



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:56 PM UTC

PDB ID : 3ORF / pdb_00003orf
Title : Crystal Structure of Dihydropteridine Reductase from Dictyostelium discoideum
Authors : Chen, C.; Zhuang, N.N.; Seo, K.H.; Park, Y.S.; Lee, K.H.
Deposited on : 2010-09-07
Resolution : 2.16 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

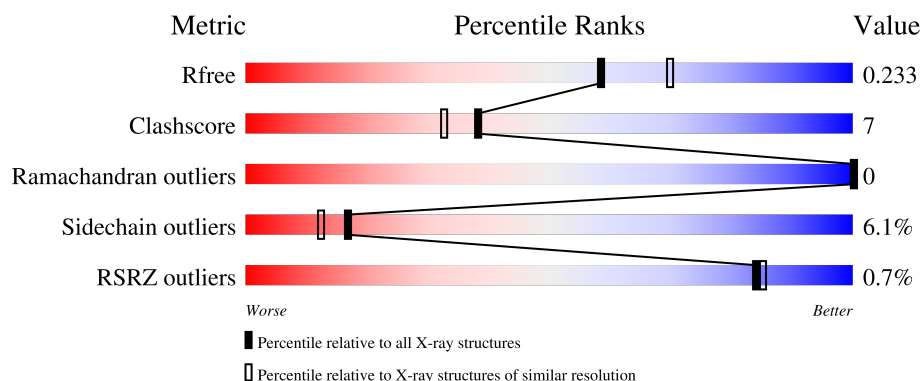
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.16 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	75% 15% 8%
1	B	251	76% 14% 8%
1	C	251	76% 15% 8%
1	D	251	73% 15% 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7229 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 Dihydropteridine reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1727	1088	290	344	5			
1	B	230	Total	C	N	O	S	0	0	0
			1727	1088	290	344	5			
1	C	230	Total	C	N	O	S	0	0	0
			1727	1088	290	344	5			
1	D	230	Total	C	N	O	S	0	0	0
			1727	1088	290	344	5			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q86A17
A	-18	GLY	-	expression tag	UNP Q86A17
A	-17	SER	-	expression tag	UNP Q86A17
A	-16	SER	-	expression tag	UNP Q86A17
A	-15	HIS	-	expression tag	UNP Q86A17
A	-14	HIS	-	expression tag	UNP Q86A17
A	-13	HIS	-	expression tag	UNP Q86A17
A	-12	HIS	-	expression tag	UNP Q86A17
A	-11	HIS	-	expression tag	UNP Q86A17
A	-10	HIS	-	expression tag	UNP Q86A17
A	-9	SER	-	expression tag	UNP Q86A17
A	-8	SER	-	expression tag	UNP Q86A17
A	-7	GLY	-	expression tag	UNP Q86A17
A	-6	LEU	-	expression tag	UNP Q86A17
A	-5	VAL	-	expression tag	UNP Q86A17
A	-4	PRO	-	expression tag	UNP Q86A17
A	-3	ARG	-	expression tag	UNP Q86A17
A	-2	GLY	-	expression tag	UNP Q86A17
A	-1	SER	-	expression tag	UNP Q86A17
A	0	HIS	-	expression tag	UNP Q86A17
B	-19	MET	-	expression tag	UNP Q86A17

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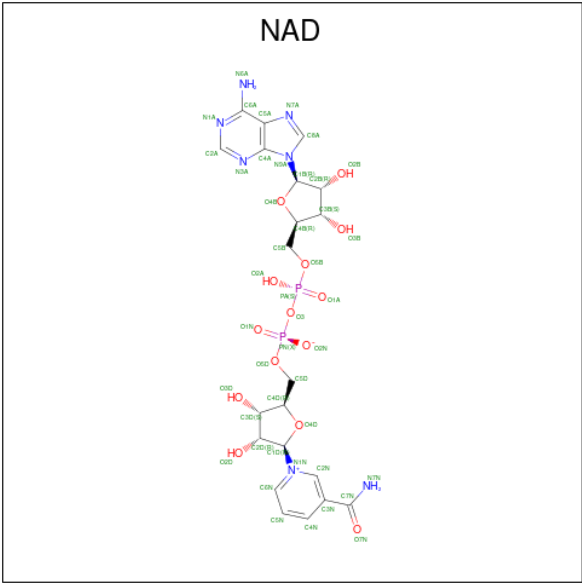
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP Q86A17
B	-17	SER	-	expression tag	UNP Q86A17
B	-16	SER	-	expression tag	UNP Q86A17
B	-15	HIS	-	expression tag	UNP Q86A17
B	-14	HIS	-	expression tag	UNP Q86A17
B	-13	HIS	-	expression tag	UNP Q86A17
B	-12	HIS	-	expression tag	UNP Q86A17
B	-11	HIS	-	expression tag	UNP Q86A17
B	-10	HIS	-	expression tag	UNP Q86A17
B	-9	SER	-	expression tag	UNP Q86A17
B	-8	SER	-	expression tag	UNP Q86A17
B	-7	GLY	-	expression tag	UNP Q86A17
B	-6	LEU	-	expression tag	UNP Q86A17
B	-5	VAL	-	expression tag	UNP Q86A17
B	-4	PRO	-	expression tag	UNP Q86A17
B	-3	ARG	-	expression tag	UNP Q86A17
B	-2	GLY	-	expression tag	UNP Q86A17
B	-1	SER	-	expression tag	UNP Q86A17
B	0	HIS	-	expression tag	UNP Q86A17
C	-19	MET	-	expression tag	UNP Q86A17
C	-18	GLY	-	expression tag	UNP Q86A17
C	-17	SER	-	expression tag	UNP Q86A17
C	-16	SER	-	expression tag	UNP Q86A17
C	-15	HIS	-	expression tag	UNP Q86A17
C	-14	HIS	-	expression tag	UNP Q86A17
C	-13	HIS	-	expression tag	UNP Q86A17
C	-12	HIS	-	expression tag	UNP Q86A17
C	-11	HIS	-	expression tag	UNP Q86A17
C	-10	HIS	-	expression tag	UNP Q86A17
C	-9	SER	-	expression tag	UNP Q86A17
C	-8	SER	-	expression tag	UNP Q86A17
C	-7	GLY	-	expression tag	UNP Q86A17
C	-6	LEU	-	expression tag	UNP Q86A17
C	-5	VAL	-	expression tag	UNP Q86A17
C	-4	PRO	-	expression tag	UNP Q86A17
C	-3	ARG	-	expression tag	UNP Q86A17
C	-2	GLY	-	expression tag	UNP Q86A17
C	-1	SER	-	expression tag	UNP Q86A17
C	0	HIS	-	expression tag	UNP Q86A17
D	-19	MET	-	expression tag	UNP Q86A17
D	-18	GLY	-	expression tag	UNP Q86A17
D	-17	SER	-	expression tag	UNP Q86A17

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP Q86A17
D	-15	HIS	-	expression tag	UNP Q86A17
D	-14	HIS	-	expression tag	UNP Q86A17
D	-13	HIS	-	expression tag	UNP Q86A17
D	-12	HIS	-	expression tag	UNP Q86A17
D	-11	HIS	-	expression tag	UNP Q86A17
D	-10	HIS	-	expression tag	UNP Q86A17
D	-9	SER	-	expression tag	UNP Q86A17
D	-8	SER	-	expression tag	UNP Q86A17
D	-7	GLY	-	expression tag	UNP Q86A17
D	-6	LEU	-	expression tag	UNP Q86A17
D	-5	VAL	-	expression tag	UNP Q86A17
D	-4	PRO	-	expression tag	UNP Q86A17
D	-3	ARG	-	expression tag	UNP Q86A17
D	-2	GLY	-	expression tag	UNP Q86A17
D	-1	SER	-	expression tag	UNP Q86A17
D	0	HIS	-	expression tag	UNP Q86A17

