



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 16, 2023 – 08:41 AM EDT

PDB ID : 1ZBQ
Title : Crystal Structure Of Human 17-Beta-Hydroxysteroid Dehydrogenase Type 4
In Complex With NAD
Authors : Lukacik, P.; Shafqat, N.; Kavanagh, K.; Bray, J.; von Delft, F.; Edwards,
A.; Arrowsmith, C.; Sundstrom, M.; Oppermann, U.; Structural Genomics
Consortium (SGC)
Deposited on : 2005-04-08
Resolution : 2.19 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](#) ①) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

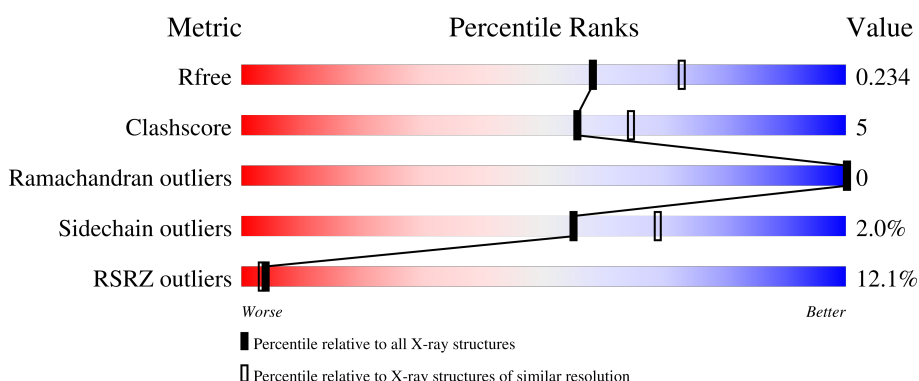
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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.



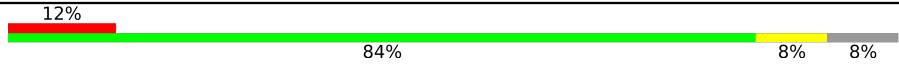
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	327	 9% 83% 9% 8%
1	B	327	 10% 86% 7% 8%
1	C	327	 10% 80% 11% 8%
1	D	327	 10% 81% 11% 8%
1	E	327	 15% 84% 9% 8%

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Mol	Chain	Length	Quality of chain
1	F	327	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a red segment on the left labeled '12%', a large green segment labeled '84%', a yellow segment labeled '8%', and a grey segment on the far right labeled '8%'.</p>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14189 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 17-beta-hydroxysteroid dehydrogenase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	302	2267	1430	409	419	9	0	2	0
1	B	302	2264	1427	410	418	9	0	1	0
1	C	302	2268	1428	409	422	9	0	1	0
1	D	302	2289	1442	419	419	9	0	3	0
1	E	302	2235	1403	408	415	9	0	1	0
1	F	302	2259	1418	407	425	9	0	2	0

There are 138 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	GLY	-	cloning artifact	UNP P51659
A	-19	SER	-	cloning artifact	UNP P51659
A	-18	SER	-	cloning artifact	UNP P51659
A	-17	HIS	-	expression tag	UNP P51659
A	-16	HIS	-	expression tag	UNP P51659
A	-15	HIS	-	expression tag	UNP P51659
A	-14	HIS	-	expression tag	UNP P51659
A	-13	HIS	-	expression tag	UNP P51659
A	-12	HIS	-	expression tag	UNP P51659
A	-11	SER	-	cloning artifact	UNP P51659
A	-10	SER	-	cloning artifact	UNP P51659
A	-9	GLY	-	cloning artifact	UNP P51659
A	-8	ARG	-	cloning artifact	UNP P51659
A	-7	GLU	-	cloning artifact	UNP P51659
A	-6	ASN	-	cloning artifact	UNP P51659
A	-5	LEU	-	cloning artifact	UNP P51659
A	-4	TYR	-	cloning artifact	UNP P51659

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	PHE	-	cloning artifact	UNP P51659
A	-2	GLN	-	cloning artifact	UNP P51659
A	-1	GLY	-	cloning artifact	UNP P51659
A	0	HIS	-	cloning artifact	UNP P51659
A	305	GLY	-	cloning artifact	UNP P51659
A	306	SER	-	cloning artifact	UNP P51659
B	-20	GLY	-	cloning artifact	UNP P51659
B	-19	SER	-	cloning artifact	UNP P51659
B	-18	SER	-	cloning artifact	UNP P51659
B	-17	HIS	-	expression tag	UNP P51659
B	-16	HIS	-	expression tag	UNP P51659
B	-15	HIS	-	expression tag	UNP P51659
B	-14	HIS	-	expression tag	UNP P51659
B	-13	HIS	-	expression tag	UNP P51659
B	-12	HIS	-	expression tag	UNP P51659
B	-11	SER	-	cloning artifact	UNP P51659
B	-10	SER	-	cloning artifact	UNP P51659
B	-9	GLY	-	cloning artifact	UNP P51659
B	-8	ARG	-	cloning artifact	UNP P51659
B	-7	GLU	-	cloning artifact	UNP P51659
B	-6	ASN	-	cloning artifact	UNP P51659
B	-5	LEU	-	cloning artifact	UNP P51659
B	-4	TYR	-	cloning artifact	UNP P51659
B	-3	PHE	-	cloning artifact	UNP P51659
B	-2	GLN	-	cloning artifact	UNP P51659
B	-1	GLY	-	cloning artifact	UNP P51659
B	0	HIS	-	cloning artifact	UNP P51659
B	305	GLY	-	cloning artifact	UNP P51659
B	306	SER	-	cloning artifact	UNP P51659
C	-20	GLY	-	cloning artifact	UNP P51659
C	-19	SER	-	cloning artifact	UNP P51659
C	-18	SER	-	cloning artifact	UNP P51659
C	-17	HIS	-	expression tag	UNP P51659
C	-16	HIS	-	expression tag	UNP P51659
C	-15	HIS	-	expression tag	UNP P51659
C	-14	HIS	-	expression tag	UNP P51659
C	-13	HIS	-	expression tag	UNP P51659
C	-12	HIS	-	expression tag	UNP P51659
C	-11	SER	-	cloning artifact	UNP P51659
C	-10	SER	-	cloning artifact	UNP P51659
C	-9	GLY	-	cloning artifact	UNP P51659
C	-8	ARG	-	cloning artifact	UNP P51659

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	GLU	-	cloning artifact	UNP P51659
C	-6	ASN	-	cloning artifact	UNP P51659
C	-5	LEU	-	cloning artifact	UNP P51659
C	-4	TYR	-	cloning artifact	UNP P51659
C	-3	PHE	-	cloning artifact	UNP P51659
C	-2	GLN	-	cloning artifact	UNP P51659
C	-1	GLY	-	cloning artifact	UNP P51659
C	0	HIS	-	cloning artifact	UNP P51659
C	305	GLY	-	cloning artifact	UNP P51659
C	306	SER	-	cloning artifact	UNP P51659
D	-20	GLY	-	cloning artifact	UNP P51659
D	-19	SER	-	cloning artifact	UNP P51659
D	-18	SER	-	cloning artifact	UNP P51659
D	-17	HIS	-	expression tag	UNP P51659
D	-16	HIS	-	expression tag	UNP P51659
D	-15	HIS	-	expression tag	UNP P51659
D	-14	HIS	-	expression tag	UNP P51659
D	-13	HIS	-	expression tag	UNP P51659
D	-12	HIS	-	expression tag	UNP P51659
D	-11	SER	-	cloning artifact	UNP P51659
D	-10	SER	-	cloning artifact	UNP P51659
D	-9	GLY	-	cloning artifact	UNP P51659
D	-8	ARG	-	cloning artifact	UNP P51659
D	-7	GLU	-	cloning artifact	UNP P51659
D	-6	ASN	-	cloning artifact	UNP P51659
D	-5	LEU	-	cloning artifact	UNP P51659
D	-4	TYR	-	cloning artifact	UNP P51659
D	-3	PHE	-	cloning artifact	UNP P51659
D	-2	GLN	-	cloning artifact	UNP P51659
D	-1	GLY	-	cloning artifact	UNP P51659
D	0	HIS	-	cloning artifact	UNP P51659
D	305	GLY	-	cloning artifact	UNP P51659
D	306	SER	-	cloning artifact	UNP P51659
E	-20	GLY	-	cloning artifact	UNP P51659
E	-19	SER	-	cloning artifact	UNP P51659
E	-18	SER	-	cloning artifact	UNP P51659
E	-17	HIS	-	expression tag	UNP P51659
E	-16	HIS	-	expression tag	UNP P51659
E	-15	HIS	-	expression tag	UNP P51659
E	-14	HIS	-	expression tag	UNP P51659
E	-13	HIS	-	expression tag	UNP P51659
E	-12	HIS	-	expression tag	UNP P51659

