



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:54 PM UTC

PDB ID : 2C8C / pdb_00002c8c
Title : Structure of the ARTT motif Q212A mutant C3bot1 Exoenzyme (NAD-bound state, crystal form I)
Authors : Stura, E.A.; Menetrey, J.; Flatau, G.; Boquet, P.; Menez, A.
Deposited on : 2005-12-03
Resolution : 2.70 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

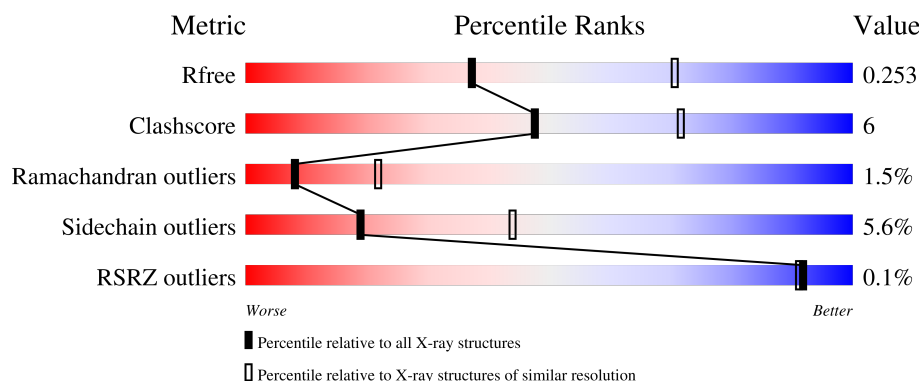
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	211	
1	B	211	
1	C	211	
1	D	211	

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	NAD	B	1248	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6581 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.

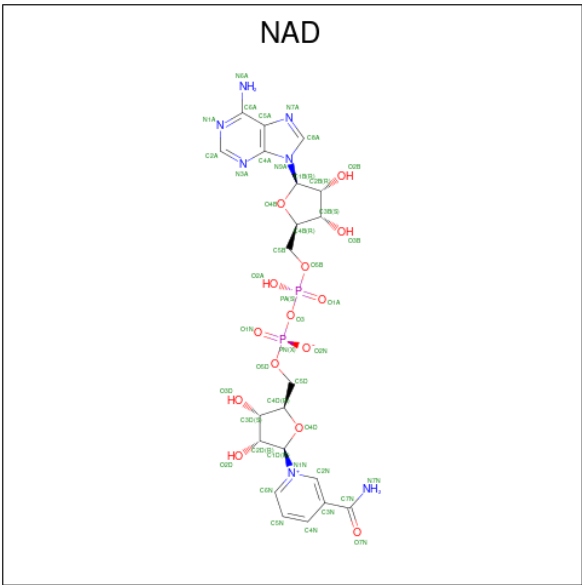
- Molecule 1 is a protein called MONO-ADP-RIBOSYLTRANSFERASE C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	1
			1595	1014	272	302	7			
1	B	205	Total	C	N	O	S	0	0	0
			1604	1018	273	306	7			
1	C	208	Total	C	N	O	S	0	0	0
			1630	1036	278	309	7			
1	D	204	Total	C	N	O	S	0	0	1
			1593	1012	272	302	7			

There are 4 discrepancies between the modelled and reference sequences:

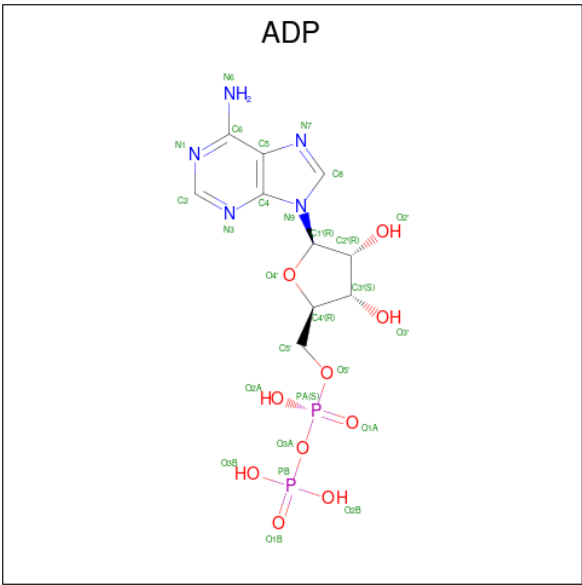
Chain	Residue	Modelled	Actual	Comment	Reference
A	212	ALA	GLN	engineered mutation	UNP P15879
B	212	ALA	GLN	engineered mutation	UNP P15879
C	212	ALA	GLN	engineered mutation	UNP P15879
D	212	ALA	GLN	engineered mutation	UNP P15879

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



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

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

Y223	Y224	G245	T246	K247	ILE	ASN	PRO	LYS
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4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	106.05Å 76.14Å 120.43Å 90.00° 102.74° 90.00°	Depositor
Resolution (Å)	39.84 – 2.70 39.84 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (39.84-2.70) 95.7 (39.84-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.241 , 0.283 0.211 , 0.253	Depositor DCC
R_{free} test set	1262 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	60.7	Xtriage
Anisotropy	0.671	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 13.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6581	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% 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, ADP

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	0.99	2/1623 (0.1%)	1.02	0/2180
1	B	0.95	1/1632 (0.1%)	1.05	1/2192 (0.0%)
1	C	1.02	0/1659	1.04	1/2228 (0.0%)
1	D	1.05	2/1621 (0.1%)	1.03	1/2177 (0.0%)
All	All	1.00	5/6535 (0.1%)	1.03	3/8777 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	244	MET	SD-CE	9.89	2.04	1.79
1	A	244	MET	SD-CE	7.44	1.98	1.79
1	D	246	THR	C-N	-7.07	1.23	1.33
1	A	247	ALA	C-N	-6.83	1.23	1.33
1	B	244	MET	SD-CE	5.10	1.92	1.79

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	203	ILE	N-CA-C	7.94	119.75	112.29
1	D	203	ILE	N-CA-C	7.22	119.83	112.90
1	B	245	GLY	N-CA-C	5.70	118.67	111.09

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	1595	0	1614	15	0
1	B	1604	0	1623	28	0
1	C	1630	0	1655	15	0
1	D	1593	0	1613	17	0
2	A	44	0	26	1	0
2	B	44	0	25	1	0
2	C	44	0	26	1	0
3	D	27	0	12	0	0
All	All	6581	0	6594	74	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.