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



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

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

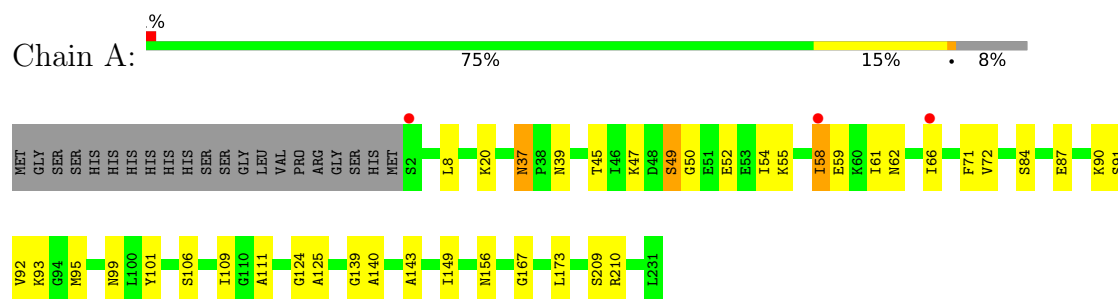
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	53	Total	O	0	0
			53	53		
3	B	16	Total	O	0	0
			16	16		
3	C	50	Total	O	0	0
			50	50		
3	D	26	Total	O	0	0
			26	26		

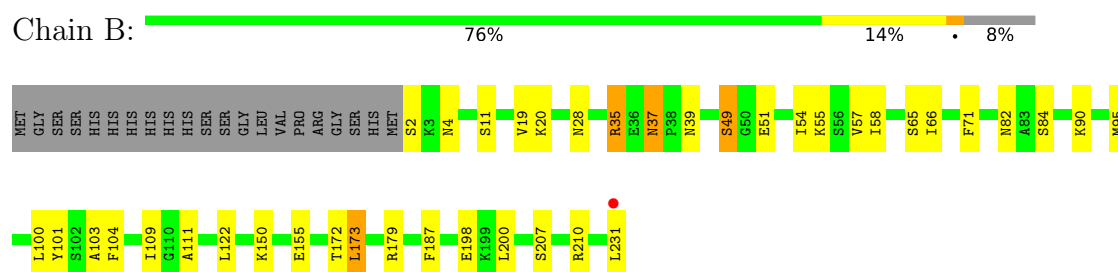
3 Residue-property plots

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.

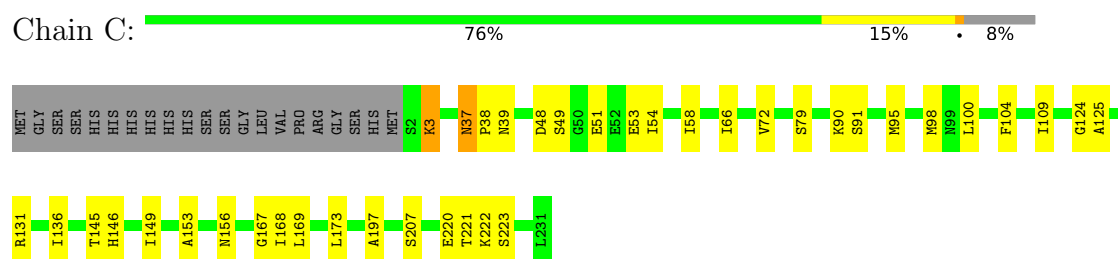
• Molecule 1: Dihydropteridine reductase



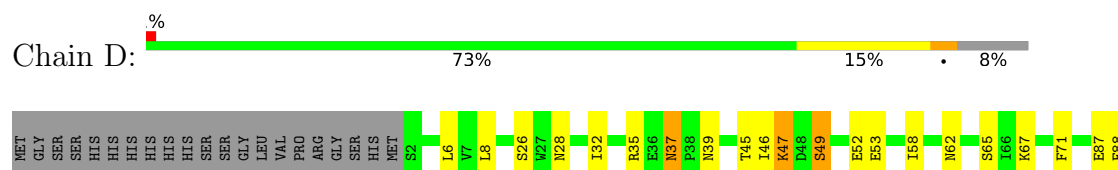
• Molecule 1: Dihydropteridine reductase



• Molecule 1: Dihydropteridine reductase



• Molecule 1: Dihydropteridine reductase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.81Å 129.90Å 78.76Å 90.00° 99.99° 90.00°	Depositor
Resolution (Å)	36.96 – 2.16 36.96 – 2.16	Depositor EDS
% Data completeness (in resolution range)	93.6 (36.96-2.16) 93.5 (36.96-2.16)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.78 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.185 , 0.240 0.181 , 0.233	Depositor DCC
R_{free} test set	2473 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 31.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7229	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.81% 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

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	1.34	4/1760 (0.2%)	1.23	10/2379 (0.4%)
1	B	1.13	1/1760 (0.1%)	1.17	4/2379 (0.2%)
1	C	1.39	5/1760 (0.3%)	1.23	3/2379 (0.1%)
1	D	1.26	2/1760 (0.1%)	1.19	4/2379 (0.2%)
All	All	1.28	12/7040 (0.2%)	1.21	21/9516 (0.2%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	197	ALA	CA-CB	6.78	1.64	1.53
1	C	220	GLU	N-CA	-6.13	1.38	1.46
1	C	136	ILE	C-O	-6.04	1.17	1.24
1	A	54	ILE	CA-CB	5.67	1.61	1.54
1	C	91	SER	CA-C	5.63	1.60	1.52
1	D	130	ASN	C-O	-5.59	1.18	1.24
1	A	140	ALA	C-O	-5.37	1.17	1.24
1	A	143	ALA	CA-CB	5.34	1.62	1.53
1	C	145	THR	CA-CB	5.33	1.61	1.53
1	D	46	ILE	CA-CB	5.12	1.62	1.55
1	B	122	LEU	N-CA	5.04	1.52	1.46
1	A	139	GLY	N-CA	5.01	1.52	1.45

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	210	ARG	CA-C-N	-8.98	111.63	120.52
1	B	210	ARG	C-N-CA	-8.98	111.63	120.52
1	A	91	SER	N-CA-C	-7.16	103.55	111.36
1	A	47	LYS	N-CA-C	-6.80	104.00	112.90
1	B	100	LEU	N-CA-C	6.25	117.89	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	88	PHE	N-CA-C	6.21	117.74	110.97
1	A	50	GLY	N-CA-C	6.14	119.09	112.33
1	D	108	HIS	N-CA-C	-6.02	104.80	111.36
1	C	153	ALA	N-CA-C	-5.91	105.57	112.89
1	A	58	ILE	CB-CA-C	-5.56	104.86	111.97
1	C	72	VAL	CA-C-N	-5.44	115.77	122.84
1	C	72	VAL	C-N-CA	-5.44	115.77	122.84
1	D	132	THR	N-CA-C	-5.37	104.00	110.44
1	B	103	ALA	N-CA-C	-5.24	105.65	111.36
1	A	8	LEU	N-CA-C	-5.12	100.96	109.46
1	A	210	ARG	CA-C-N	-5.11	114.39	120.11
1	A	210	ARG	C-N-CA	-5.11	114.39	120.11
1	D	121	VAL	N-CA-C	5.09	115.30	107.77
1	A	72	VAL	CA-C-N	-5.06	116.05	122.77
1	A	72	VAL	C-N-CA	-5.06	116.05	122.77
1	A	209	SER	N-CA-C	-5.01	107.17	113.28

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	1727	0	1708	28	0
1	B	1727	0	1708	23	0
1	C	1727	0	1708	26	0
1	D	1727	0	1708	27	0
2	A	44	0	26	5	0
2	B	44	0	26	1	0
2	C	44	0	26	0	0
2	D	44	0	26	1	0
3	A	53	0	0	2	0
3	B	16	0	0	0	0
3	C	50	0	0	1	0
3	D	26	0	0	1	0
All	All	7229	0	6936	97	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 7.