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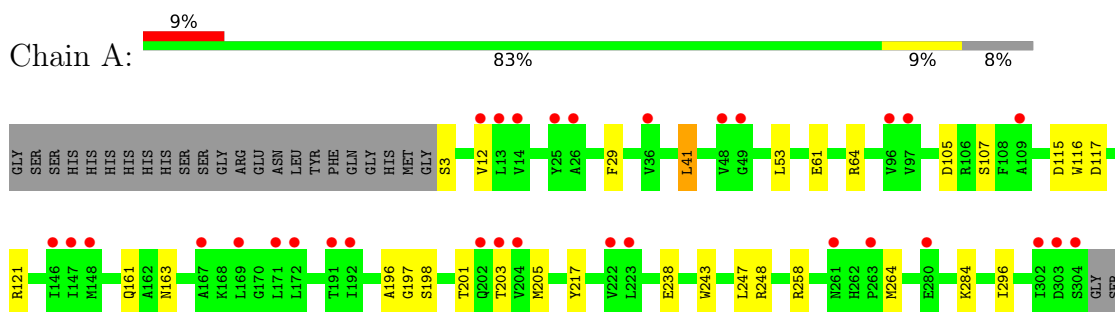
Chain	Residue	Modelled	Actual	Comment	Reference
E	-11	SER	-	cloning artifact	UNP P51659
E	-10	SER	-	cloning artifact	UNP P51659
E	-9	GLY	-	cloning artifact	UNP P51659
E	-8	ARG	-	cloning artifact	UNP P51659
E	-7	GLU	-	cloning artifact	UNP P51659
E	-6	ASN	-	cloning artifact	UNP P51659
E	-5	LEU	-	cloning artifact	UNP P51659
E	-4	TYR	-	cloning artifact	UNP P51659
E	-3	PHE	-	cloning artifact	UNP P51659
E	-2	GLN	-	cloning artifact	UNP P51659
E	-1	GLY	-	cloning artifact	UNP P51659
E	0	HIS	-	cloning artifact	UNP P51659
E	305	GLY	-	cloning artifact	UNP P51659
E	306	SER	-	cloning artifact	UNP P51659
F	-20	GLY	-	cloning artifact	UNP P51659
F	-19	SER	-	cloning artifact	UNP P51659
F	-18	SER	-	cloning artifact	UNP P51659
F	-17	HIS	-	expression tag	UNP P51659
F	-16	HIS	-	expression tag	UNP P51659
F	-15	HIS	-	expression tag	UNP P51659
F	-14	HIS	-	expression tag	UNP P51659
F	-13	HIS	-	expression tag	UNP P51659
F	-12	HIS	-	expression tag	UNP P51659
F	-11	SER	-	cloning artifact	UNP P51659
F	-10	SER	-	cloning artifact	UNP P51659
F	-9	GLY	-	cloning artifact	UNP P51659
F	-8	ARG	-	cloning artifact	UNP P51659
F	-7	GLU	-	cloning artifact	UNP P51659
F	-6	ASN	-	cloning artifact	UNP P51659
F	-5	LEU	-	cloning artifact	UNP P51659
F	-4	TYR	-	cloning artifact	UNP P51659
F	-3	PHE	-	cloning artifact	UNP P51659
F	-2	GLN	-	cloning artifact	UNP P51659
F	-1	GLY	-	cloning artifact	UNP P51659
F	0	HIS	-	cloning artifact	UNP P51659
F	305	GLY	-	cloning artifact	UNP P51659
F	306	SER	-	cloning artifact	UNP P51659

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).

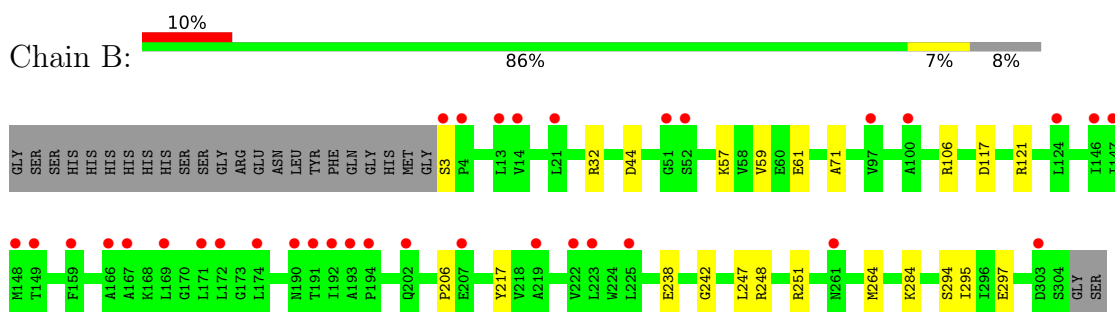
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

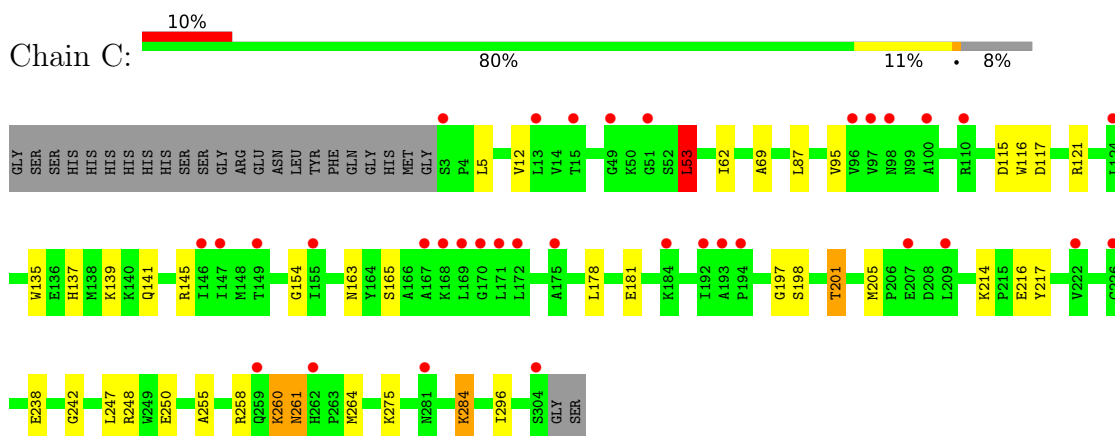
- Molecule 1: 17-beta-hydroxysteroid dehydrogenase 4



