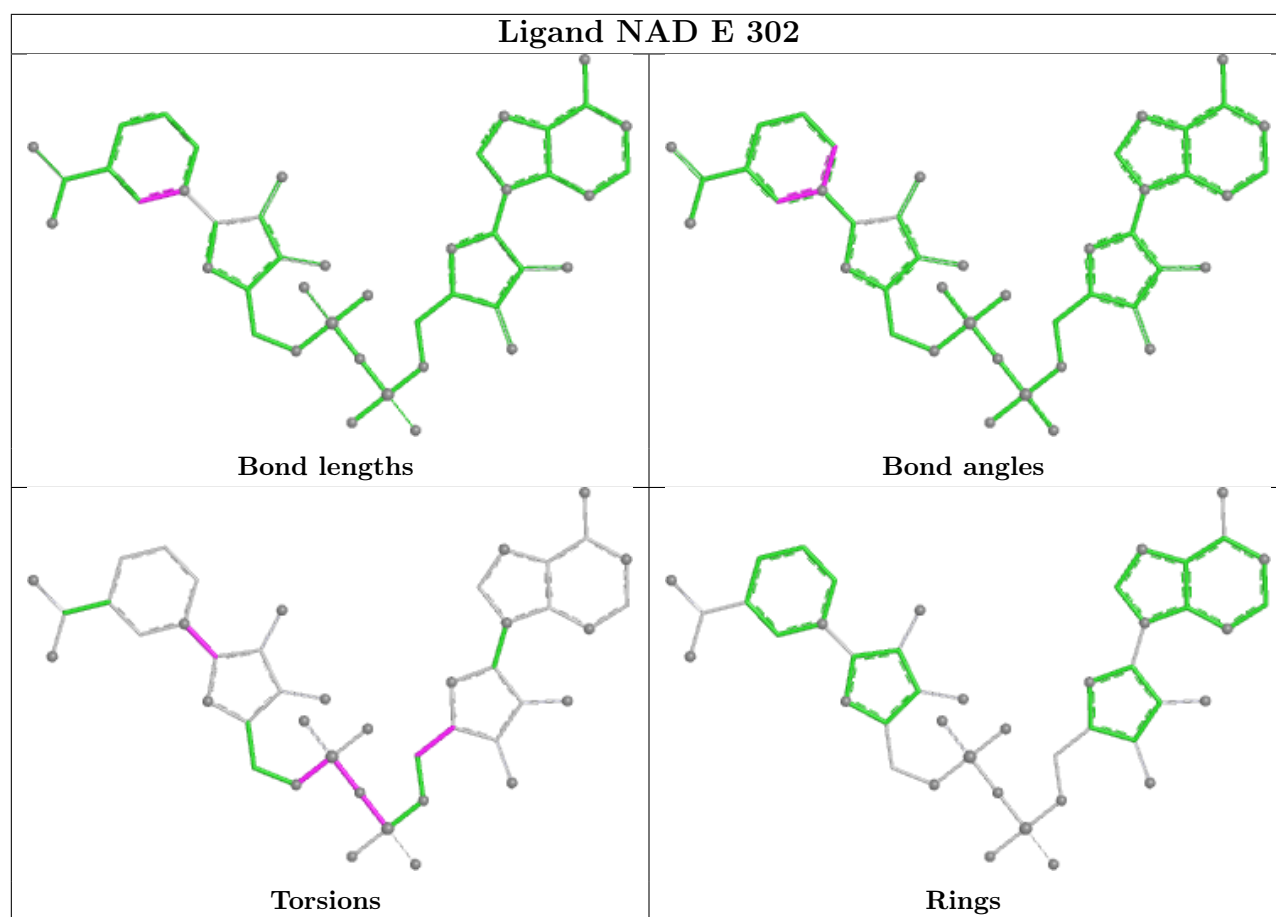
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	302	NAD	2	0
3	D	302	NAD	1	0