All (97) 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:A:61:ILE:CG2	1:A:66:ILE:HD11	1.77	1.13
1:A:58:ILE:HD11	1:A:109:ILE:HG12	1.32	1.07
1:A:61:ILE:HG23	1:A:66:ILE:CD1	1.87	1.02
1:C:58:ILE:HD11	1:C:109:ILE:HG12	1.42	1.01
1:A:61:ILE:HG23	1:A:66:ILE:HD11	0.99	0.97
1:A:61:ILE:CG2	1:A:66:ILE:CD1	2.48	0.87
1:B:58:ILE:HD11	1:B:109:ILE:HG12	1.58	0.85
1:D:156:ASN:H	1:D:156:ASN:HD22	1.27	0.81
1:C:51:GLU:OE1	1:D:90:LYS:HD3	1.81	0.80
1:D:182:MET:HE2	1:D:185:ALA:HB2	1.61	0.80
1:D:37:ASN:C	1:D:37:ASN:HD22	1.92	0.77
1:D:37:ASN:HD22	1:D:39:ASN:H	1.31	0.76
1:A:58:ILE:HD11	1:A:109:ILE:CG1	2.16	0.72
1:B:35:ARG:HG2	1:B:35:ARG:HH11	1.55	0.72
1:C:58:ILE:HD11	1:C:109:ILE:CG1	2.20	0.70
1:D:37:ASN:ND2	1:D:39:ASN:H	1.89	0.69
1:D:176:PRO:O	1:D:179:ARG:HB2	1.91	0.69
1:A:37:ASN:HD22	1:A:37:ASN:C	2.02	0.67
1:B:35:ARG:HH11	1:B:35:ARG:CG	2.06	0.67
1:A:125:ALA:HA	2:A:901:NAD:H5N	1.78	0.67
1:D:195:GLU:HG2	3:D:248:HOH:O	1.95	0.66
1:C:37:ASN:C	1:C:37:ASN:HD22	2.02	0.66
1:C:146:HIS:HD2	3:C:266:HOH:O	1.83	0.61
1:C:149:ILE:HD13	1:C:167:GLY:HA3	1.81	0.61
1:D:187:PHE:O	1:D:190:TRP:HB2	2.02	0.60
1:B:4:ASN:HD22	1:B:28:ASN:HB3	1.67	0.59
1:A:55:LYS:O	1:A:59:GLU:HG3	2.02	0.58
1:A:149:ILE:HD13	1:A:167:GLY:HA3	1.85	0.58
1:C:95:MET:CE	1:C:98:MET:HE3	2.34	0.58
1:D:58:ILE:CD1	1:D:108:HIS:HD2	2.15	0.58
1:D:58:ILE:CD1	1:D:108:HIS:CD2	2.87	0.58
1:B:37:ASN:HD22	1:B:37:ASN:C	2.11	0.57
1:A:58:ILE:CD1	1:A:109:ILE:HG12	2.22	0.57
1:D:182:MET:HE2	1:D:185:ALA:CB	2.35	0.57
1:D:95:MET:HA	1:D:95:MET:HE2	1.87	0.55
1:D:156:ASN:H	1:D:156:ASN:ND2	2.00	0.54
1:A:95:MET:HE2	1:A:95:MET:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:SER:HB3	1:B:101:TYR:HB3	1.92	0.52
1:C:48:ASP:H	1:C:53:GLU:HG3	1.75	0.52
1:C:221:THR:O	1:C:222:LYS:HD3	2.09	0.52
1:B:19:VAL:O	1:B:20:LYS:C	2.53	0.51
1:C:37:ASN:C	1:C:37:ASN:ND2	2.69	0.51
1:A:173:LEU:H	2:A:901:NAD:H72N	1.59	0.50
1:B:71:PHE:CD2	1:B:71:PHE:C	2.89	0.50
1:C:125:ALA:H	1:C:146:HIS:HE1	1.60	0.49
1:D:149:ILE:HD13	1:D:167:GLY:HA3	1.95	0.49
1:A:156:ASN:HD21	1:C:156:ASN:HD21	1.61	0.48
1:C:222:LYS:O	1:C:223:SER:C	2.56	0.48
1:A:37:ASN:HD21	1:A:39:ASN:HB3	1.78	0.48
1:A:71:PHE:CE2	1:A:106:SER:HB3	2.48	0.47
1:A:87:GLU:HG3	3:A:264:HOH:O	2.14	0.47
1:D:182:MET:O	1:D:183:SER:C	2.56	0.47
1:C:95:MET:HE2	1:C:98:MET:HE3	1.97	0.47
1:B:37:ASN:C	1:B:37:ASN:ND2	2.72	0.47
1:B:37:ASN:ND2	1:B:39:ASN:H	2.12	0.47
1:C:58:ILE:CD1	1:C:109:ILE:HG12	2.29	0.47
1:A:61:ILE:CG2	1:A:66:ILE:HD12	2.42	0.47
1:C:37:ASN:ND2	1:C:39:ASN:H	2.13	0.47
1:A:125:ALA:CB	2:A:901:NAD:H5N	2.44	0.47
1:C:104:PHE:CD1	1:D:92:VAL:HG13	2.50	0.47
1:C:100:LEU:HD11	1:C:104:PHE:CE1	2.51	0.46
1:D:37:ASN:C	1:D:37:ASN:ND2	2.66	0.46
1:B:35:ARG:CG	1:B:35:ARG:NH1	2.72	0.46
1:C:131:ARG:HA	1:C:131:ARG:NE	2.30	0.46
1:C:54:ILE:O	1:C:58:ILE:HD13	2.16	0.46
1:A:125:ALA:CA	2:A:901:NAD:H5N	2.45	0.46
1:D:49:SER:HB3	1:D:101:TYR:HB3	1.97	0.45
1:D:8:LEU:HD12	1:D:32:ILE:HB	1.99	0.45
1:B:155:GLU:HA	1:B:155:GLU:OE1	2.17	0.45
1:B:173:LEU:HB2	2:B:902:NAD:C7N	2.46	0.45
1:C:3:LYS:HE2	1:C:3:LYS:HB3	1.87	0.45
1:B:11:SER:OG	1:B:37:ASN:HB2	2.18	0.44
1:A:99:ASN:HB3	3:A:243:HOH:O	2.17	0.44
1:A:84:SER:HB3	1:B:111:ALA:HB1	1.98	0.43
1:D:47:LYS:HB2	1:D:53:GLU:CD	2.43	0.43
1:A:92:VAL:HG13	1:B:104:PHE:CD1	2.52	0.43
1:D:71:PHE:CD2	1:D:71:PHE:C	2.97	0.43
1:B:95:MET:HA	1:B:95:MET:HE2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:123:THR:HG21	2:D:904:NAD:H4D	2.01	0.43
1:B:4:ASN:ND2	1:B:28:ASN:HB3	2.33	0.43
1:D:62:ASN:HD21	1:D:67:LYS:NZ	2.17	0.42
1:B:54:ILE:O	1:B:57:VAL:HG12	2.19	0.42
1:D:6:LEU:HD11	1:D:32:ILE:HG13	2.01	0.42
1:B:179:ARG:HG2	1:B:187:PHE:CZ	2.55	0.42
1:A:111:ALA:HB1	1:B:84:SER:HB3	2.00	0.42
1:A:37:ASN:C	1:A:37:ASN:ND2	2.67	0.42
1:A:124:GLY:O	2:A:901:NAD:H6N	2.19	0.42
1:C:124:GLY:HA3	1:C:146:HIS:HE1	1.84	0.41
1:C:104:PHE:CE2	1:D:137:ALA:HA	2.55	0.41
1:D:154:SER:HB2	1:D:156:ASN:ND2	2.34	0.41
1:C:168:ILE:C	1:C:169:LEU:HD23	2.46	0.41
1:B:82:ASN:OD1	1:B:82:ASN:C	2.64	0.41
1:C:37:ASN:HD22	1:C:38:PRO:N	2.18	0.41
1:A:58:ILE:O	1:A:62:ASN:HB2	2.21	0.40
1:A:49:SER:HB3	1:A:101:TYR:HB3	2.04	0.40
1:B:51:GLU:OE2	1:B:55:LYS:HE3	2.20	0.40
1:C:124:GLY:HA3	1:C:146:HIS:CE1	2.56	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	228/251 (91%)	224 (98%)	4 (2%)	0	100	100
1	B	228/251 (91%)	222 (97%)	6 (3%)	0	100	100
1	C	228/251 (91%)	222 (97%)	6 (3%)	0	100	100
1	D	228/251 (91%)	220 (96%)	8 (4%)	0	100	100
All	All	912/1004 (91%)	888 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	188/206 (91%)	181 (96%)	7 (4%)	30	30
1	B	188/206 (91%)	174 (93%)	14 (7%)	13	8
1	C	188/206 (91%)	180 (96%)	8 (4%)	26	24
1	D	188/206 (91%)	171 (91%)	17 (9%)	9	5
All	All	752/824 (91%)	706 (94%)	46 (6%)	17	12