- Molecule 1: 17-beta-hydroxysteroid dehydrogenase 4

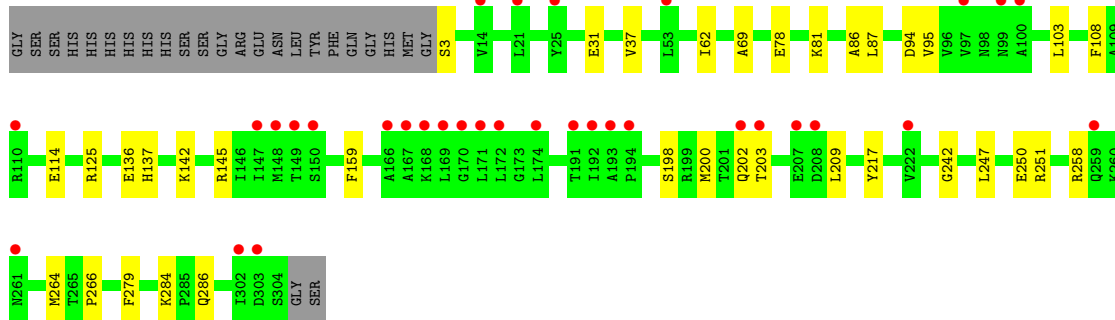


- Molecule 1: 17-beta-hydroxysteroid dehydrogenase 4



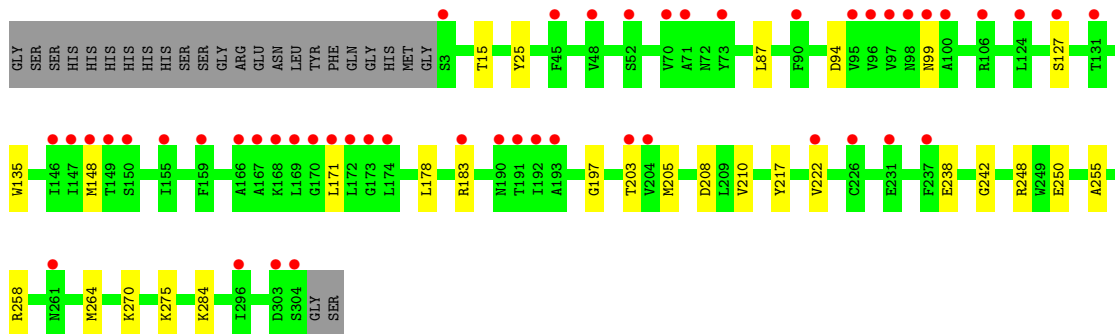
- Molecule 1: 17-beta-hydroxysteroid dehydrogenase 4

Chain D:



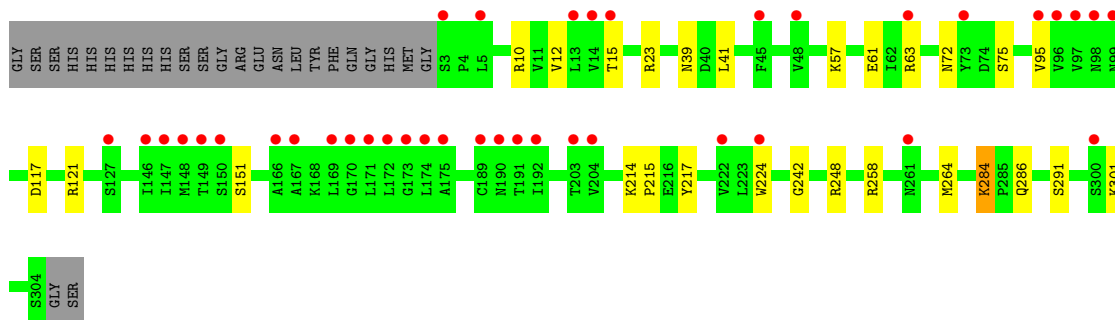
- Molecule 1: 17-beta-hydroxysteroid dehydrogenase 4

Chain E:



- Molecule 1: 17-beta-hydroxysteroid dehydrogenase 4

Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	50.83Å 50.77Å 183.78Å 87.52° 87.07° 70.75°	Depositor
Resolution (Å)	50.57 – 2.19 32.68 – 2.19	Depositor EDS
% Data completeness (in resolution range)	76.2 (50.57-2.19) 76.3 (32.68-2.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.26 (at 2.20Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.188 , 0.236 0.186 , 0.234	Depositor DCC
R_{free} test set	3383 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	35.7	Xtrriage
Anisotropy	0.123	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.019 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14189	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% 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 i

5.1 Standard geometry i

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	0.59	0/2310	0.65	0/3126
1	B	0.62	0/2307	0.67	0/3120
1	C	0.62	0/2311	0.67	1/3128 (0.0%)
1	D	0.58	1/2339 (0.0%)	0.67	1/3159 (0.0%)
1	E	0.53	0/2278	0.61	0/3089
1	F	0.61	2/2305 (0.1%)	0.65	2/3124 (0.1%)
All	All	0.59	3/13850 (0.0%)	0.65	4/18746 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	63	ARG	CZ-NH1	9.30	1.45	1.33
1	F	10	ARG	NE-CZ	5.88	1.40	1.33
1	D	250	GLU	CB-CG	-5.08	1.42	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	63	ARG	NE-CZ-NH2	-9.62	115.49	120.30
1	F	63	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	D	94	ASP	CB-CG-OD2	5.28	123.05	118.30
1	C	53	LEU	CA-CB-CG	5.12	127.07	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	260	LYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2267	0	2227	31	0
1	B	2264	0	2226	24	0
1	C	2268	0	2229	38	0
1	D	2289	0	2282	27	0
1	E	2235	0	2158	32	0
1	F	2259	0	2184	22	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	C	44	0	26	0	0
2	D	44	0	26	0	0
2	E	44	0	26	1	0
2	F	44	0	26	0	0
3	A	61	0	0	1	0
3	B	67	0	0	2	0
3	C	66	0	0	0	0
3	D	64	0	0	2	0
3	E	42	0	0	0	0
3	F	43	0	0	2	0
All	All	14189	0	13462	139	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 5.