All (74) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:244:MET:SD	1:D:244:MET:CE	2.04	1.44
1:B:147:ASN:HD22	1:B:147:ASN:H	1.32	0.75
1:B:49:PHE:HE1	1:B:124:ILE:HD11	1.56	0.70
1:D:147:ASN:ND2	1:D:149:THR:H	1.95	0.65
1:A:161:LYS:HE2	1:A:162:PHE:CZ	2.33	0.63
1:B:147:ASN:HD22	1:B:147:ASN:N	1.96	0.62
1:C:147:ASN:HD21	1:C:149:THR:HG23	1.65	0.61
1:A:138:GLU:HG2	1:A:139:PHE:CD1	2.37	0.60
1:D:147:ASN:HD22	1:D:148:GLY:N	2.00	0.59
1:A:131:ASP:HB3	1:A:132:PRO:HD2	1.85	0.58
1:A:114:SER:HB3	1:A:118:MET:HE2	1.85	0.57
1:B:105:ILE:HG12	1:B:109:GLU:OE2	2.07	0.55
1:B:49:PHE:CE1	1:B:124:ILE:HD11	2.41	0.54
1:B:45:THR:HG23	1:B:123:ASN:HD22	1.74	0.53
1:B:125:MET:HE2	1:B:193:LYS:HA	1.93	0.51
1:A:131:ASP:HB3	1:A:132:PRO:CD	2.40	0.51
1:C:190:THR:HG21	1:C:192:PHE:CZ	2.46	0.51
1:C:172:TYR:CZ	1:C:219:ARG:HD3	2.46	0.51
1:D:125:MET:CE	1:D:193:LYS:HG2	2.41	0.51
1:C:126:LEU:CD2	1:C:177:LEU:HD23	2.41	0.51
1:D:181:SER:O	1:D:182:GLN:C	2.53	0.50
1:B:44:ASN:O	1:B:45:THR:HG22	2.12	0.50
1:B:69:SER:O	1:B:73:LYS:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:102:SER:O	1:B:105:ILE:HG22	2.12	0.49
1:D:147:ASN:HD22	1:D:147:ASN:C	2.19	0.49
1:C:126:LEU:HD12	1:C:194:VAL:HG21	1.94	0.49
1:B:195:ALA:O	1:B:198:SER:OG	2.21	0.49
1:C:147:ASN:ND2	1:C:149:THR:HG23	2.28	0.48
1:B:147:ASN:H	1:B:147:ASN:ND2	2.06	0.48
1:B:143:LEU:HD21	1:B:188:ILE:HD11	1.94	0.48
1:D:104:LEU:O	1:D:105:ILE:C	2.56	0.48
1:C:46:TYR:CE2	1:C:193:LYS:HB3	2.49	0.48
1:B:217:LEU:CD1	1:B:243:MET:HE3	2.44	0.47
1:D:131:ASP:HB3	1:D:132:PRO:CD	2.45	0.47
1:B:139:PHE:O	1:B:140:GLN:C	2.56	0.47
1:C:201:GLY:O	1:C:215:MET:HA	2.14	0.47
1:B:44:ASN:O	1:B:45:THR:CB	2.63	0.47
1:A:50:THR:HB	1:D:47:GLN:NE2	2.30	0.46
1:C:125:MET:HE3	1:C:125:MET:HB3	1.92	0.46
1:B:125:MET:HE2	1:B:193:LYS:HG2	1.98	0.46
1:C:204:ASP:N	1:C:205:PRO:CD	2.79	0.45
1:B:189:ILE:HB	1:B:238:ILE:HD13	1.97	0.45
1:D:58:TRP:O	1:D:62:GLN:HG2	2.16	0.45
1:C:189:ILE:HD11	1:C:236:GLN:NE2	2.32	0.45
1:A:220:HIS:CD2	1:A:247:ALA:HB3	2.52	0.45
1:A:139:PHE:CE2	1:A:158:ALA:HB2	2.52	0.45
1:C:220:HIS:HD2	1:C:247:ALA:HB3	1.82	0.44
1:A:186:ARG:O	1:A:236:GLN:NE2	2.50	0.44
1:D:145:ASN:HD21	1:D:151:ASN:HD22	1.65	0.44
1:A:166:ASP:OD1	1:A:224:HIS:ND1	2.38	0.44
1:B:49:PHE:HE1	1:B:124:ILE:CD1	2.29	0.44
1:A:147:ASN:ND2	1:A:149:THR:HG23	2.33	0.44
1:A:113:LYS:O	1:A:114:SER:C	2.62	0.43
1:D:46:TYR:CD2	1:D:123:ASN:HB3	2.53	0.43
1:B:170:TYR:O	1:B:219:ARG:HB2	2.19	0.43
1:B:131:ASP:HB3	1:B:132:PRO:CD	2.49	0.43
1:A:104:LEU:HD12	1:A:104:LEU:HA	1.80	0.43
1:B:125:MET:CE	1:B:193:LYS:HG2	2.49	0.43
1:B:132:PRO:HG3	1:B:143:LEU:HD23	2.01	0.42
1:C:128:ARG:HB2	2:C:1252:NAD:O7N	2.19	0.42
1:A:172:TYR:HB3	1:A:216:LEU:HD11	2.01	0.42
1:C:134:TYR:OH	1:C:223:TYR:OH	2.27	0.42
1:D:125:MET:HE2	1:D:193:LYS:HG2	2.01	0.42
1:D:134:TYR:HH	1:D:223:TYR:HH	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:TYR:CD2	1:B:123:ASN:HB3	2.55	0.42
1:A:128:ARG:HA	2:A:1248:NAD:O7N	2.20	0.41
1:D:93:ASN:ND2	1:D:100:PHE:CE1	2.88	0.41
1:D:139:PHE:O	1:D:140:GLN:C	2.64	0.41
1:B:214:GLU:OE2	2:B:1248:NAD:H6N	2.20	0.41
1:B:243:MET:HE2	1:B:243:MET:HB2	1.94	0.41
1:D:134:TYR:CZ	1:D:167:ARG:NH1	2.88	0.41
1:B:44:ASN:O	1:B:45:THR:HB	2.20	0.40
1:B:204:ASP:N	1:B:205:PRO:CD	2.84	0.40
1:C:101:PRO:O	1:C:102:SER:C	2.65	0.40