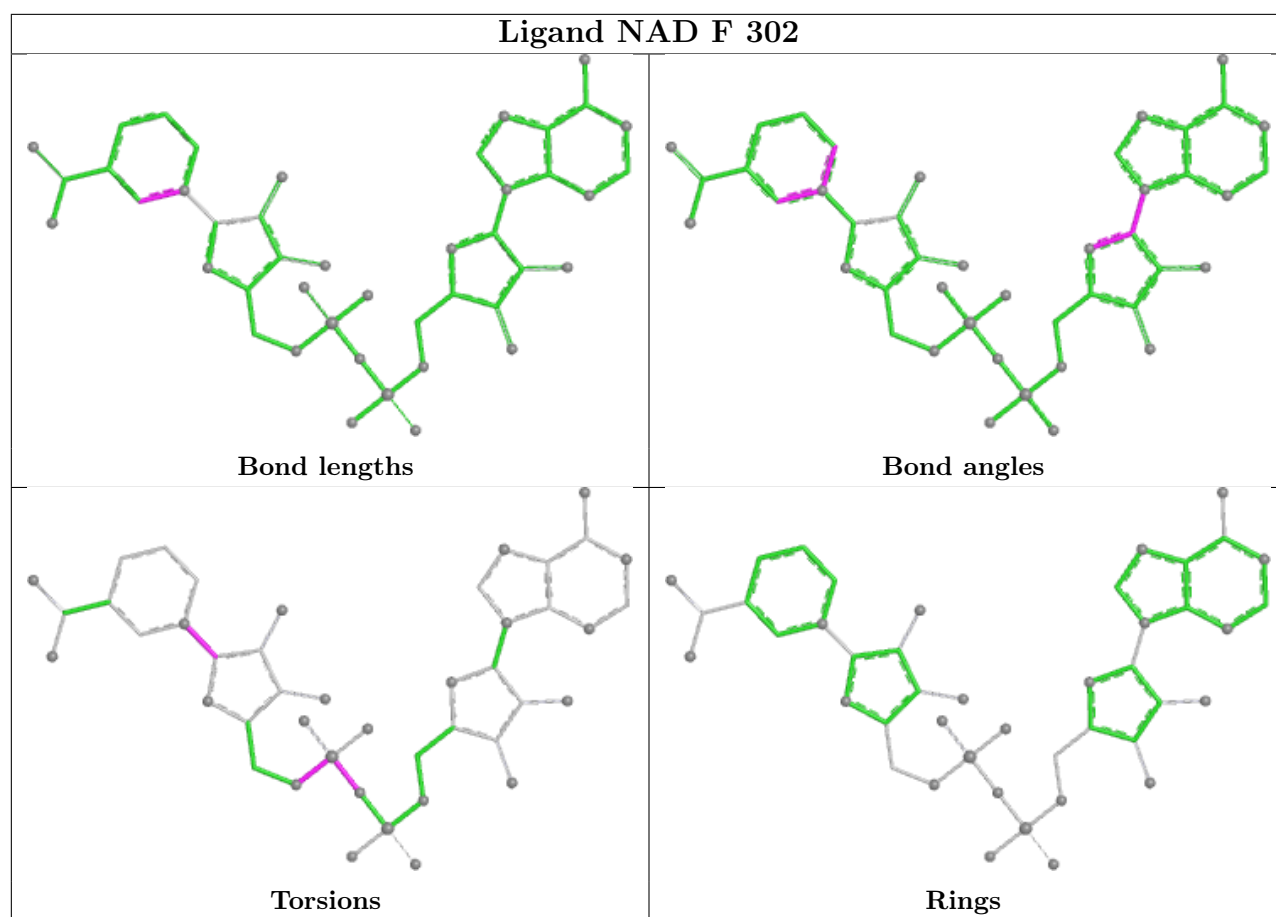
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