All (139) 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:E:258:ARG:HB2	1:E:264:MET:HE2	1.46	0.94
1:E:148:MET:HE1	1:E:171:LEU:HD22	1.57	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:264:MET:CE	1:F:242:GLY:HA2	2.04	0.86
1:F:258:ARG:HB2	1:F:264:MET:HE2	1.58	0.85
1:E:264:MET:HE1	1:F:242:GLY:HA2	1.58	0.83
1:A:117:ASP:O	1:A:121:ARG:HG3	1.79	0.83
1:E:148:MET:CE	1:E:171:LEU:HD22	2.08	0.83
1:C:258:ARG:HB2	1:C:264:MET:HE2	1.62	0.82
1:A:217:TYR:HA	1:B:264:MET:CE	2.10	0.81
1:A:217:TYR:HA	1:B:264:MET:HE3	1.65	0.77
1:C:242:GLY:HA2	1:D:264:MET:CE	2.14	0.77
1:B:206:PRO:HA	3:B:1063:HOH:O	1.86	0.74
1:A:198:SER:H	1:A:201:THR:HG22	1.51	0.74
1:E:242:GLY:HA2	1:F:264:MET:HE1	1.69	0.74
1:E:242:GLY:HA2	1:F:264:MET:CE	2.22	0.69
1:A:217:TYR:CB	1:B:264:MET:HE1	2.22	0.68
1:D:258:ARG:HB2	1:D:264:MET:HE2	1.76	0.68
1:C:242:GLY:HA2	1:D:264:MET:HE1	1.77	0.67
1:C:264:MET:CE	1:D:242:GLY:HA2	2.24	0.67
1:A:217:TYR:HB3	1:B:264:MET:HE1	1.76	0.67
1:A:258:ARG:HD3	1:A:264:MET:HE2	1.77	0.66
1:C:115:ASP:O	1:C:163[B]:ASN:ND2	2.27	0.66
1:C:264:MET:HE1	1:D:242:GLY:HA2	1.78	0.64
1:C:198:SER:H	1:C:201:THR:HG22	1.62	0.63
1:A:217:TYR:HA	1:B:264:MET:HE1	1.82	0.61
1:C:242:GLY:HA2	1:D:264:MET:HE2	1.81	0.61
1:F:258:ARG:HD3	1:F:264:MET:HE2	1.83	0.60
1:A:196:ALA:O	1:A:201:THR:HG21	2.02	0.59
1:E:258:ARG:HD3	1:E:264:MET:CE	2.33	0.58
1:C:117:ASP:O	1:C:121:ARG:HG3	2.04	0.58
1:E:264:MET:HE2	1:F:242:GLY:HA2	1.85	0.58
1:A:217:TYR:CA	1:B:264:MET:HE1	2.34	0.57
1:C:248:ARG:HG2	1:D:279:PHE:CE2	2.39	0.57
1:A:198:SER:H	1:A:201:THR:CG2	2.17	0.57
1:E:250:GLU:HG3	1:E:284:LYS:NZ	2.20	0.56
1:C:250:GLU:HG3	1:C:284:LYS:HZ3	1.71	0.56
1:C:250:GLU:HG3	1:C:284:LYS:NZ	2.21	0.56
1:A:264:MET:HE3	1:B:217:TYR:HA	1.90	0.54
1:F:57:LYS:O	1:F:61:GLU:HG3	2.07	0.54
1:C:135:TRP:NE1	1:C:139:LYS:HD2	2.23	0.54
1:E:264:MET:HE1	1:F:217:TYR:HB3	1.90	0.54
1:B:57:LYS:O	1:B:61:GLU:HG3	2.08	0.53
1:C:296:ILE:HD13	1:D:209:LEU:HD21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:95:VAL:HG22	1:D:145:ARG:HB2	1.89	0.53
1:A:198:SER:N	1:A:201:THR:HG22	2.22	0.53
1:A:238:GLU:HG3	1:A:247:LEU:HD11	1.90	0.53
1:A:61:GLU:OE1	1:A:64:ARG:NH1	2.42	0.52
1:C:5:LEU:HD12	1:D:266:PRO:HB2	1.90	0.52
1:C:238:GLU:OE2	1:D:251:ARG:HD2	2.09	0.52
1:A:115:ASP:O	1:A:163[B]:ASN:ND2	2.40	0.52
1:B:117:ASP:O	1:B:121:ARG:HG3	2.10	0.52
1:E:248:ARG:CZ	1:E:284:LYS:HG2	2.40	0.52
1:E:250:GLU:HG3	1:E:284:LYS:HZ2	1.74	0.51
1:F:258:ARG:HD3	1:F:264:MET:CE	2.40	0.51
1:C:264:MET:HE1	1:D:217:TYR:HB3	1.92	0.51
1:F:248:ARG:CZ	1:F:284:LYS:HG2	2.41	0.51
1:B:248:ARG:CZ	1:B:284:LYS:HG2	2.41	0.51
1:B:294:SER:HA	1:B:297:GLU:HG2	1.93	0.51
1:A:116:TRP:HA	1:A:163[B]:ASN:ND2	2.26	0.50
1:E:197:GLY:HA2	1:E:205:MET:HE1	1.92	0.50
1:A:41:LEU:HB3	3:A:1011:HOH:O	2.12	0.49
1:F:117:ASP:O	1:F:121:ARG:HG2	2.12	0.49
1:D:37:VAL:HG21	1:D:86:ALA:HB2	1.94	0.49
1:B:247:LEU:HD12	1:B:247:LEU:N	2.26	0.49
1:D:103:LEU:HD11	1:D:200:MET:HG3	1.93	0.49
1:F:23[A]:ARG:HD3	3:F:1024:HOH:O	2.11	0.49
1:E:148:MET:HE2	1:E:171:LEU:HD22	1.92	0.49
1:A:264:MET:CE	1:B:242:GLY:HA2	2.42	0.49
1:A:201:THR:HG23	1:A:205:MET:HE2	1.95	0.49
1:A:264:MET:CE	1:B:217:TYR:HA	2.43	0.49
1:C:12:VAL:HG22	1:C:95:VAL:HB	1.96	0.48
1:E:270:LYS:HG3	1:F:224:TRP:CH2	2.49	0.48
1:D:87:LEU:HD11	1:D:137:HIS:CE1	2.49	0.47
1:C:247:LEU:CD1	1:D:251:ARG:HG3	2.45	0.47
1:E:217:TYR:HB3	1:F:264:MET:HE1	1.95	0.47
1:C:260:LYS:HA	1:C:261:ASN:HD22	1.80	0.46
1:E:258:ARG:CB	1:E:264:MET:HE2	2.33	0.46
1:A:197:GLY:HA2	1:A:201:THR:CG2	2.45	0.46
1:F:12:VAL:HG22	1:F:95:VAL:HB	1.96	0.46
1:E:25:TYR:CZ	1:E:222:VAL:HG21	2.51	0.46
1:B:238:GLU:HG3	1:B:247:LEU:HD11	1.97	0.46
1:D:142:LYS:HE3	3:D:1046:HOH:O	2.15	0.46
1:A:197:GLY:HA2	1:A:201:THR:HG21	1.97	0.46
1:C:116:TRP:HA	1:C:163[B]:ASN:ND2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:258:ARG:HD3	1:E:264:MET:HE3	1.96	0.46
1:C:154:GLY:HA2	1:C:165:SER:HB2	1.98	0.45
1:E:148:MET:HE2	1:E:148:MET:HB3	1.67	0.45
1:A:264:MET:HE1	1:B:242:GLY:HA2	1.99	0.45
1:B:59:VAL:HG21	1:B:71:ALA:HB2	1.98	0.45
1:C:178:LEU:HD21	1:D:108:PHE:CD1	2.52	0.45
1:E:255:ALA:HB2	1:E:275:LYS:HD3	1.99	0.45
1:C:217:TYR:HB3	1:D:264:MET:HE1	1.99	0.45
1:D:125:ARG:HD3	3:D:1013:HOH:O	2.17	0.45
1:E:127:SER:HB3	1:E:148:MET:HE1	1.98	0.44
1:E:208:ASP:OD1	1:E:208:ASP:N	2.50	0.44
1:C:197:GLY:HA2	1:C:201:THR:HG21	2.00	0.44
1:F:41:LEU:HD13	1:F:75:SER:HB2	1.99	0.44
1:C:95:VAL:HG22	1:C:145:ARG:HB2	2.00	0.44
1:E:148:MET:HE1	1:E:171:LEU:CD2	2.38	0.44
2:E:1005:NAD:O1N	2:E:1005:NAD:N7N	2.49	0.44
1:C:238:GLU:HG3	1:C:247:LEU:HD11	2.00	0.44
1:C:135:TRP:HE1	1:C:139:LYS:HD2	1.81	0.43
1:F:39:ASN:ND2	1:F:72:ASN:OD1	2.48	0.43
1:D:78:GLU:HB3	1:D:81:LYS:HG3	2.00	0.43
1:D:62:ILE:HG21	1:D:69:ALA:HB2	2.01	0.43
1:A:12:VAL:HG11	1:A:29:PHE:CD1	2.54	0.43
1:C:197:GLY:HA2	1:C:201:THR:CG2	2.49	0.43
1:E:205:MET:HE3	1:E:210:VAL:HA	2.01	0.43
1:A:248:ARG:CZ	1:A:284:LYS:HG2	2.50	0.42
1:B:32[A]:ARG:HG2	1:B:32[A]:ARG:HH11	1.85	0.42
1:B:251:ARG:NH1	3:B:1026:HOH:O	2.52	0.42
1:E:15:THR:O	1:E:99:ASN:HB3	2.20	0.42
1:A:105:ASP:OD1	1:A:161:GLN:HG2	2.19	0.42
1:D:198:SER:O	1:D:202:GLN:HG3	2.19	0.42
1:E:127:SER:HB3	1:E:148:MET:CE	2.49	0.42
1:A:264:MET:HE1	1:B:217:TYR:HB3	2.01	0.42
1:D:103:LEU:CD1	1:D:200:MET:HG3	2.49	0.42
1:E:238:GLU:OE1	1:F:291:SER:OG	2.37	0.42
1:A:258:ARG:HB2	1:A:264:MET:HE2	2.02	0.42
1:C:87:LEU:HD11	1:C:137:HIS:CE1	2.54	0.42
1:C:62:ILE:HG21	1:C:69:ALA:HB2	2.02	0.41
1:C:248:ARG:CZ	1:C:284:LYS:HG2	2.50	0.41
1:F:151:SER:HB2	3:F:1035:HOH:O	2.20	0.41
1:A:243:TRP:CE3	1:B:295:ILE:HD12	2.55	0.41
1:A:258:ARG:HD3	1:A:264:MET:CE	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:TYR:CE1	1:E:222:VAL:HG21	2.55	0.41
1:C:53:LEU:HD23	1:C:53:LEU:H	1.86	0.41
1:C:248:ARG:HG2	1:D:279:PHE:CZ	2.55	0.41
1:D:247:LEU:HD12	1:D:247:LEU:N	2.36	0.41
1:E:135:TRP:CZ3	1:E:178:LEU:HD22	2.56	0.41
1:E:258:ARG:HD3	1:E:264:MET:HE2	2.01	0.41
1:C:141:GLN:HE21	1:C:141:GLN:HB2	1.67	0.40
1:C:181:GLU:HG2	1:D:159:PHE:CD1	2.56	0.40
1:B:294:SER:O	1:B:297:GLU:HG2	2.21	0.40
1:F:15:THR:HA	1:F:39:ASN:HB3	2.02	0.40
1:C:255:ALA:HB2	1:C:275:LYS:HD3	2.04	0.40
1:F:214:LYS:HA	1:F:215:PRO:HD2	1.88	0.40
1:B:44:ASP:OD1	1:B:44:ASP:C	2.60	0.40
1:C:214:LYS:HB3	1:C:216:GLU:HG2	2.04	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	302/327 (92%)	295 (98%)	7 (2%)	0	100	100
1	B	301/327 (92%)	297 (99%)	4 (1%)	0	100	100
1	C	301/327 (92%)	296 (98%)	5 (2%)	0	100	100
1	D	303/327 (93%)	296 (98%)	7 (2%)	0	100	100
1	E	301/327 (92%)	294 (98%)	7 (2%)	0	100	100
1	F	302/327 (92%)	296 (98%)	6 (2%)	0	100	100
All	All	1810/1962 (92%)	1774 (98%)	36 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	222/258 (86%)	216 (97%)	6 (3%)	44	57
1	B	222/258 (86%)	220 (99%)	2 (1%)	78	88
1	C	225/258 (87%)	220 (98%)	5 (2%)	52	65
1	D	229/258 (89%)	222 (97%)	7 (3%)	40	51
1	E	216/258 (84%)	212 (98%)	4 (2%)	57	71
1	F	221/258 (86%)	218 (99%)	3 (1%)	67	80
All	All	1335/1548 (86%)	1308 (98%)	27 (2%)	55	69