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LYS
1	A	37	ASN
1	A	45	THR
1	A	49	SER
1	A	52	GLU
1	A	90	LYS
1	A	93	LYS
1	B	2	SER
1	B	35	ARG
1	B	37	ASN
1	B	49	SER
1	B	65	SER
1	B	66	ILE
1	B	90	LYS
1	B	150	LYS
1	B	172	THR
1	B	173	LEU
1	B	198	GLU
1	B	200	LEU
1	B	207	SER
1	B	231	LEU
1	C	3	LYS

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Mol	Chain	Res	Type
1	C	37	ASN
1	C	49	SER
1	C	66	ILE
1	C	79	SER
1	C	90	LYS
1	C	173	LEU
1	C	207	SER
1	D	26	SER
1	D	28	ASN
1	D	35	ARG
1	D	37	ASN
1	D	45	THR
1	D	47	LYS
1	D	49	SER
1	D	52	GLU
1	D	65	SER
1	D	87	GLU
1	D	90	LYS
1	D	154	SER
1	D	156	ASN
1	D	173	LEU
1	D	195	GLU
1	D	200	LEU
1	D	231	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	ASN
1	A	62	ASN
1	B	4	ASN
1	B	37	ASN
1	B	39	ASN
1	B	62	ASN
1	B	115	ASN
1	B	230	ASN
1	C	28	ASN
1	C	37	ASN
1	C	108	HIS
1	C	115	ASN
1	C	146	HIS
1	C	156	ASN

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Mol	Chain	Res	Type
1	C	206	ASN
1	C	230	ASN
1	D	37	ASN
1	D	39	ASN
1	D	62	ASN
1	D	108	HIS
1	D	156	ASN
1	D	206	ASN
1	D	230	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	$\# Z > 2$
2	NAD	C	903	-	46,48,48	1.95	13 (28%)	64,73,73	1.78	16 (25%)
2	NAD	D	904	-	46,48,48	1.87	5 (10%)	64,73,73	2.09	17 (26%)
2	NAD	B	902	-	46,48,48	2.00	9 (19%)	64,73,73	1.53	12 (18%)
2	NAD	A	901	-	46,48,48	2.23	6 (13%)	64,73,73	2.24	19 (29%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	C	903	-	-	3/30/62/62	0/5/5/5
2	NAD	D	904	-	-	8/30/62/62	0/5/5/5
2	NAD	B	902	-	-	4/30/62/62	0/5/5/5
2	NAD	A	901	-	-	7/30/62/62	0/5/5/5

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	NAD	C2N-N1N	10.89	1.46	1.35
2	D	904	NAD	C2N-N1N	10.04	1.46	1.35
2	C	903	NAD	C2N-N1N	8.69	1.44	1.35
2	B	902	NAD	C2N-N1N	6.37	1.42	1.35
2	A	901	NAD	PN-O3	-5.03	1.54	1.59
2	B	902	NAD	O4D-C1D	4.51	1.46	1.40
2	A	901	NAD	O4D-C1D	4.38	1.46	1.40
2	B	902	NAD	PN-O3	-4.23	1.54	1.59
2	B	902	NAD	C3N-C7N	4.16	1.56	1.50
2	A	901	NAD	C3N-C7N	3.49	1.55	1.50
2	A	901	NAD	C2N-C3N	3.35	1.44	1.39
2	B	902	NAD	C6N-N1N	3.34	1.43	1.35
2	B	902	NAD	PA-O3	3.04	1.62	1.59
2	A	901	NAD	C6N-N1N	3.01	1.42	1.35
2	C	903	NAD	PN-O3	-2.87	1.56	1.59
2	C	903	NAD	C7N-N7N	2.87	1.38	1.33
2	D	904	NAD	C6N-N1N	2.85	1.41	1.35
2	C	903	NAD	O5D-C5D	2.85	1.55	1.44
2	C	903	NAD	C5A-N7A	-2.78	1.34	1.39
2	B	902	NAD	C5A-N7A	-2.76	1.34	1.39
2	B	902	NAD	C7N-N7N	2.74	1.38	1.33
2	C	903	NAD	O2D-C2D	2.56	1.49	1.43
2	D	904	NAD	C5A-N7A	-2.36	1.34	1.39
2	C	903	NAD	PA-O1A	-2.34	1.42	1.50
2	C	903	NAD	C4A-N9A	-2.21	1.33	1.37
2	B	902	NAD	C5N-C4N	2.17	1.42	1.38
2	C	903	NAD	O3B-C3B	2.17	1.48	1.43
2	C	903	NAD	C5N-C4N	2.17	1.42	1.38
2	C	903	NAD	O4B-C1B	2.09	1.46	1.42
2	C	903	NAD	C6N-N1N	2.05	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	903	NAD	PA-O2A	-2.04	1.45	1.55
2	D	904	NAD	O4D-C4D	2.03	1.49	1.45
2	D	904	NAD	C6N-C5N	2.01	1.42	1.38