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	203/211 (96%)	189 (93%)	11 (5%)	3 (2%)	8	22
1	B	203/211 (96%)	189 (93%)	9 (4%)	5 (2%)	4	11
1	C	206/211 (98%)	191 (93%)	12 (6%)	3 (2%)	8	22
1	D	202/211 (96%)	192 (95%)	9 (4%)	1 (0%)	24	48
All	All	814/844 (96%)	761 (94%)	41 (5%)	12 (2%)	8	22

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	181	SER
1	A	247	ALA
1	C	94	LYS
1	B	182	GLN
1	B	234	GLY

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Mol	Chain	Res	Type
1	A	94	LYS
1	B	98	ASN
1	B	200	ALA
1	B	233	ASP
1	C	200	ALA
1	C	232	SER
1	D	105	ILE

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	171/178 (96%)	163 (95%)	8 (5%)	23	51
1	B	173/178 (97%)	162 (94%)	11 (6%)	16	38
1	C	176/178 (99%)	169 (96%)	7 (4%)	28	56
1	D	172/178 (97%)	159 (92%)	13 (8%)	12	30
All	All	692/712 (97%)	653 (94%)	39 (6%)	19	44

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	GLN
1	A	60	ASN
1	A	71	SER
1	A	92	GLN
1	A	125	MET
1	A	142	THR
1	A	220	HIS
1	A	226	ASP
1	B	45	THR
1	B	78	SER
1	B	84	SER
1	B	104	LEU
1	B	125	MET
1	B	147	ASN

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Mol	Chain	Res	Type
1	B	159	LYS
1	B	186	ARG
1	B	225	ILE
1	B	232	SER
1	B	242	THR
1	C	47	GLN
1	C	54	GLN
1	C	74	GLU
1	C	82	SER
1	C	152	LYS
1	C	220	HIS
1	C	246	THR
1	D	64	LYS
1	D	82	SER
1	D	84	SER
1	D	92	GLN
1	D	94	LYS
1	D	102	SER
1	D	104	LEU
1	D	125	MET
1	D	147	ASN
1	D	182	GLN
1	D	183	PHE
1	D	207	SER
1	D	244	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	GLN
1	A	60	ASN
1	A	92	GLN
1	A	116	ASN
1	A	182	GLN
1	A	220	HIS
1	B	44	ASN
1	B	54	GLN
1	B	92	GLN
1	B	103	ASN
1	B	107	GLN
1	B	147	ASN
1	B	182	GLN

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Mol	Chain	Res	Type
1	C	44	ASN
1	C	47	GLN
1	C	51	ASN
1	C	92	GLN
1	C	98	ASN
1	C	147	ASN
1	C	182	GLN
1	C	220	HIS
1	C	236	GLN
1	C	249	ASN
1	D	47	GLN
1	D	107	GLN
1	D	116	ASN
1	D	140	GLN
1	D	141	ASN
1	D	145	ASN
1	D	147	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](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ADP	D	1247	-	28,29,29	1.78	4 (14%)	43,45,45	1.73	9 (20%)
2	NAD	B	1248	-	46,48,48	1.71	8 (17%)	64,73,73	1.73	16 (25%)
2	NAD	C	1252	-	46,48,48	1.81	7 (15%)	64,73,73	1.72	15 (23%)
2	NAD	A	1248	-	46,48,48	2.00	8 (17%)	64,73,73	1.70	14 (21%)

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	ADP	D	1247	-	-	3/16/32/32	0/3/3/3
2	NAD	B	1248	-	1/1/11/11	6/30/62/62	0/5/5/5
2	NAD	C	1252	-	-	3/30/62/62	0/5/5/5
2	NAD	A	1248	-	-	3/30/62/62	0/5/5/5

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1248	NAD	O7N-C7N	9.27	1.41	1.24
2	C	1252	NAD	O7N-C7N	7.94	1.38	1.24
2	B	1248	NAD	O7N-C7N	7.45	1.38	1.24
3	D	1247	ADP	PA-O3A	6.60	1.66	1.59
2	A	1248	NAD	PN-O3	4.67	1.64	1.59
2	A	1248	NAD	PA-O3	4.55	1.64	1.59
2	B	1248	NAD	PN-O3	3.66	1.63	1.59
2	C	1252	NAD	C2N-N1N	3.61	1.38	1.35
2	C	1252	NAD	C2A-N3A	3.60	1.40	1.33
3	D	1247	ADP	C2-N1	3.36	1.39	1.33
2	C	1252	NAD	C2A-N1A	3.25	1.39	1.33
3	D	1247	ADP	C2-N3	3.22	1.39	1.33
2	C	1252	NAD	C8A-N7A	3.17	1.37	1.31
2	B	1248	NAD	C2A-N1A	3.09	1.39	1.33
2	A	1248	NAD	O4D-C1D	3.00	1.44	1.40
2	B	1248	NAD	C2A-N3A	2.81	1.38	1.33
2	C	1252	NAD	PN-O3	2.80	1.62	1.59
2	B	1248	NAD	PA-O3	2.73	1.62	1.59
2	B	1248	NAD	C8A-N7A	2.72	1.36	1.31
2	A	1248	NAD	C2A-N3A	2.70	1.38	1.33
2	A	1248	NAD	C2A-N1A	2.57	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1247	ADP	C8-N7	2.40	1.36	1.31
2	B	1248	NAD	C2N-N1N	2.31	1.37	1.35
2	C	1252	NAD	O4D-C1D	2.20	1.43	1.40
2	A	1248	NAD	C8A-N7A	2.16	1.35	1.31
2	B	1248	NAD	O4D-C1D	2.13	1.43	1.40
2	A	1248	NAD	C2N-N1N	2.09	1.37	1.35