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	SER
1	A	41	LEU
1	A	53	LEU
1	A	107	SER
1	A	203	THR
1	A	296	ILE
1	B	3	SER
1	B	106	ARG
1	C	53	LEU
1	C	201	THR
1	C	205	MET
1	C	261	ASN
1	C	284	LYS
1	D	3	SER
1	D	31	GLU
1	D	114	GLU
1	D	136	GLU
1	D	203	THR
1	D	284	LYS
1	D	286	GLN
1	E	87	LEU
1	E	94	ASP

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Mol	Chain	Res	Type
1	E	183	ARG
1	E	203	THR
1	F	284	LYS
1	F	286	GLN
1	F	301	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	HIS
1	B	120	HIS
1	B	141	GLN
1	C	120	HIS
1	C	137	HIS
1	C	141	GLN
1	C	195	ASN
1	C	261	ASN
1	D	120	HIS
1	D	137	HIS
1	E	137	HIS
1	F	141	GLN
1	F	272	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	B	1002	-	42,48,48	1.69	3 (7%)	50,73,73	1.43	5 (10%)
2	NAD	F	1006	-	42,48,48	1.81	4 (9%)	50,73,73	1.31	6 (12%)
2	NAD	E	1005	-	42,48,48	1.73	3 (7%)	50,73,73	1.42	5 (10%)
2	NAD	C	1003	-	42,48,48	1.73	3 (7%)	50,73,73	1.45	5 (10%)
2	NAD	A	1001	-	42,48,48	1.84	4 (9%)	50,73,73	1.36	4 (8%)
2	NAD	D	1004	-	42,48,48	1.78	4 (9%)	50,73,73	1.48	7 (14%)

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	B	1002	-	-	6/26/62/62	0/5/5/5
2	NAD	F	1006	-	-	4/26/62/62	0/5/5/5
2	NAD	E	1005	-	-	6/26/62/62	0/5/5/5
2	NAD	C	1003	-	-	4/26/62/62	0/5/5/5
2	NAD	A	1001	-	-	4/26/62/62	0/5/5/5
2	NAD	D	1004	-	-	4/26/62/62	0/5/5/5

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	NAD	O7N-C7N	8.91	1.41	1.24
2	C	1003	NAD	O7N-C7N	8.66	1.40	1.24
2	F	1006	NAD	O7N-C7N	8.64	1.40	1.24
2	B	1002	NAD	O7N-C7N	8.64	1.40	1.24
2	E	1005	NAD	O7N-C7N	8.57	1.40	1.24
2	D	1004	NAD	O7N-C7N	8.20	1.39	1.24
2	A	1001	NAD	C2A-N3A	4.91	1.40	1.32
2	F	1006	NAD	C2A-N3A	4.51	1.39	1.32
2	E	1005	NAD	C2A-N3A	4.24	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1004	NAD	C2A-N3A	3.88	1.38	1.32
2	C	1003	NAD	C2A-N3A	3.68	1.38	1.32
2	B	1002	NAD	C2A-N3A	3.50	1.37	1.32
2	A	1001	NAD	C2A-N1A	3.04	1.39	1.33
2	F	1006	NAD	C2A-N1A	2.91	1.39	1.33
2	D	1004	NAD	C2A-N1A	2.67	1.38	1.33
2	D	1004	NAD	C2N-N1N	2.64	1.38	1.35
2	F	1006	NAD	C2N-N1N	2.63	1.38	1.35
2	C	1003	NAD	C2A-N1A	2.42	1.38	1.33
2	E	1005	NAD	C2A-N1A	2.38	1.38	1.33
2	A	1001	NAD	C2N-N1N	2.31	1.37	1.35
2	B	1002	NAD	C2A-N1A	2.03	1.37	1.33

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1005	NAD	N3A-C2A-N1A	-6.67	118.25	128.68
2	B	1002	NAD	N3A-C2A-N1A	-6.55	118.44	128.68
2	C	1003	NAD	N3A-C2A-N1A	-6.15	119.06	128.68
2	F	1006	NAD	N3A-C2A-N1A	-6.15	119.06	128.68
2	A	1001	NAD	N3A-C2A-N1A	-5.72	119.74	128.68
2	D	1004	NAD	N3A-C2A-N1A	-5.69	119.79	128.68
2	D	1004	NAD	C3N-C7N-N7N	3.75	122.25	117.75
2	C	1003	NAD	C3N-C7N-N7N	3.66	122.14	117.75
2	A	1001	NAD	C1B-N9A-C4A	-3.27	120.90	126.64
2	F	1006	NAD	C3N-C7N-N7N	3.15	121.53	117.75
2	E	1005	NAD	PN-O3-PA	-2.96	122.68	132.83
2	D	1004	NAD	O7N-C7N-C3N	-2.82	116.26	119.63
2	C	1003	NAD	O2N-PN-O1N	2.81	126.12	112.24
2	B	1002	NAD	PN-O3-PA	-2.74	123.44	132.83
2	E	1005	NAD	O4D-C1D-C2D	-2.67	103.02	106.93
2	C	1003	NAD	PN-O3-PA	-2.67	123.68	132.83
2	D	1004	NAD	C1B-N9A-C4A	-2.59	122.10	126.64
2	A	1001	NAD	O4D-C1D-C2D	-2.53	103.23	106.93
2	C	1003	NAD	O7N-C7N-C3N	-2.48	116.66	119.63
2	D	1004	NAD	O4D-C1D-C2D	-2.46	103.34	106.93
2	F	1006	NAD	PN-O3-PA	-2.23	125.18	132.83
2	D	1004	NAD	C6N-N1N-C2N	-2.22	119.95	121.97
2	A	1001	NAD	C4A-C5A-N7A	-2.20	107.10	109.40
2	B	1002	NAD	C1B-N9A-C4A	-2.20	122.78	126.64
2	F	1006	NAD	O7N-C7N-C3N	-2.18	117.02	119.63
2	E	1005	NAD	C3N-C7N-N7N	2.16	120.34	117.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1004	NAD	C5N-C4N-C3N	-2.14	117.82	120.34
2	F	1006	NAD	O2N-PN-O1N	2.11	122.65	112.24
2	E	1005	NAD	C2N-C3N-C4N	2.07	120.60	118.26
2	B	1002	NAD	C3N-C7N-N7N	2.03	120.18	117.75
2	F	1006	NAD	O4D-C1D-C2D	-2.02	103.97	106.93
2	B	1002	NAD	O3B-C3B-C4B	-2.00	105.26	111.05

There are no chirality outliers.