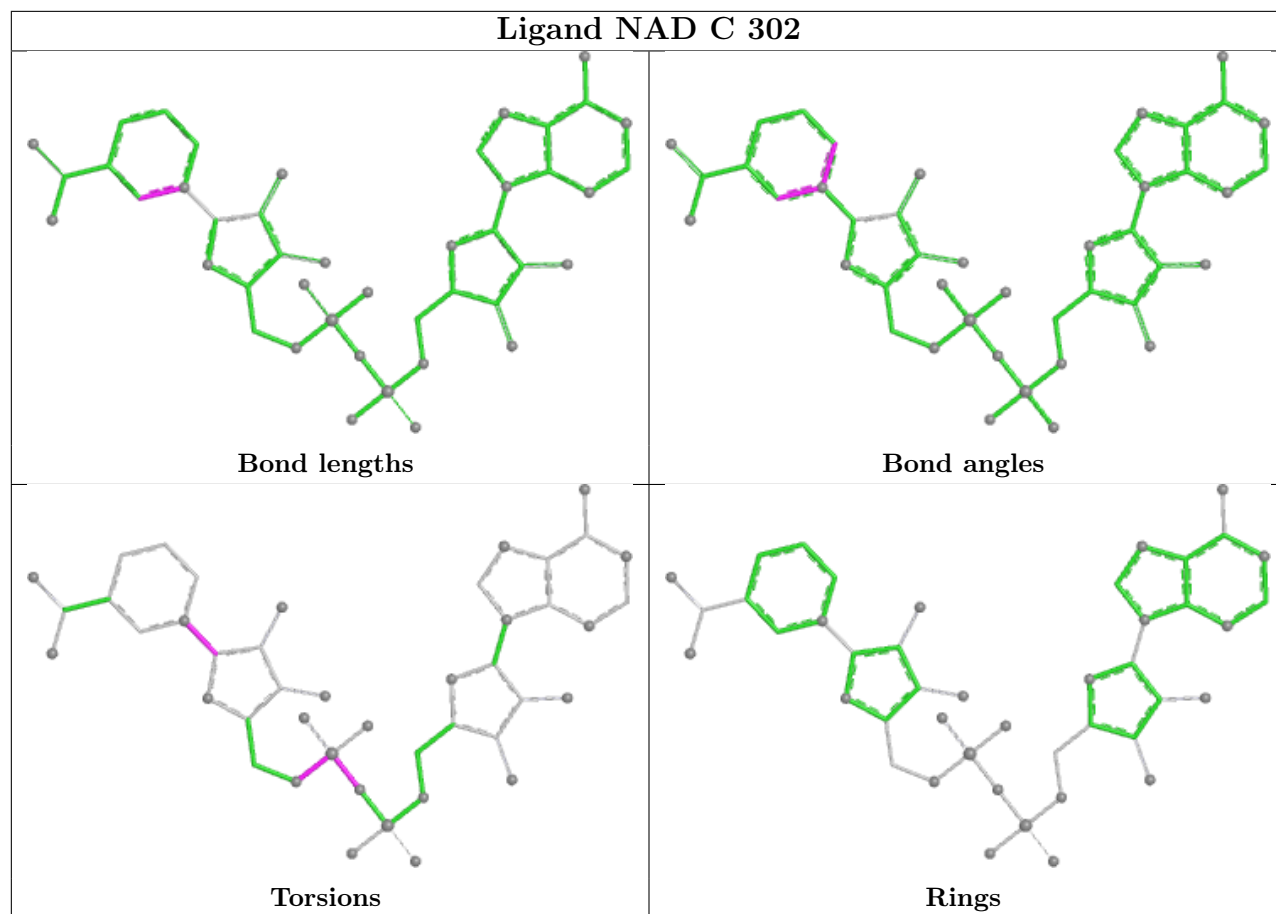


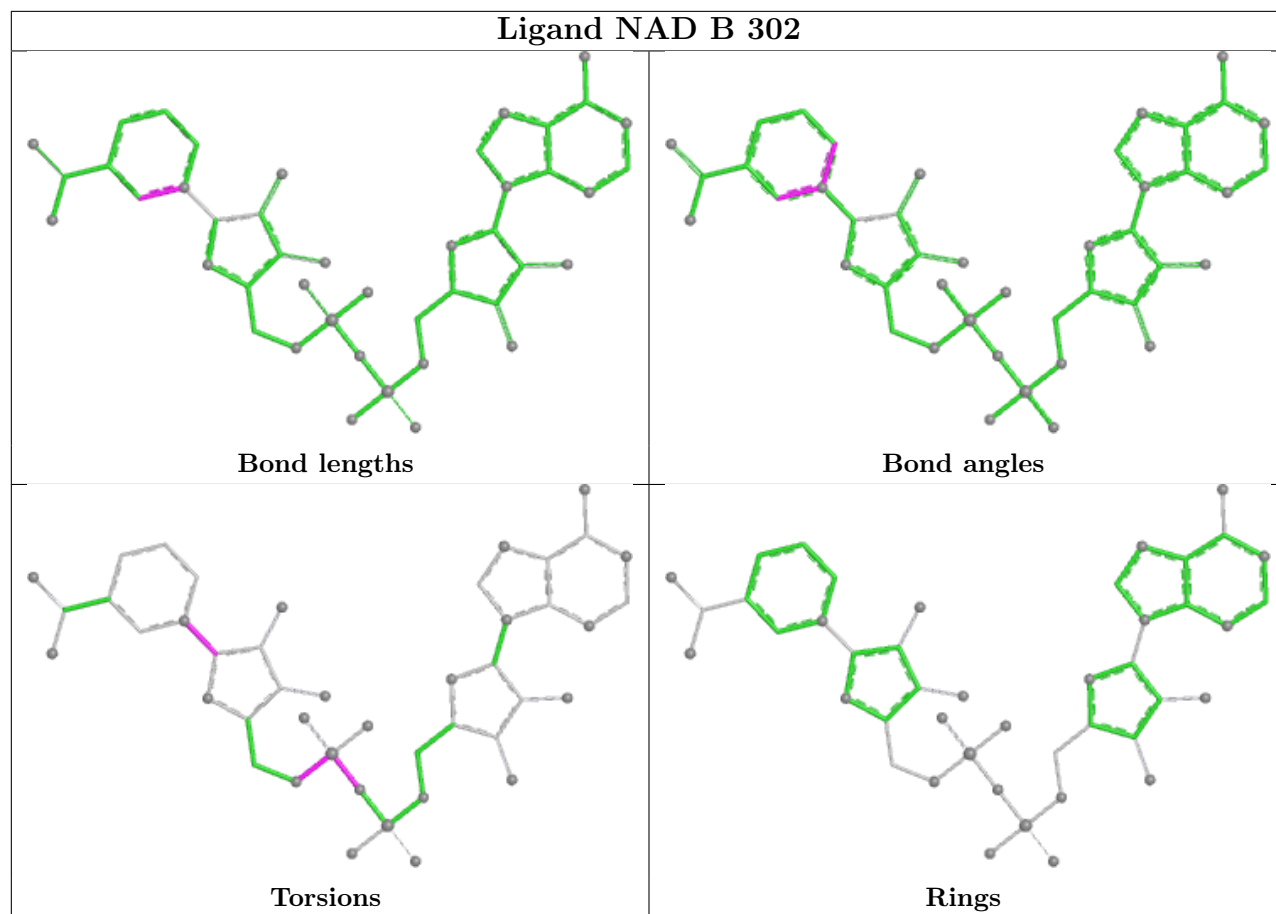


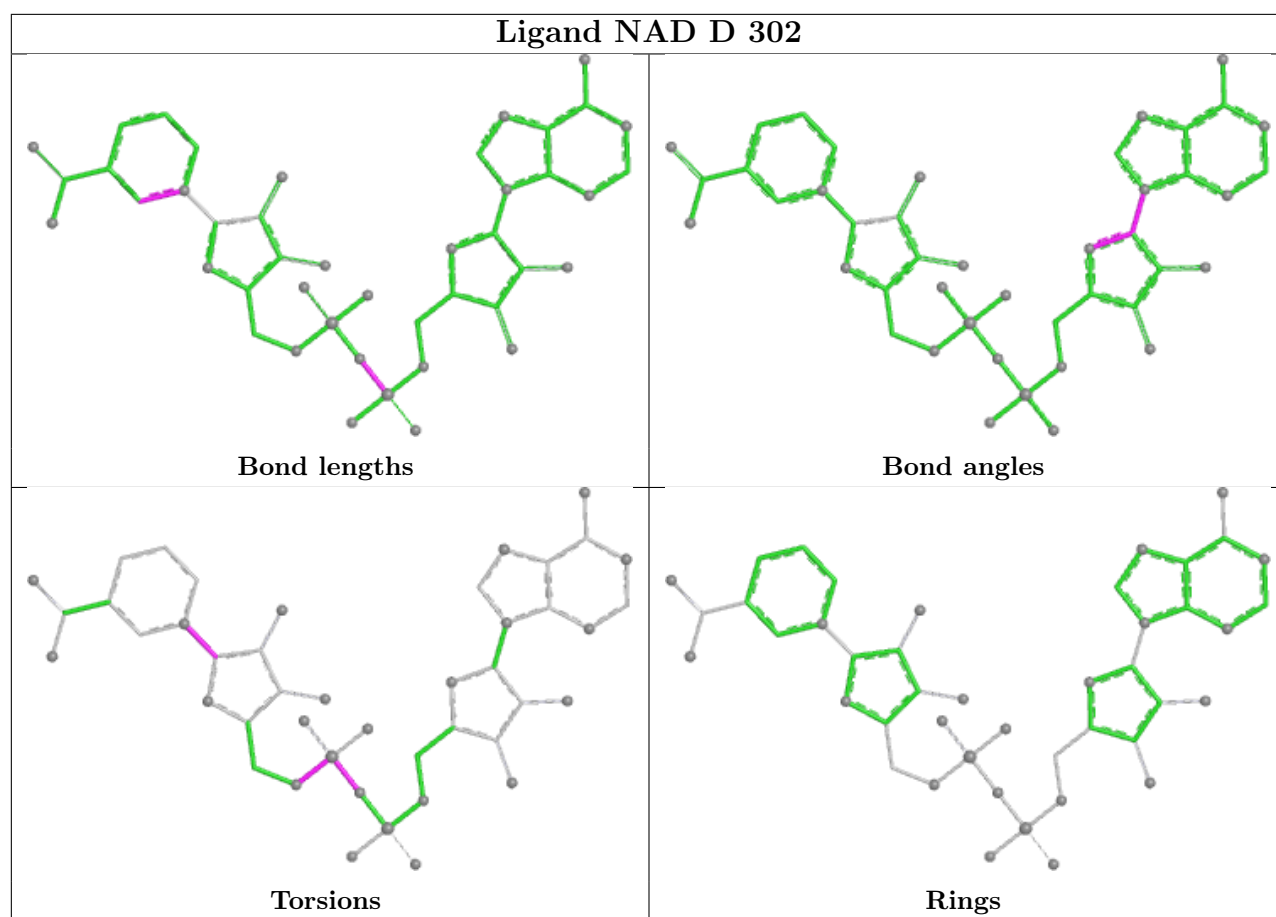












5.7 Other polymers [i](#)

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, 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	251/251 (100%)	-1.59	0 100 100	14, 29, 58, 76	1 (0%)
1	B	251/251 (100%)	-1.55	0 100 100	10, 31, 52, 74	1 (0%)
1	C	251/251 (100%)	-1.59	0 100 100	9, 30, 54, 71	1 (0%)
1	D	251/251 (100%)	-1.58	0 100 100	9, 29, 56, 75	1 (0%)
1	E	251/251 (100%)	-1.53	0 100 100	18, 32, 57, 78	1 (0%)
1	F	250/251 (99%)	-1.56	0 100 100	14, 29, 65, 93	1 (0%)
1	G	251/251 (100%)	-1.56	0 100 100	12, 32, 56, 64	1 (0%)
1	H	251/251 (100%)	-1.54	0 100 100	17, 32, 66, 95	1 (0%)
All	All	2007/2008 (99%)	-1.56	0 100 100	9, 31, 58, 95	8 (0%)

There are no RSRZ outliers to report.