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1252	NAD	N3A-C2A-N1A	-5.26	120.62	128.58
2	A	1248	NAD	N3A-C2A-N1A	-5.07	120.91	128.58
2	B	1248	NAD	C5A-C4A-N3A	-4.93	119.93	126.72
3	D	1247	ADP	N3-C2-N1	-4.70	121.47	128.58
2	B	1248	NAD	C6N-N1N-C2N	-4.69	117.89	121.88
3	D	1247	ADP	C5-C4-N3	-4.35	120.73	126.72
2	B	1248	NAD	N3A-C2A-N1A	-4.30	122.08	128.58
2	A	1248	NAD	C5A-C4A-N3A	-4.29	120.81	126.72
2	C	1252	NAD	C5A-C4A-N3A	-4.07	121.11	126.72
2	C	1252	NAD	N9A-C8A-N7A	-3.95	108.33	113.94
2	A	1248	NAD	N9A-C8A-N7A	-3.86	108.45	113.94
3	D	1247	ADP	C5-N7-C8	3.31	108.66	103.45
2	B	1248	NAD	N3A-C4A-N9A	3.29	132.76	127.17
2	A	1248	NAD	C6N-N1N-C2N	-3.27	119.09	121.88
3	D	1247	ADP	N9-C8-N7	-3.27	109.30	113.94
2	A	1248	NAD	N3A-C4A-N9A	3.19	132.58	127.17
2	A	1248	NAD	C2A-N3A-C4A	3.17	119.58	111.83
2	C	1252	NAD	N3A-C4A-N9A	3.17	132.56	127.17
2	C	1252	NAD	O2N-PN-O1N	3.12	126.95	112.44
2	A	1248	NAD	C5A-N7A-C8A	3.10	108.33	103.45
2	C	1252	NAD	C3N-C7N-N7N	3.04	121.48	117.74
2	C	1252	NAD	C5A-N7A-C8A	3.01	108.17	103.45
2	B	1248	NAD	C2A-N3A-C4A	2.99	119.12	111.83
2	C	1252	NAD	C6N-N1N-C2N	-2.98	119.34	121.88
2	C	1252	NAD	C2A-N3A-C4A	2.93	118.98	111.83
2	B	1248	NAD	C3N-C7N-N7N	2.89	121.30	117.74
3	D	1247	ADP	C2-N3-C4	2.86	118.81	111.83
2	B	1248	NAD	O7N-C7N-N7N	-2.80	118.56	122.62
2	B	1248	NAD	O2A-PA-O5B	2.73	119.92	107.57
2	A	1248	NAD	C5D-C4D-C3D	-2.71	105.45	115.21
3	D	1247	ADP	O2A-PA-O3A	2.70	114.58	107.27
2	B	1248	NAD	C5N-C4N-C3N	-2.67	117.74	120.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1247	ADP	N3-C4-N9	2.66	131.69	127.17
2	B	1248	NAD	C6N-N1N-C1D	2.62	124.87	119.73
3	D	1247	ADP	C4-C5-N7	-2.62	107.59	110.58
2	A	1248	NAD	O2B-C2B-C1B	2.61	119.09	110.10
2	B	1248	NAD	O2B-C2B-C1B	2.55	118.88	110.10
2	A	1248	NAD	C2N-C3N-C4N	2.52	121.19	118.26
2	B	1248	NAD	N9A-C8A-N7A	-2.49	110.40	113.94
2	A	1248	NAD	O2N-PN-O3	2.43	113.84	107.27
3	D	1247	ADP	C6-C5-C4	2.42	120.48	117.18
2	B	1248	NAD	O4B-C1B-N9A	2.41	112.72	108.09
2	B	1248	NAD	C6A-C5A-C4A	2.38	120.43	117.18
2	A	1248	NAD	C3N-C7N-N7N	2.28	120.55	117.74
2	B	1248	NAD	C2D-C3D-C4D	2.26	106.98	102.61
2	C	1252	NAD	C2N-C3N-C4N	2.26	120.89	118.26
2	A	1248	NAD	C4A-N9A-C8A	2.20	108.05	105.74
2	C	1252	NAD	C5A-C6A-N6A	-2.14	118.00	123.29
2	A	1248	NAD	C6A-C5A-C4A	2.13	120.09	117.18
2	C	1252	NAD	C4A-N9A-C8A	2.12	107.96	105.74
2	C	1252	NAD	C4D-O4D-C1D	-2.10	108.00	109.92
2	B	1248	NAD	C5A-N7A-C8A	2.06	106.69	103.45
2	C	1252	NAD	O7N-C7N-N7N	-2.04	119.67	122.62
2	C	1252	NAD	O4B-C4B-C5B	-2.02	102.88	109.33

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	1248	NAD	C1D

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1248	NAD	C2D-C1D-N1N-C2N
2	B	1248	NAD	C2D-C1D-N1N-C6N
2	B	1248	NAD	O4D-C4D-C5D-O5D
2	B	1248	NAD	C3D-C4D-C5D-O5D
2	A	1248	NAD	C2B-C1B-N9A-C8A
2	C	1252	NAD	C2B-C1B-N9A-C8A
2	B	1248	NAD	C2B-C1B-N9A-C8A
3	D	1247	ADP	C2'-C1'-N9-C8
2	A	1248	NAD	C2B-C1B-N9A-C4A
3	D	1247	ADP	C2'-C1'-N9-C4
2	B	1248	NAD	O4B-C1B-N9A-C8A