All (28) torsion outliers are listed below:

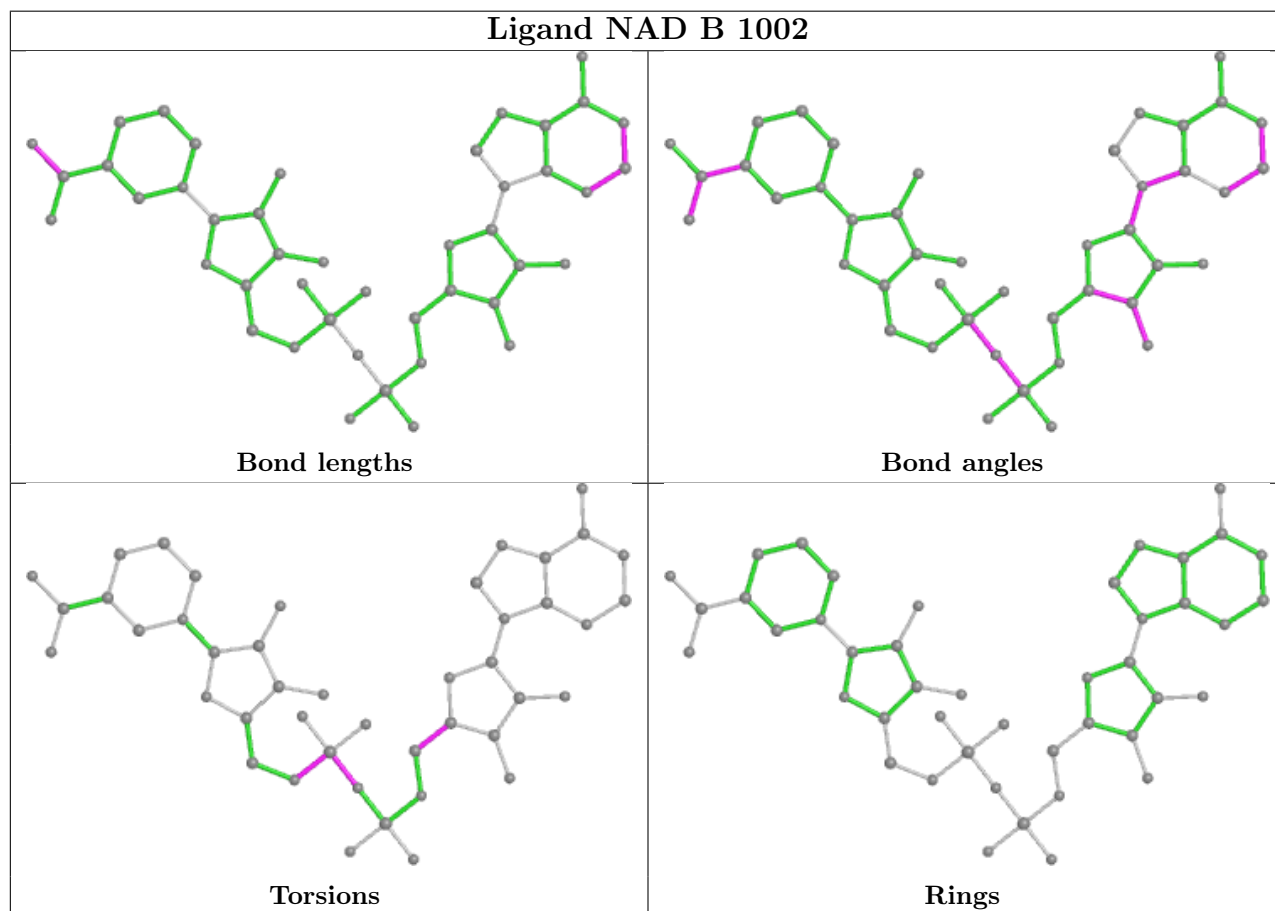
Mol	Chain	Res	Type	Atoms
2	B	1002	NAD	C5D-O5D-PN-O3
2	B	1002	NAD	C5D-O5D-PN-O1N
2	B	1002	NAD	C5D-O5D-PN-O2N
2	C	1003	NAD	C5D-O5D-PN-O1N
2	C	1003	NAD	C5D-O5D-PN-O2N
2	D	1004	NAD	C5D-O5D-PN-O1N
2	D	1004	NAD	C5D-O5D-PN-O2N
2	E	1005	NAD	C5D-O5D-PN-O1N
2	E	1005	NAD	C5D-O5D-PN-O2N
2	F	1006	NAD	C5D-O5D-PN-O2N
2	D	1004	NAD	C5D-O5D-PN-O3
2	F	1006	NAD	C5D-O5D-PN-O3
2	B	1002	NAD	PA-O3-PN-O2N
2	E	1005	NAD	PA-O3-PN-O2N
2	C	1003	NAD	O4B-C4B-C5B-O5B
2	A	1001	NAD	C5D-O5D-PN-O3
2	C	1003	NAD	C5D-O5D-PN-O3
2	E	1005	NAD	C5D-O5D-PN-O3
2	A	1001	NAD	O4B-C4B-C5B-O5B
2	B	1002	NAD	O4B-C4B-C5B-O5B
2	D	1004	NAD	O4B-C4B-C5B-O5B
2	F	1006	NAD	O4B-C4B-C5B-O5B
2	A	1001	NAD	PA-O3-PN-O1N
2	B	1002	NAD	PA-O3-PN-O1N
2	E	1005	NAD	PA-O3-PN-O1N
2	F	1006	NAD	PA-O3-PN-O1N
2	A	1001	NAD	C5D-O5D-PN-O1N
2	E	1005	NAD	O4B-C4B-C5B-O5B

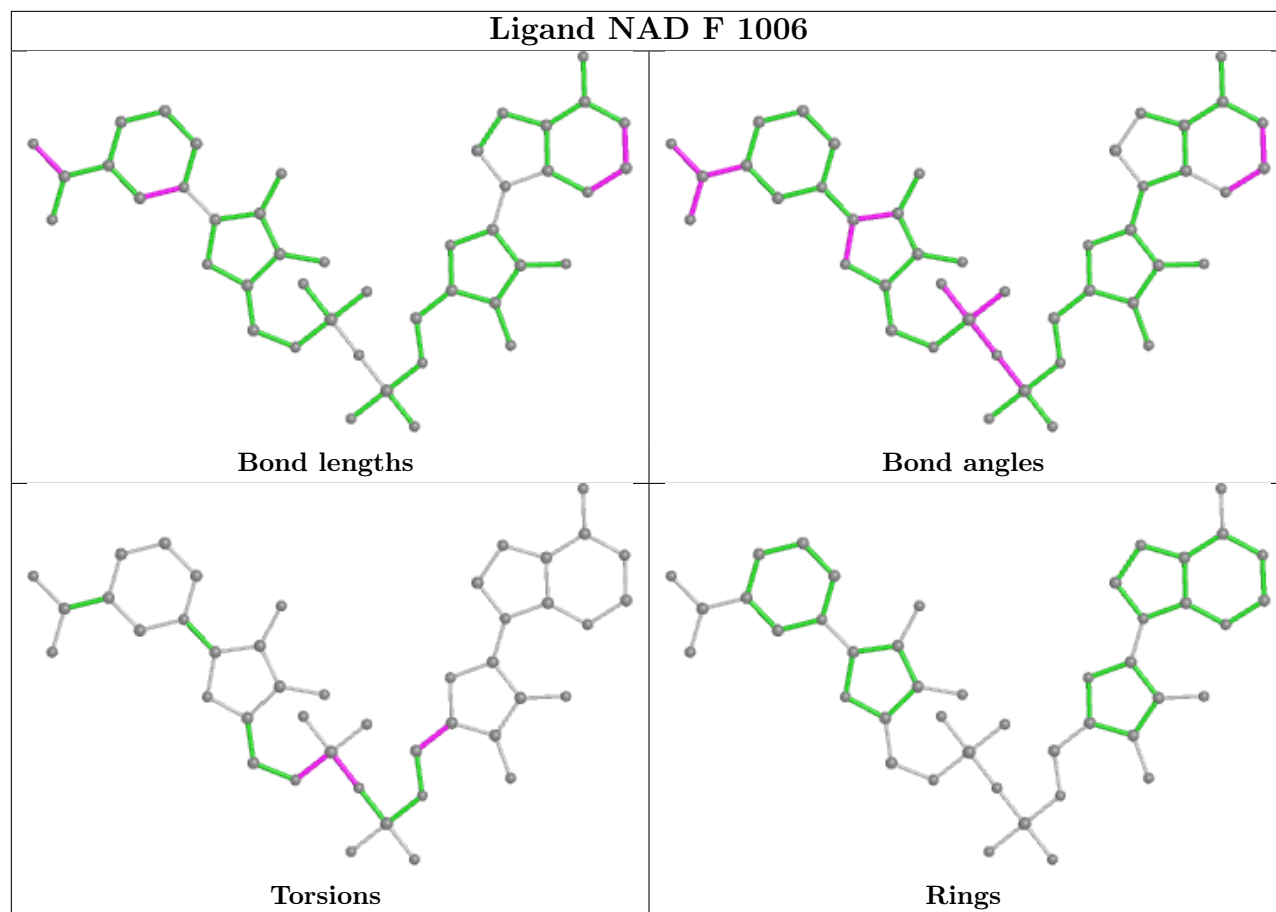
There are no ring outliers.