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](#)

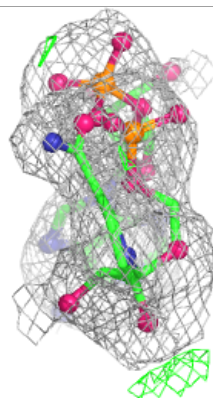
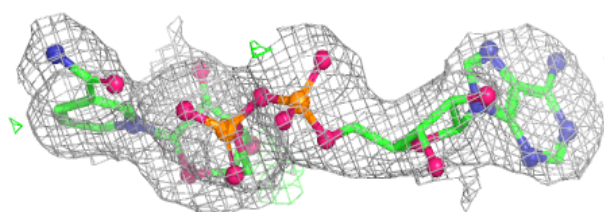
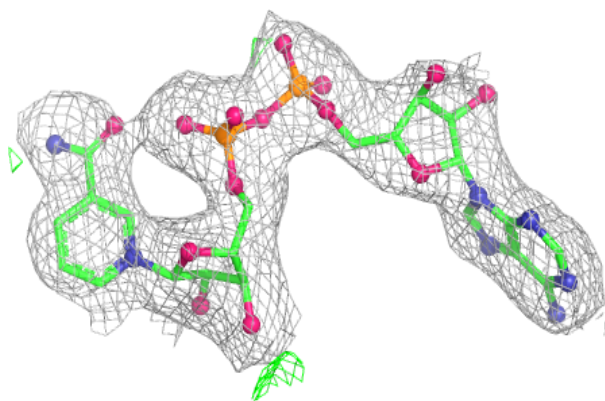
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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
4	ZN	A	305	1/1	0.96	0.04	81,81,81,81	0
2	IPA	B	301	4/4	0.99	0.04	24,26,26,27	0
2	IPA	D	301	4/4	0.99	0.06	25,26,26,26	0
2	IPA	G	301	4/4	0.99	0.04	23,24,24,24	0
3	NAD	B	302	44/44	0.99	0.02	23,29,33,35	0
3	NAD	C	302	44/44	0.99	0.02	20,26,30,31	0
3	NAD	D	302	44/44	0.99	0.03	22,28,30,31	0
3	NAD	E	302	44/44	0.99	0.03	23,32,38,43	0
3	NAD	F	302	44/44	0.99	0.03	22,28,35,37	0
3	NAD	G	302	44/44	0.99	0.03	26,34,38,41	0
3	NAD	H	302	44/44	0.99	0.03	18,28,37,45	0
4	ZN	A	303	1/1	0.99	0.02	56,56,56,56	0
4	ZN	A	304	1/1	0.99	0.01	33,33,33,33	0