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Mol	Chain	Res	Type	Atoms
3	D	1247	ADP	O4'-C1'-N9-C8
2	C	1252	NAD	C2B-C1B-N9A-C4A
2	C	1252	NAD	O4B-C1B-N9A-C8A
2	A	1248	NAD	O4B-C1B-N9A-C8A

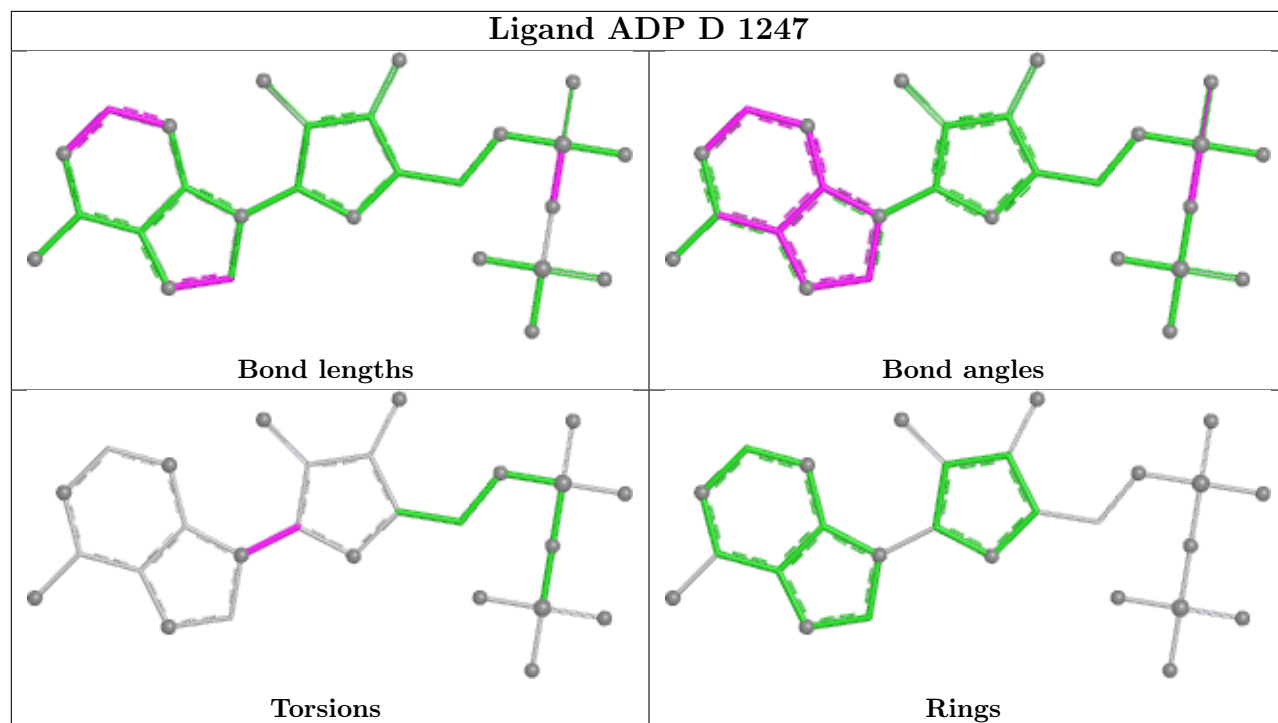
There are no ring outliers.

3 monomers are involved in 3 short contacts:

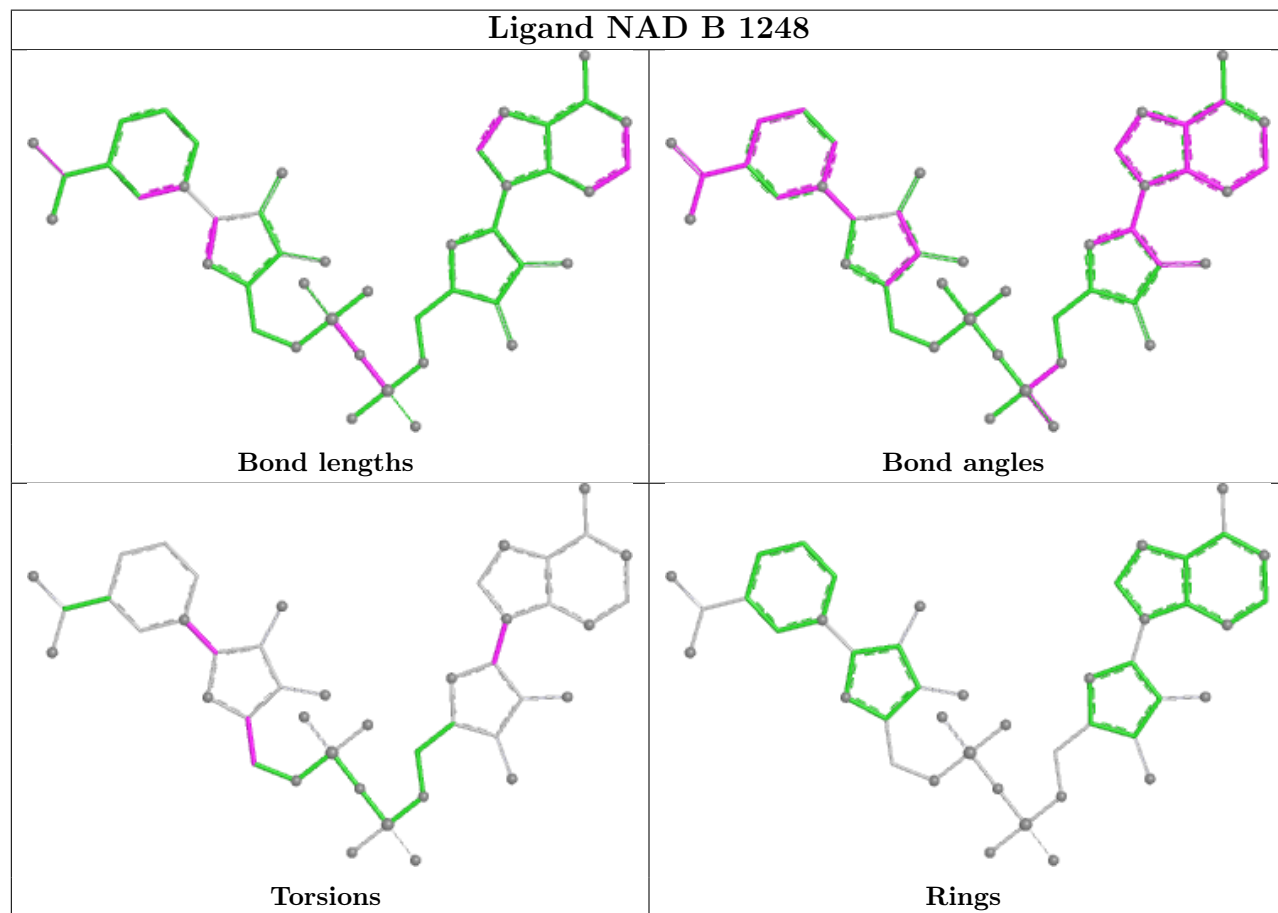
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1248	NAD	1	0
2	C	1252	NAD	1	0
2	A	1248	NAD	1	0