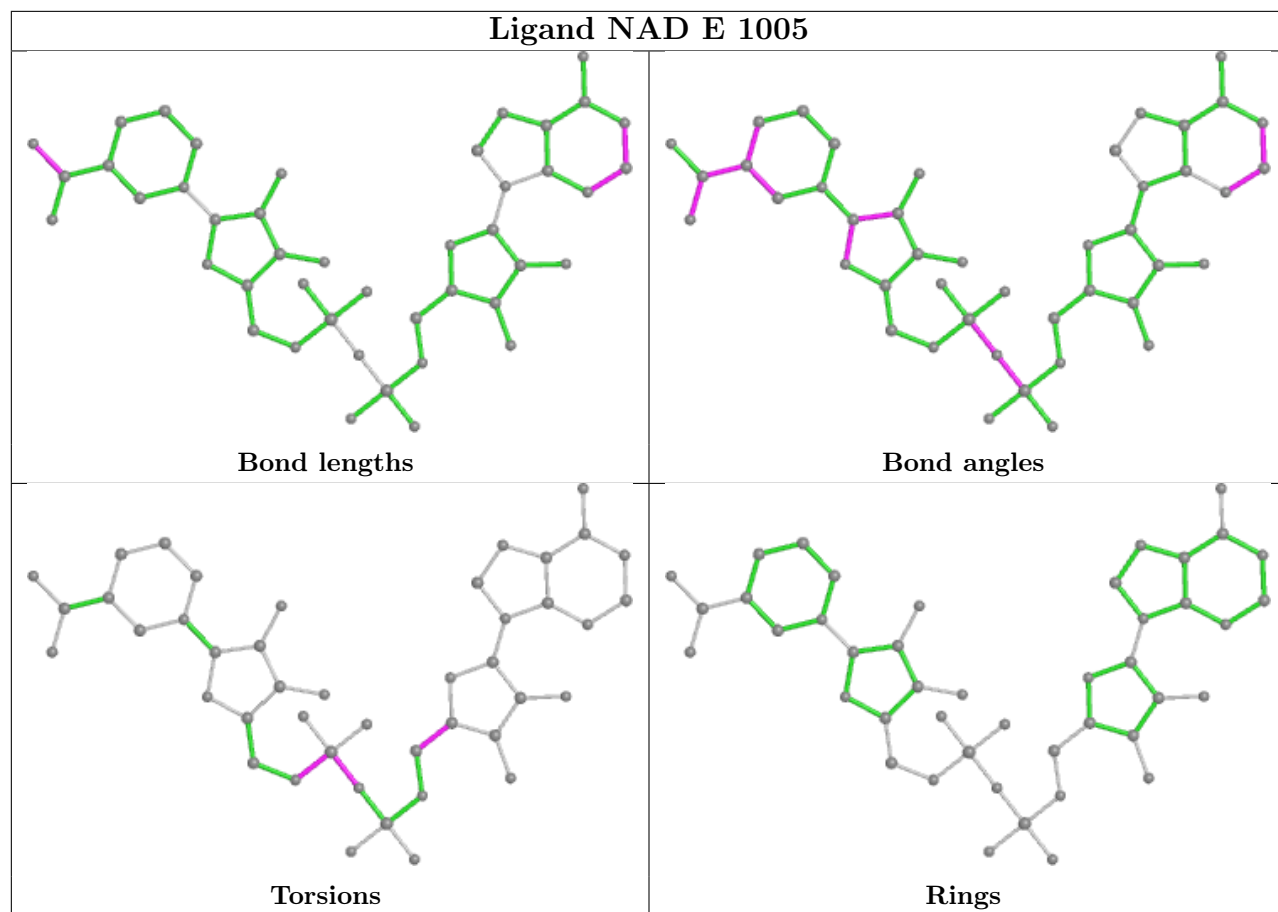
1 monomer is involved in 1 short contact:

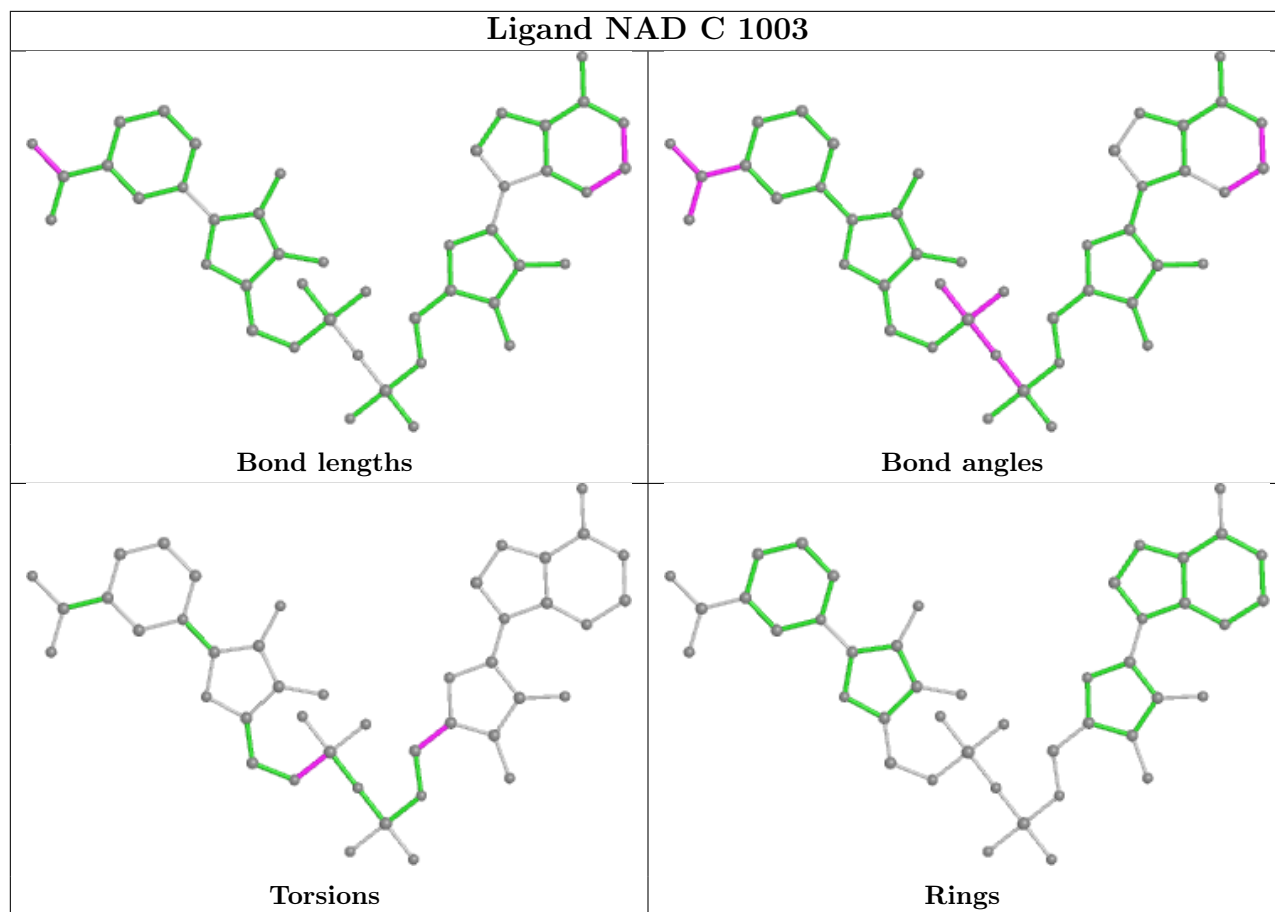
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1005	NAD	1	0