2	IPA	A	301	4/4	0.99	0.03	32,33,33,34	0
4	ZN	A	306	1/1	0.99	0.01	60,60,60,60	0
4	ZN	B	304	1/1	0.99	0.02	57,57,57,57	0
4	ZN	B	305	1/1	0.99	0.02	53,53,53,53	0
4	ZN	B	306	1/1	0.99	0.02	59,59,59,59	0
4	ZN	C	304	1/1	0.99	0.02	49,49,49,49	0
4	ZN	C	306	1/1	0.99	0.02	54,54,54,54	0
4	ZN	D	303	1/1	0.99	0.02	53,53,53,53	0
4	ZN	E	303	1/1	0.99	0.01	61,61,61,61	0
4	ZN	F	304	1/1	0.99	0.03	66,66,66,66	0
4	ZN	G	303	1/1	0.99	0.02	53,53,53,53	0
4	ZN	H	303	1/1	0.99	0.01	63,63,63,63	0
3	NAD	A	302	44/44	1.00	0.02	22,28,33,35	0
4	ZN	C	305	1/1	1.00	0.01	43,43,43,43	0
2	IPA	E	301	4/4	1.00	0.03	23,24,24,24	0
4	ZN	B	303	1/1	1.00	0.01	25,25,25,25	0
2	IPA	F	301	4/4	1.00	0.03	26,27,27,28	0
4	ZN	F	303	1/1	1.00	0.01	33,33,33,33	0
2	IPA	C	301	4/4	1.00	0.03	25,25,26,26	0
2	IPA	H	301	4/4	1.00	0.04	33,34,35,35	0
4	ZN	C	303	1/1	1.00	0.02	29,29,29,29	0