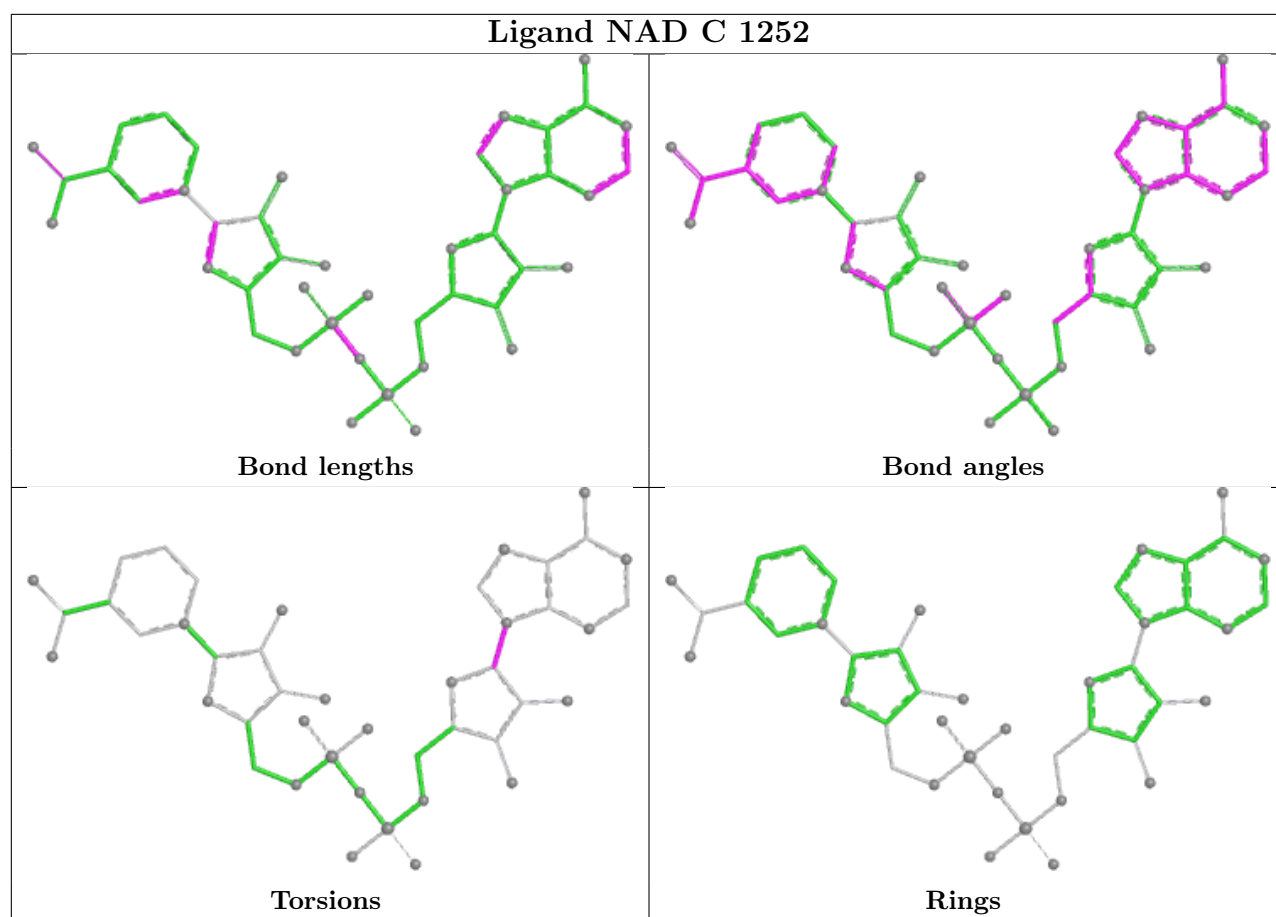
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