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	NAD	C4D-O4D-C1D	-6.34	104.12	109.92
2	A	901	NAD	C5A-C4A-N3A	-5.92	118.56	126.72
2	D	904	NAD	N3A-C2A-N1A	-5.45	120.33	128.58
2	D	904	NAD	N9A-C8A-N7A	-5.39	106.29	113.94
2	D	904	NAD	C5A-C4A-N3A	-5.15	119.63	126.72
2	D	904	NAD	C5A-N7A-C8A	5.14	111.53	103.45
2	A	901	NAD	N9A-C8A-N7A	-4.98	106.87	113.94
2	D	904	NAD	C4A-C5A-N7A	-4.76	105.14	110.58
2	A	901	NAD	N3A-C2A-N1A	-4.67	121.51	128.58
2	C	903	NAD	C5A-C4A-N3A	-4.44	120.60	126.72
2	A	901	NAD	C2A-N3A-C4A	4.20	122.09	111.83
2	A	901	NAD	N3A-C4A-N9A	4.14	134.20	127.17
2	B	902	NAD	C4D-O4D-C1D	-4.12	106.15	109.92
2	A	901	NAD	C4A-N9A-C8A	4.01	109.95	105.74
2	A	901	NAD	C5A-N7A-C8A	3.99	109.72	103.45
2	D	904	NAD	C2A-N3A-C4A	3.95	121.47	111.83
2	C	903	NAD	N9A-C8A-N7A	-3.85	108.47	113.94
2	C	903	NAD	O3-PA-O1A	-3.80	99.28	110.70
2	A	901	NAD	C4A-C5A-N7A	-3.75	106.29	110.58
2	C	903	NAD	N3A-C2A-N1A	-3.70	122.98	128.58
2	D	904	NAD	C4A-N9A-C8A	3.69	109.61	105.74
2	B	902	NAD	C5A-C4A-N3A	-3.66	121.67	126.72
2	B	902	NAD	N3A-C2A-N1A	-3.64	123.07	128.58
2	A	901	NAD	C6N-N1N-C2N	-3.62	118.80	121.88
2	D	904	NAD	N3A-C4A-N9A	3.37	132.91	127.17
2	D	904	NAD	C5N-C6N-N1N	-3.36	115.80	120.38
2	D	904	NAD	C3N-C7N-N7N	-3.28	113.70	117.74
2	C	903	NAD	O2N-PN-O3	3.14	115.75	107.27
2	C	903	NAD	C5A-N7A-C8A	3.08	108.29	103.45
2	D	904	NAD	C6N-C5N-C4N	3.03	123.82	119.45
2	B	902	NAD	N9A-C8A-N7A	-3.02	109.65	113.94
2	C	903	NAD	C2N-C3N-C4N	3.00	121.74	118.26
2	D	904	NAD	C4D-O4D-C1D	-2.98	107.19	109.92
2	B	902	NAD	N3A-C4A-N9A	2.90	132.09	127.17
2	C	903	NAD	C2A-N3A-C4A	2.84	118.76	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	903	NAD	C4A-C5A-N7A	-2.82	107.36	110.58
2	C	903	NAD	O2A-PA-O1A	2.72	125.08	112.44
2	B	902	NAD	C3N-C7N-N7N	-2.70	114.42	117.74
2	A	901	NAD	C2N-N1N-C1D	2.69	125.08	119.13
2	C	903	NAD	O7N-C7N-C3N	-2.63	116.38	119.60
2	C	903	NAD	N3A-C4A-N9A	2.61	131.61	127.17
2	A	901	NAD	C3N-C7N-N7N	-2.54	114.61	117.74
2	B	902	NAD	C4A-N9A-C8A	2.52	108.38	105.74
2	B	902	NAD	C6N-N1N-C2N	-2.50	119.75	121.88
2	A	901	NAD	O3-PN-O1N	-2.48	103.25	110.70
2	A	901	NAD	O3B-C3B-C2B	-2.46	103.93	111.82
2	A	901	NAD	O2A-PA-O3	2.45	113.89	107.27
2	A	901	NAD	O2N-PN-O1N	2.44	123.78	112.44
2	A	901	NAD	O4B-C1B-N9A	-2.43	103.42	108.09
2	D	904	NAD	C2A-N1A-C6A	2.43	122.72	118.73
2	C	903	NAD	C5N-C6N-N1N	-2.38	117.13	120.38
2	B	902	NAD	O2A-PA-O3	2.36	113.65	107.27
2	D	904	NAD	O4B-C1B-N9A	-2.36	103.56	108.09
2	D	904	NAD	O2A-PA-O1A	2.36	123.40	112.44
2	B	902	NAD	C2A-N3A-C4A	2.30	117.45	111.83
2	A	901	NAD	O2N-PN-O3	2.28	113.44	107.27
2	C	903	NAD	C4A-N9A-C8A	2.20	108.05	105.74
2	B	902	NAD	C5D-C4D-C3D	-2.13	107.53	115.21
2	D	904	NAD	C6A-C5A-N7A	2.11	136.16	132.09
2	A	901	NAD	O7N-C7N-N7N	2.08	125.62	122.62
2	D	904	NAD	O3D-C3D-C2D	-2.07	105.17	111.82
2	C	903	NAD	O7N-C7N-N7N	2.04	125.57	122.62
2	C	903	NAD	C4D-O4D-C1D	2.02	111.77	109.92
2	B	902	NAD	C5A-N7A-C8A	2.01	106.61	103.45

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	NAD	C5D-O5D-PN-O2N
2	D	904	NAD	C5D-O5D-PN-O3
2	D	904	NAD	C5D-O5D-PN-O1N
2	D	904	NAD	C5D-O5D-PN-O2N
2	D	904	NAD	O4D-C1D-N1N-C2N
2	B	902	NAD	O4D-C4D-C5D-O5D
2	A	901	NAD	C4N-C3N-C7N-N7N
2	B	902	NAD	C3D-C4D-C5D-O5D

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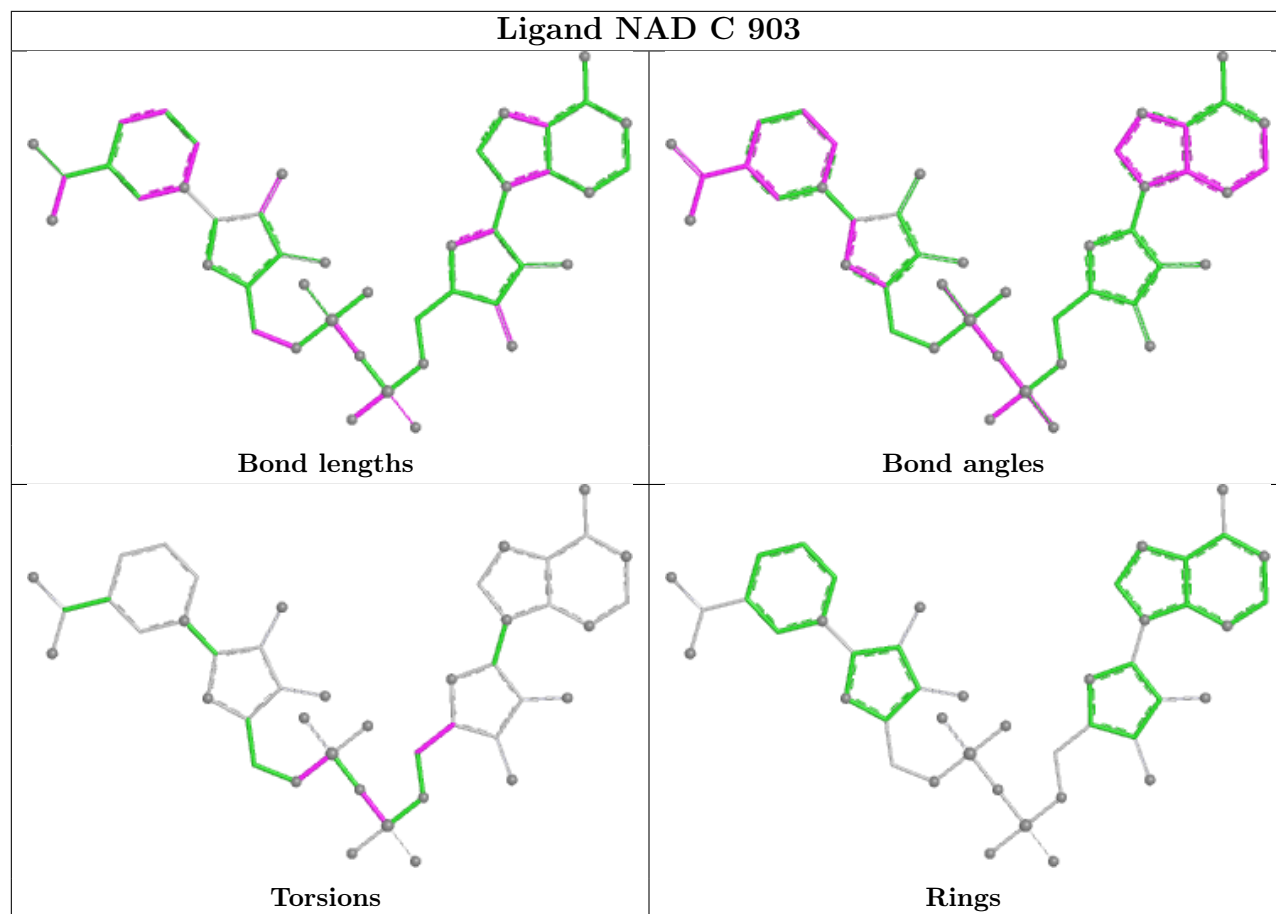
Mol	Chain	Res	Type	Atoms
2	A	901	NAD	C4N-C3N-C7N-O7N
2	A	901	NAD	C2N-C3N-C7N-N7N
2	A	901	NAD	C5D-O5D-PN-O3
2	C	903	NAD	C5D-O5D-PN-O3
2	D	904	NAD	PN-O3-PA-O2A
2	D	904	NAD	O4D-C1D-N1N-C6N
2	B	902	NAD	PN-O3-PA-O1A
2	B	902	NAD	PN-O3-PA-O2A
2	D	904	NAD	PN-O3-PA-O1A
2	A	901	NAD	C2N-C3N-C7N-O7N
2	C	903	NAD	PN-O3-PA-O2A
2	D	904	NAD	O4B-C4B-C5B-O5B
2	C	903	NAD	O4B-C4B-C5B-O5B
2	A	901	NAD	O4B-C4B-C5B-O5B