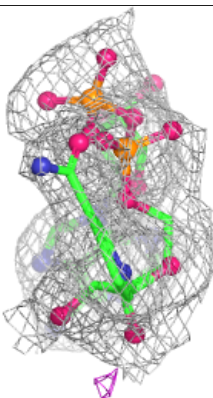
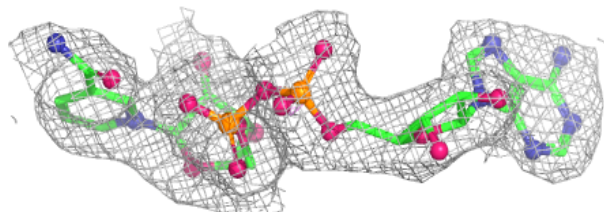
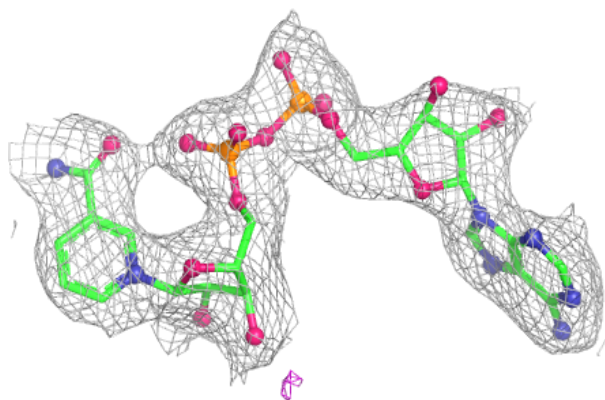
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAD B 302:

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

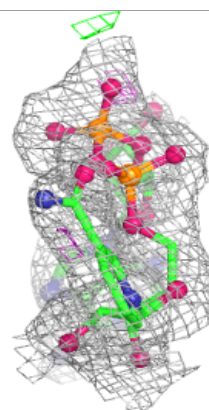
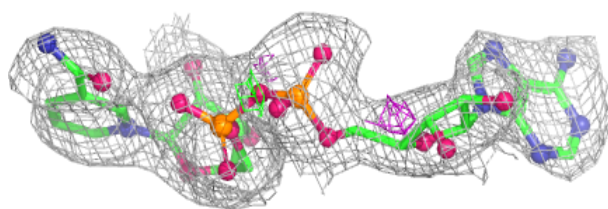
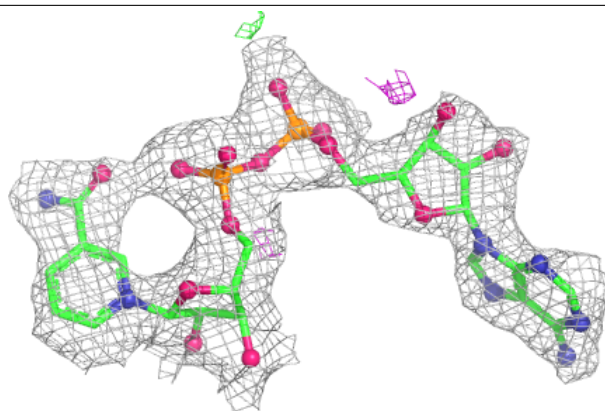
**Electron density around NAD C 302:**