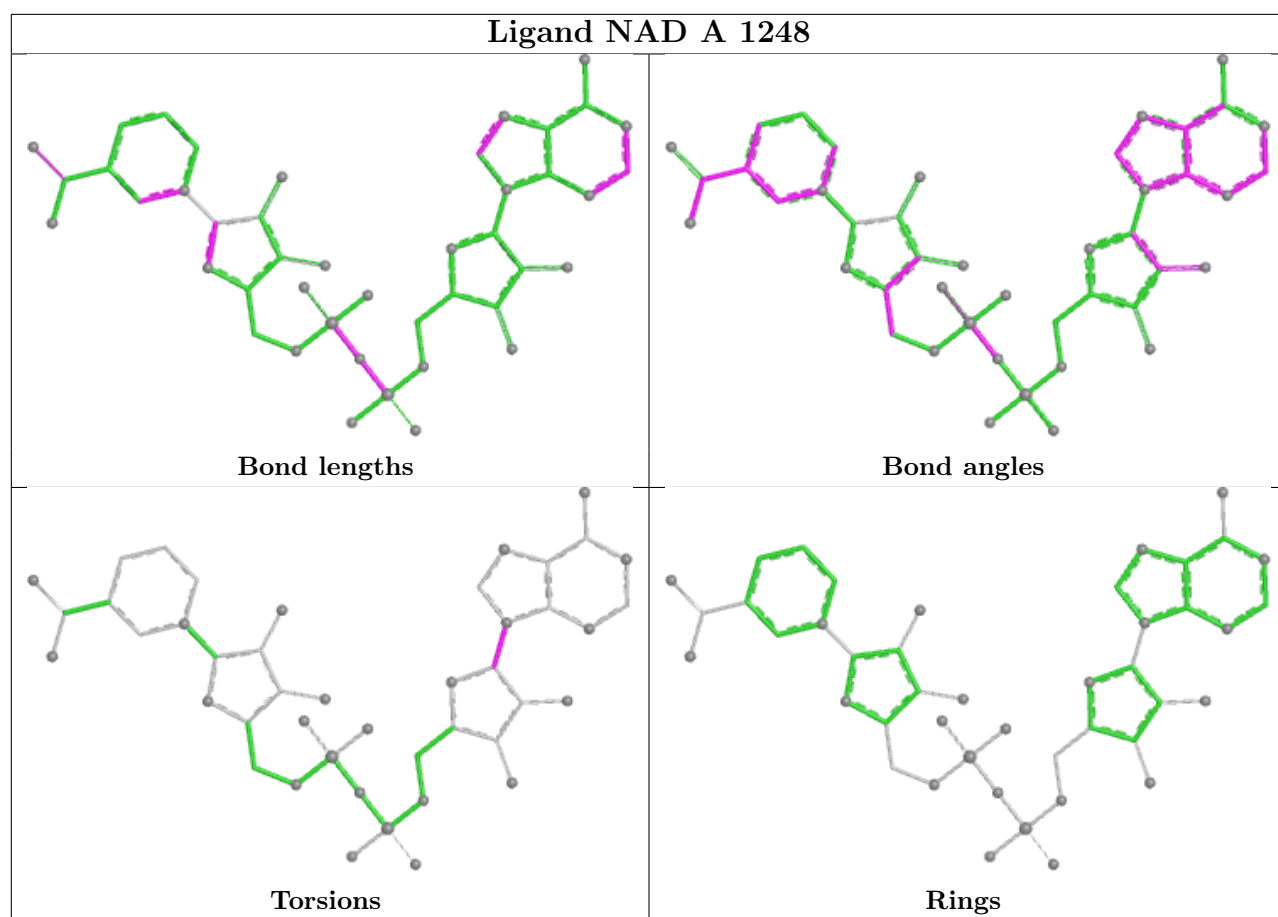
Ligand ADP D 1247



Ligand NAD B 1248







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	205/211 (97%)	-0.34	1 (0%) 87 86	36, 58, 76, 84	0
1	B	205/211 (97%)	-0.18	0 100 100	41, 63, 86, 94	0
1	C	208/211 (98%)	-0.34	0 100 100	37, 56, 84, 92	0
1	D	204/211 (96%)	-0.40	0 100 100	36, 55, 77, 90	0
All	All	822/844 (97%)	-0.32	1 (0%) 92 91	36, 59, 82, 94	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	247	ALA	2.3

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(Å ²)	Q<0.9
3	ADP	D	1247	27/27	0.81	0.10	78,86,92,94	0

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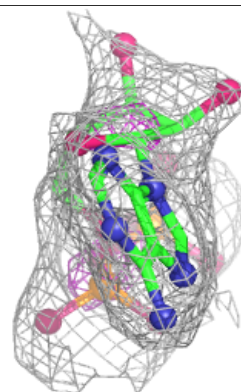
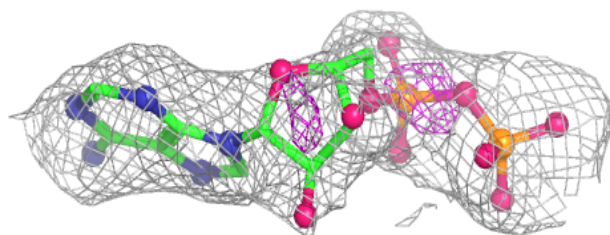
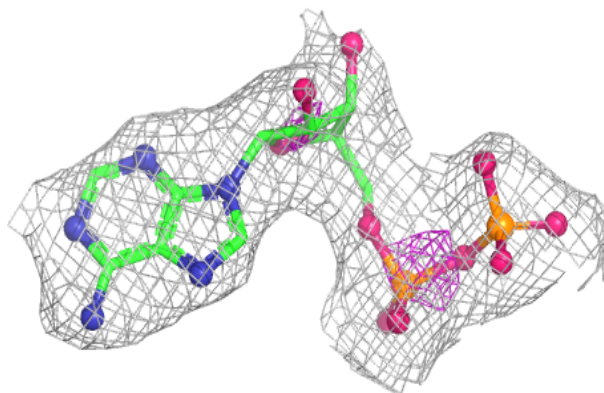
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAD	C	1252	44/44	0.84	0.12	33,46,50,52	44
2	NAD	B	1248	44/44	0.89	0.08	50,63,75,77	0
2	NAD	A	1248	44/44	0.91	0.10	32,43,50,51	44

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.