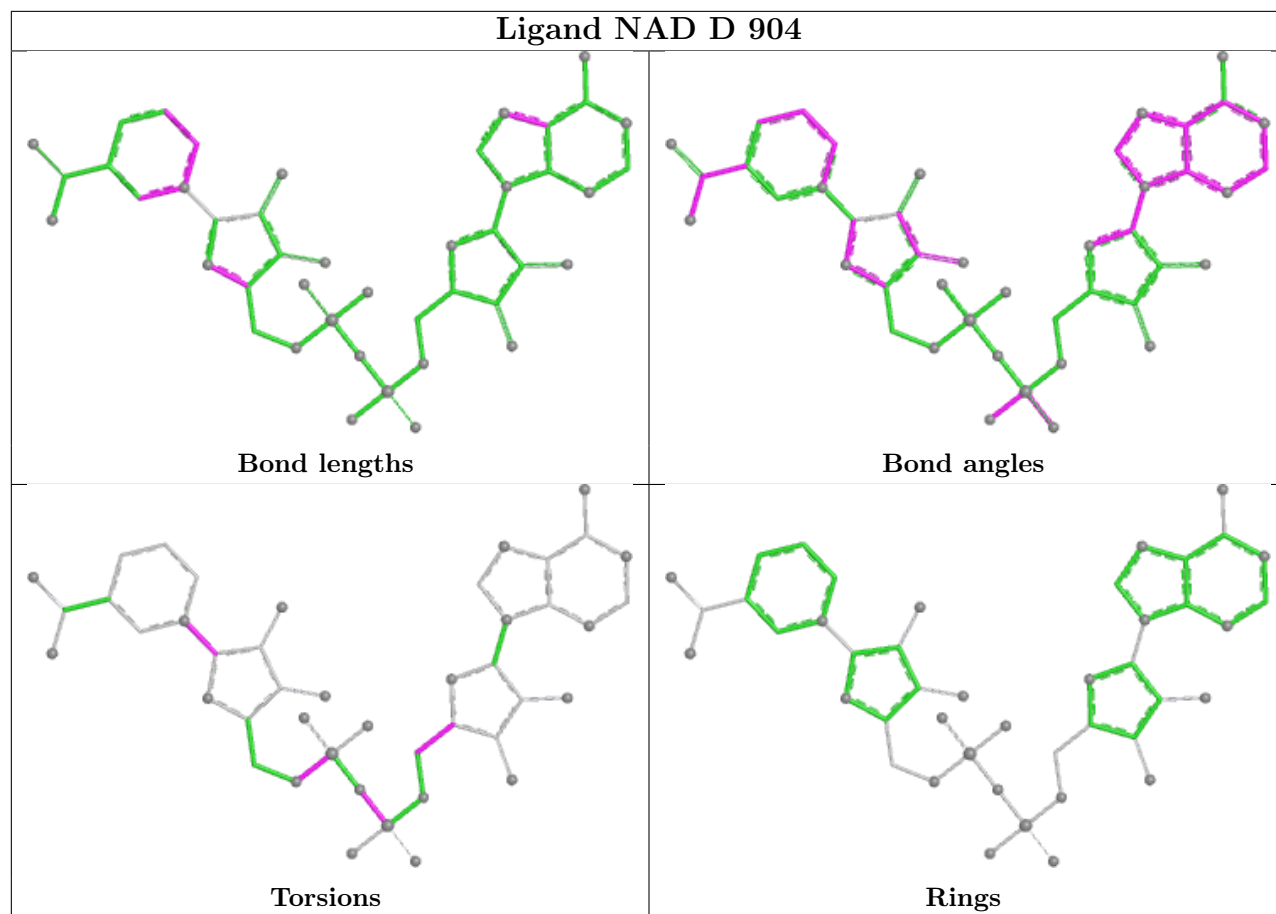
There are no ring outliers.