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

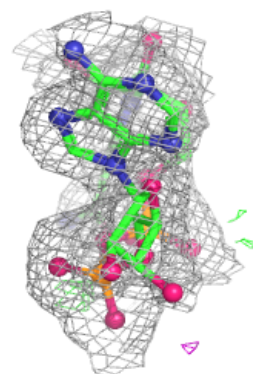
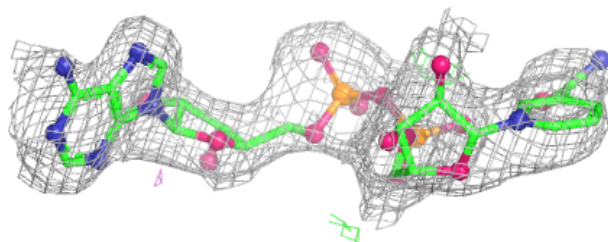
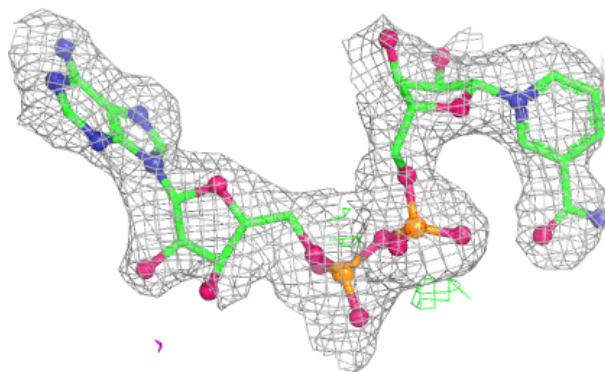


Electron density around NAD D 302:

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

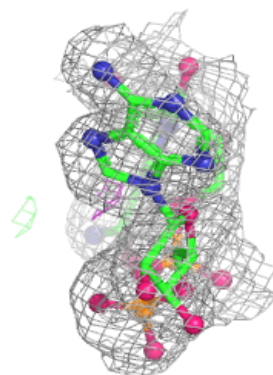
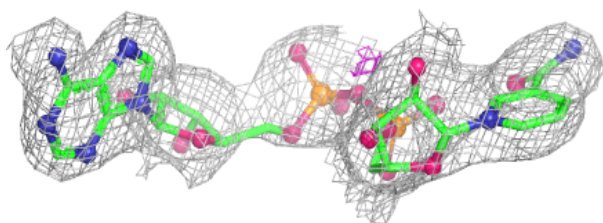
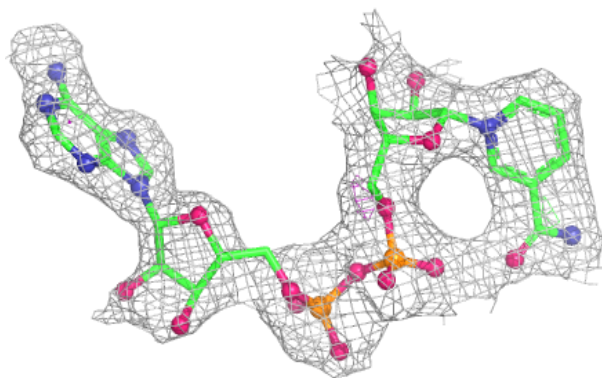
**Electron density around NAD E 302:**