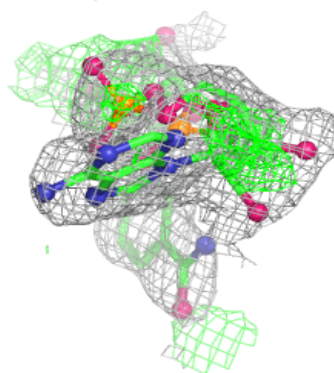
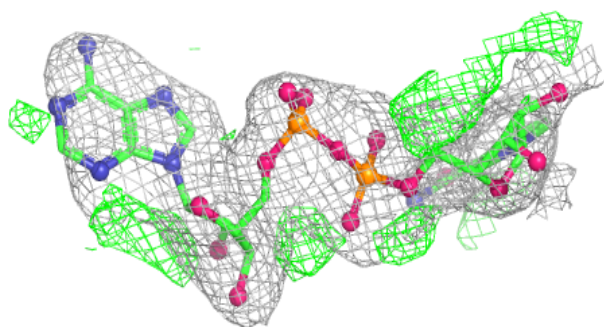
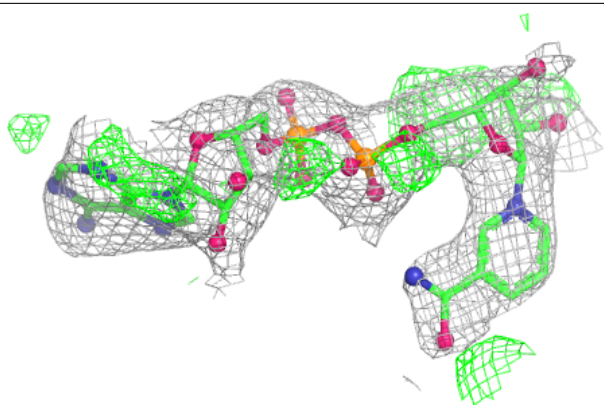
Electron density around ADP D 1247:

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

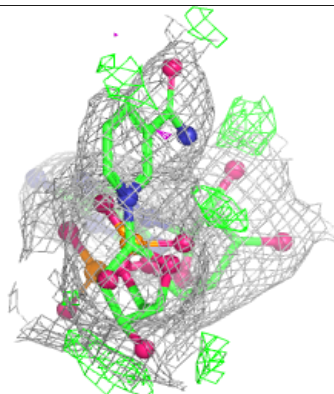
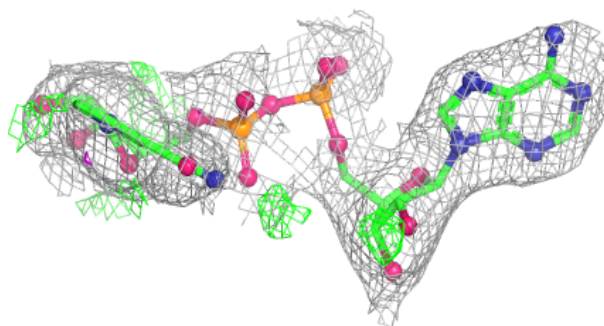
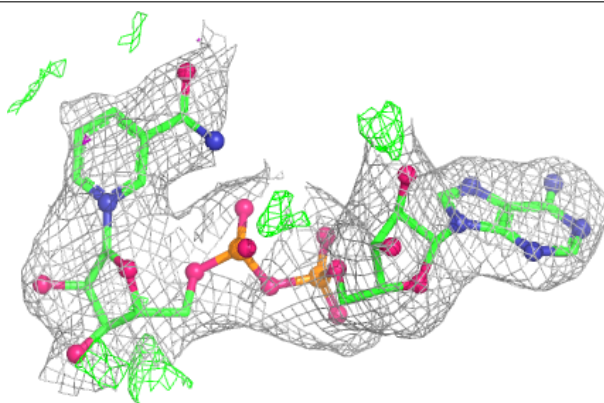


Electron density around NAD C 1252:

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

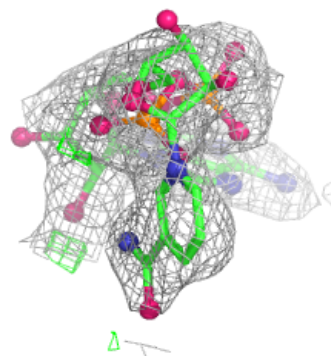
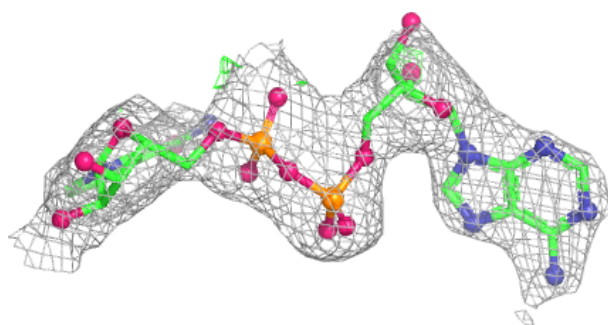
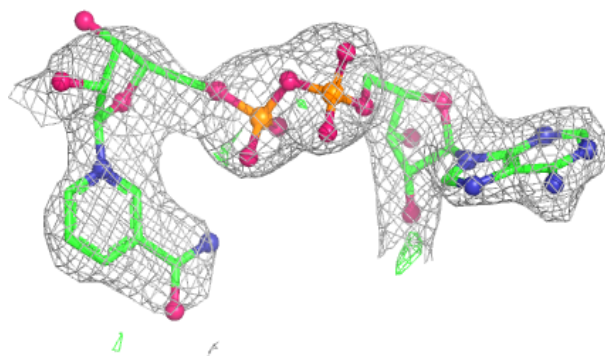
**Electron density around NAD B 1248:**

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



Electron density around NAD A 1248:

$2mF_o-DF_c$ (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.