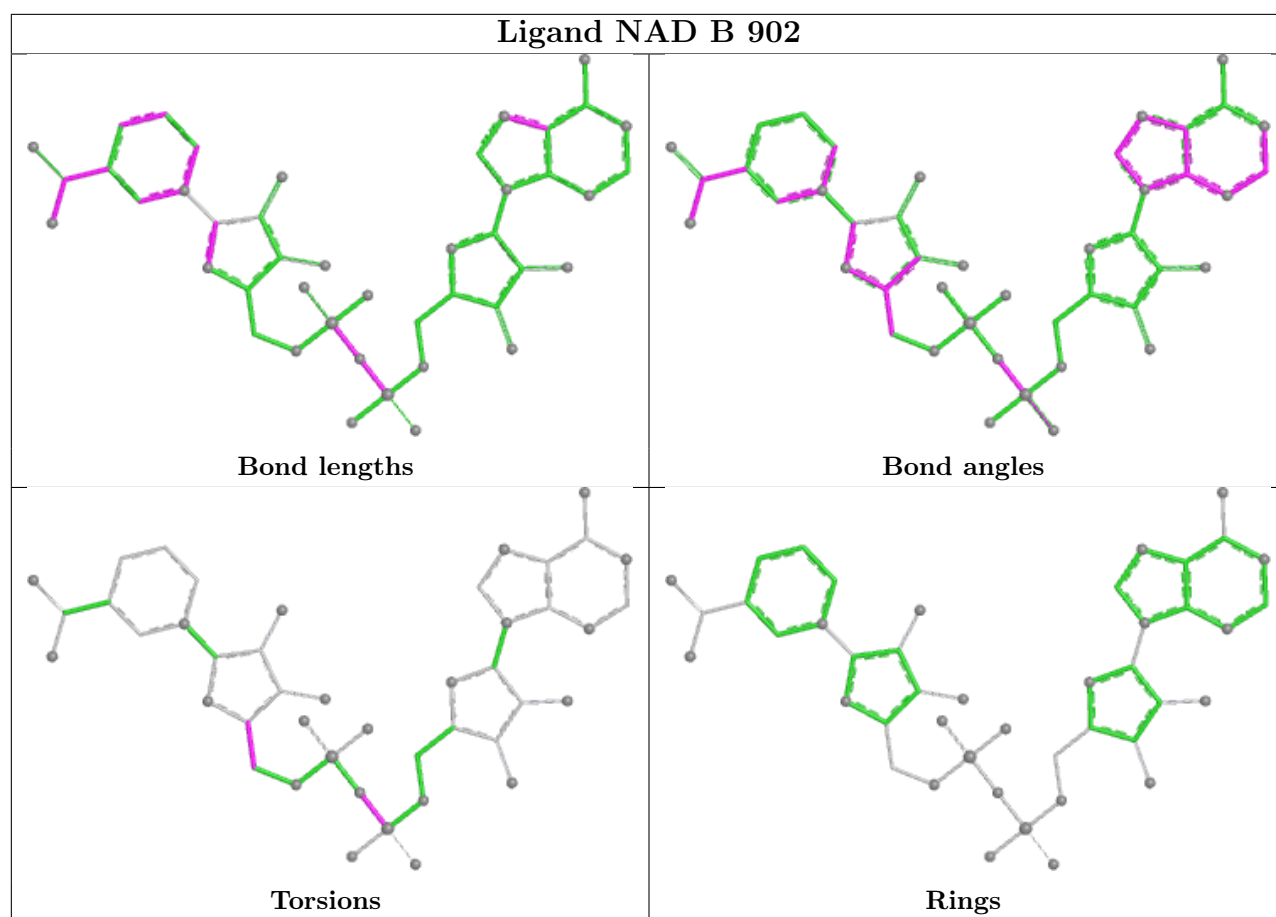
3 monomers are involved in 7 short contacts:

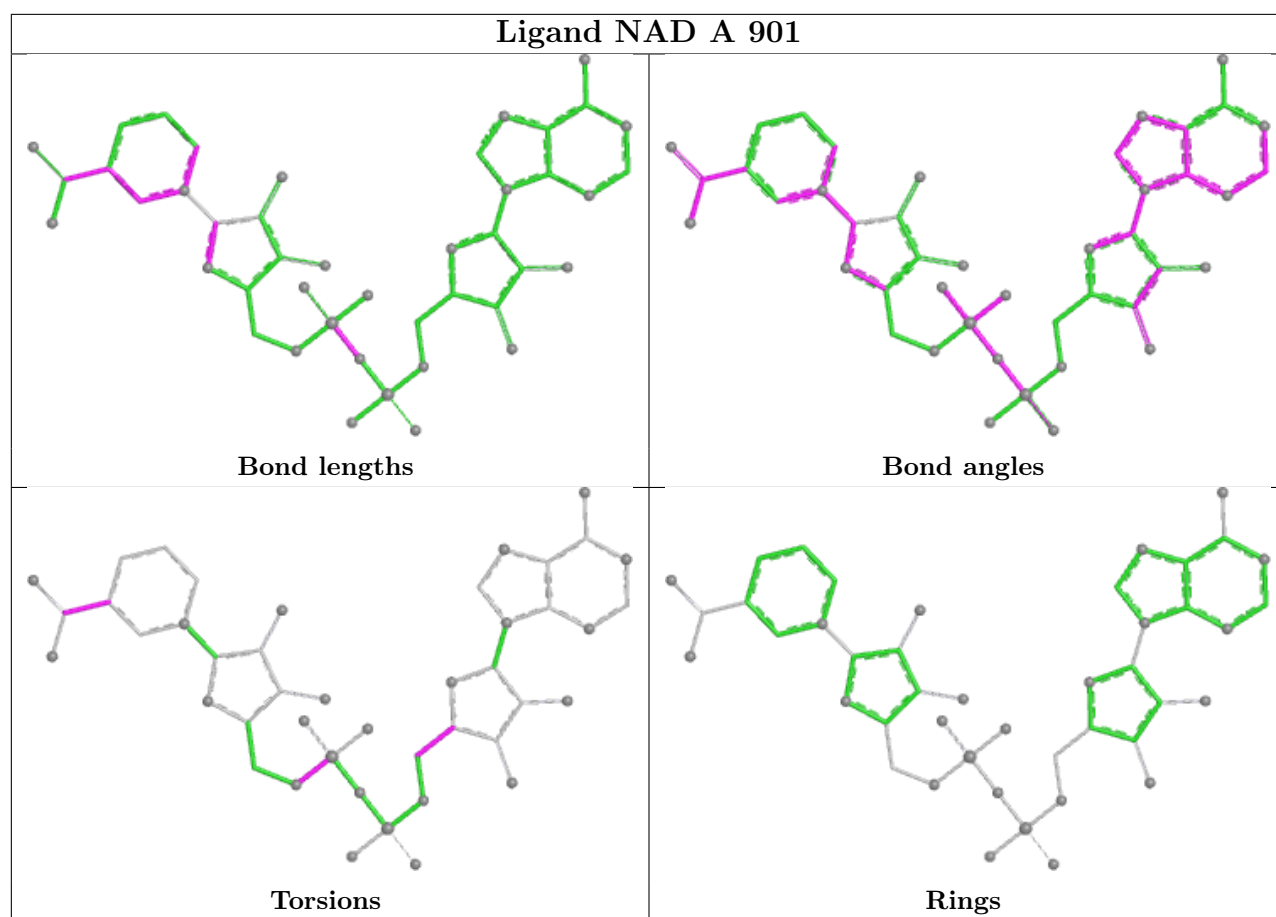
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	904	NAD	1	0
2	B	902	NAD	1	0
2	A	901	NAD	5	0

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	230/251 (91%)	-0.44	3 (1%) 75 78	20, 33, 55, 68	0
1	B	230/251 (91%)	0.03	1 (0%) 88 90	26, 52, 83, 95	0
1	C	230/251 (91%)	-0.54	0 100 100	18, 31, 49, 60	0
1	D	230/251 (91%)	-0.22	2 (0%) 81 83	18, 38, 60, 75	0
All	All	920/1004 (91%)	-0.29	6 (0%) 84 85	18, 37, 68, 95	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	182	MET	2.6
1	A	2	SER	2.2
1	A	66	ILE	2.2
1	B	231	LEU	2.2
1	A	58	ILE	2.1
1	D	187	PHE	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