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

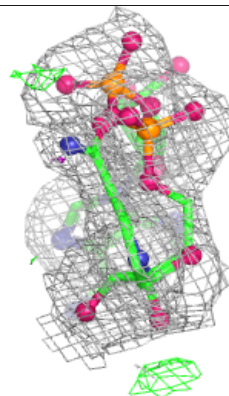
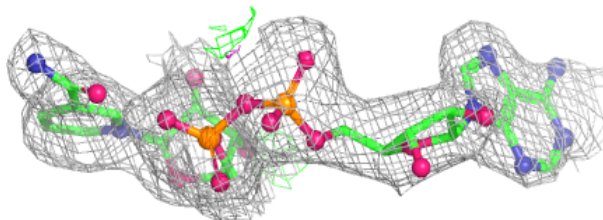
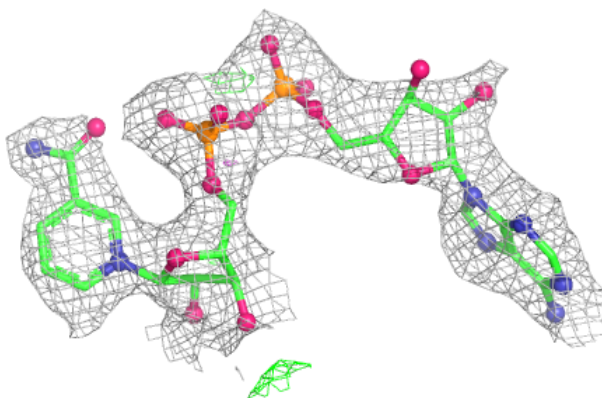


Electron density around NAD F 302:

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

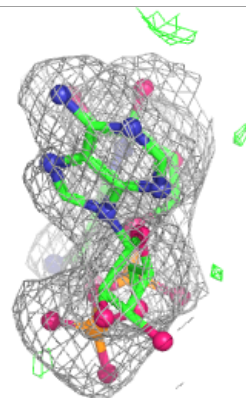
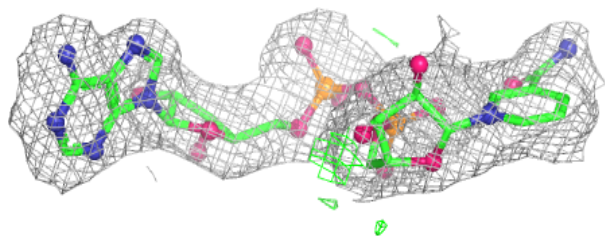
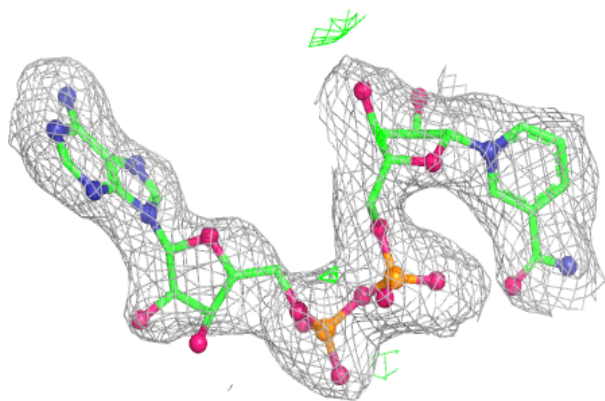
**Electron density around NAD G 302:**

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

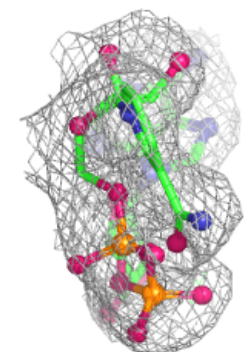
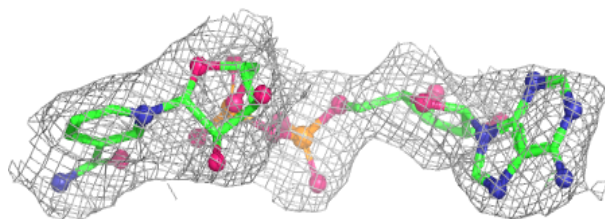
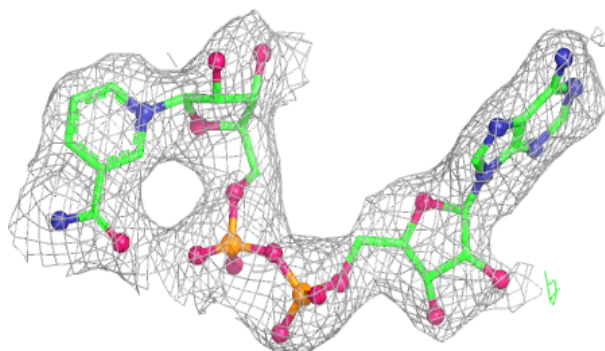


Electron density around NAD H 302:

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

**Electron density around NAD A 302:**

$2mF_o-DF_c$ (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.