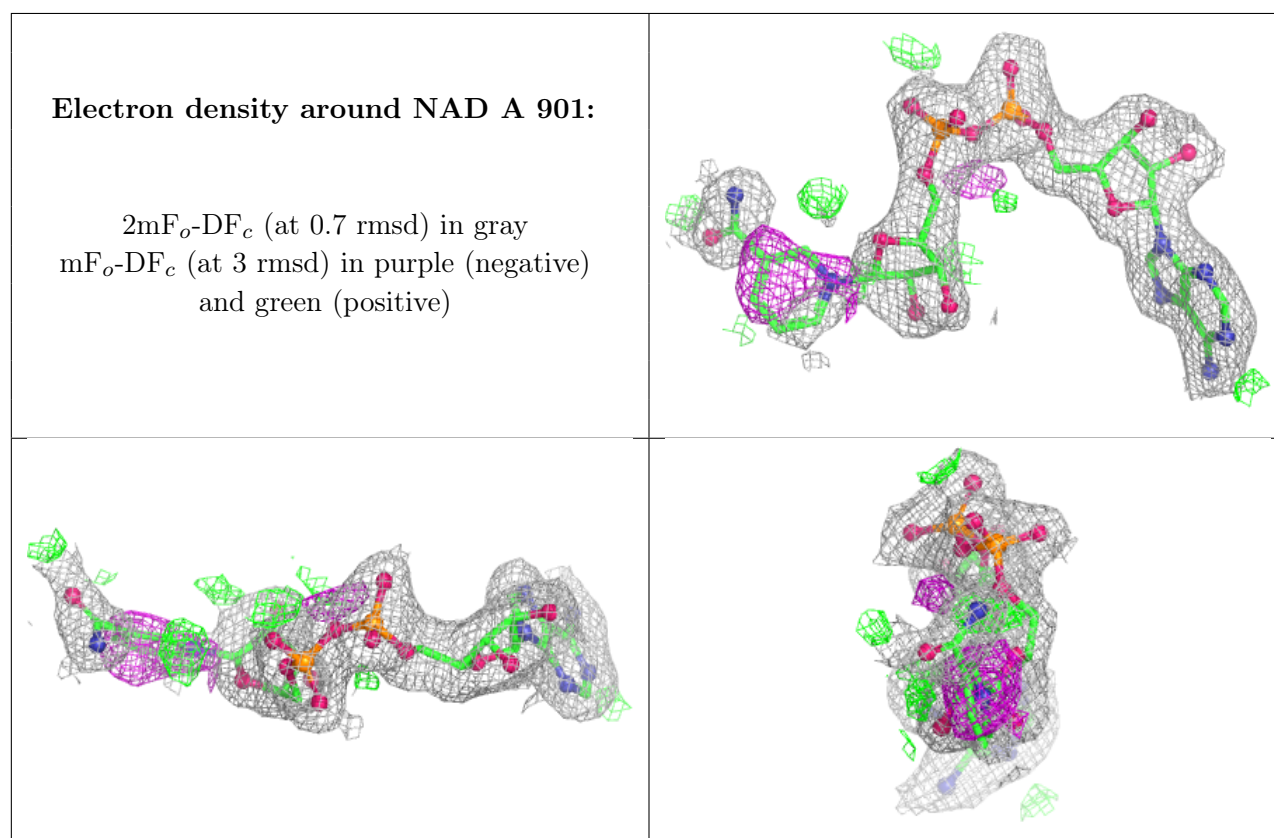
6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

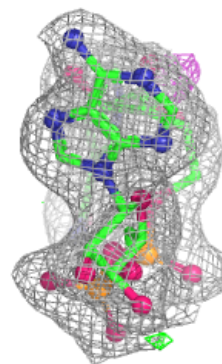
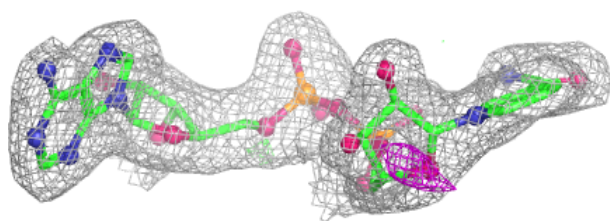
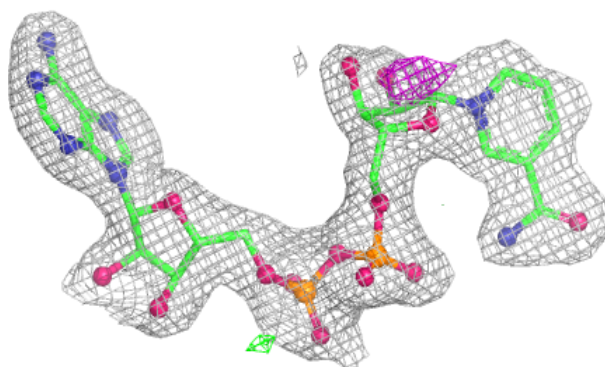
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAD	A	901	44/44	0.94	0.09	31,38,62,63	0
2	NAD	D	904	44/44	0.96	0.05	31,37,42,45	0
2	NAD	B	902	44/44	0.97	0.06	39,46,51,55	0
2	NAD	C	903	44/44	0.98	0.05	21,28,30,34	0

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.

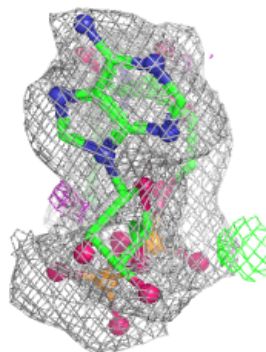
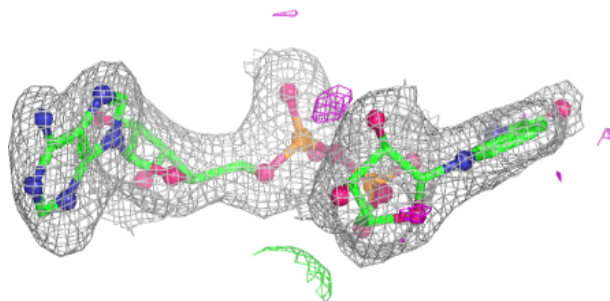
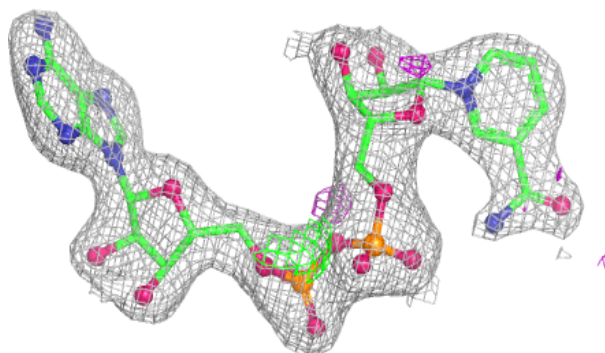


Electron density around NAD D 904:

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

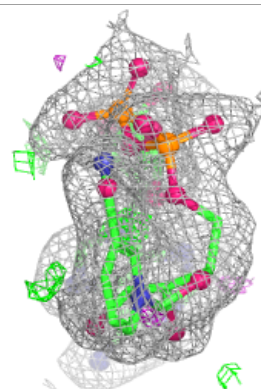
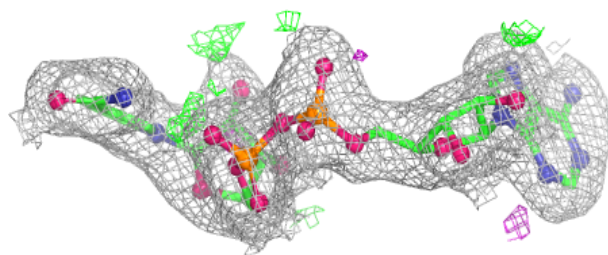
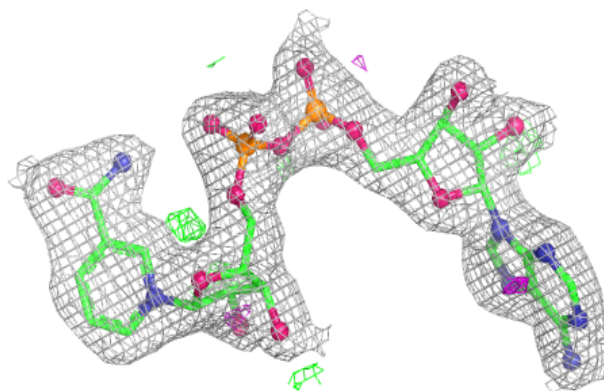
**Electron density around NAD B 902:**

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



Electron density around NAD C 903:

$2mF_o-DF_c$ (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.