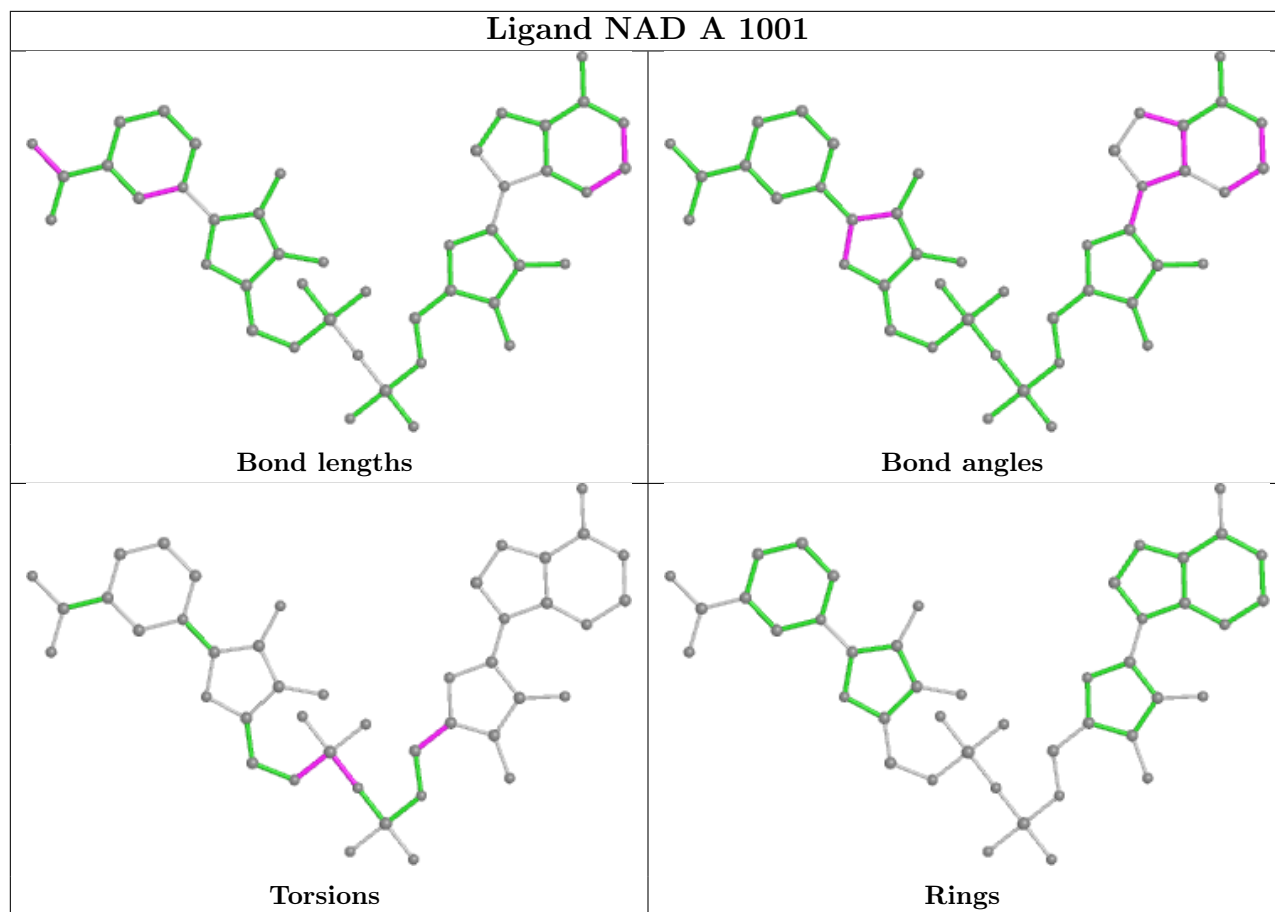
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

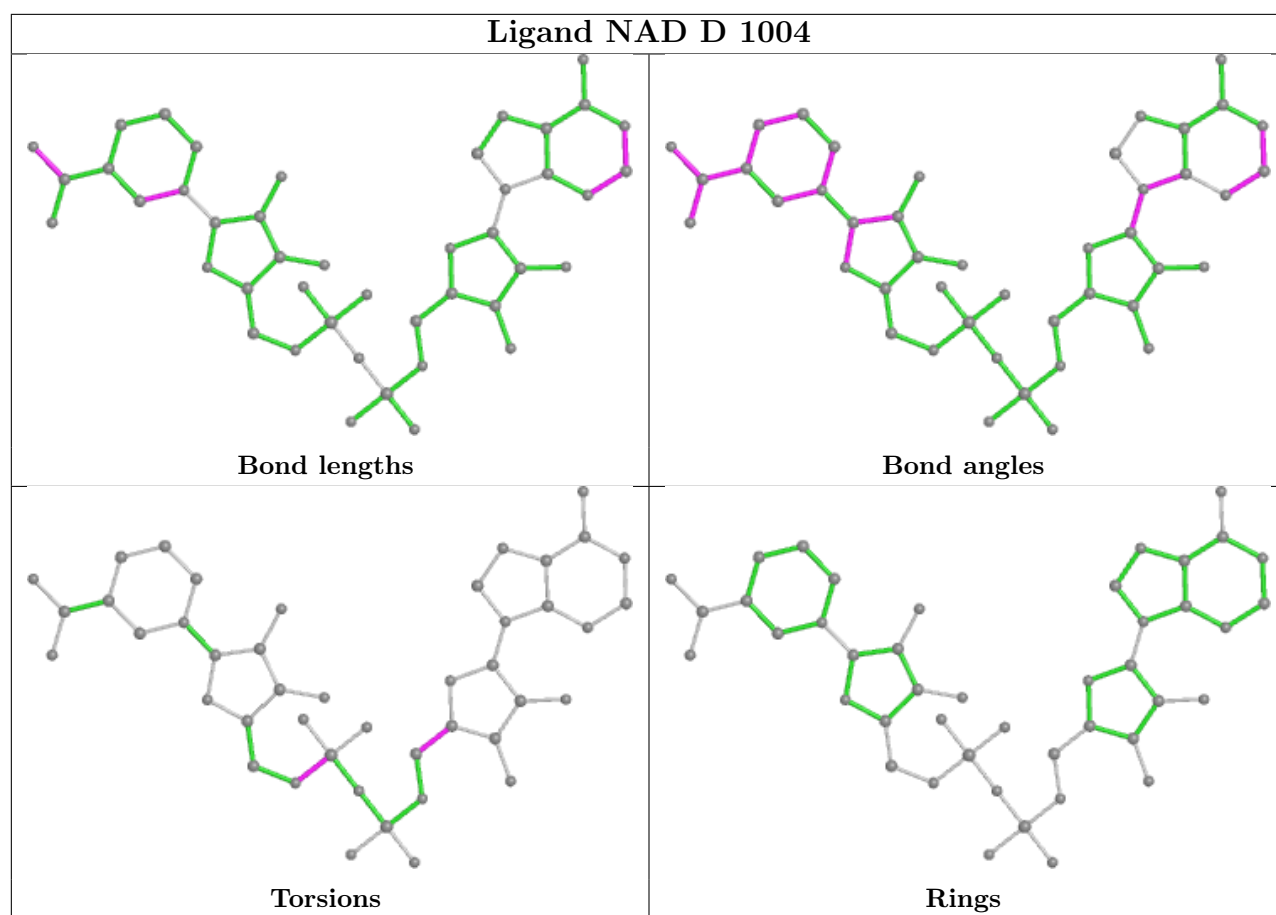












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	302/327 (92%)	0.66	31 (10%) 6 5	33, 39, 47, 54	0
1	B	302/327 (92%)	0.68	34 (11%) 5 4	33, 39, 47, 54	0
1	C	302/327 (92%)	0.64	34 (11%) 5 4	32, 39, 46, 54	0
1	D	302/327 (92%)	0.64	33 (10%) 5 5	33, 39, 47, 54	1 (0%)
1	E	302/327 (92%)	0.87	49 (16%) 1 1	33, 39, 47, 54	0
1	F	302/327 (92%)	0.84	39 (12%) 3 3	33, 39, 46, 54	0
All	All	1812/1962 (92%)	0.72	220 (12%) 4 3	32, 39, 47, 54	1 (0%)

All (220) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	147	ILE	5.5
1	F	97	VAL	5.5
1	B	147	ILE	5.4
1	E	169	LEU	5.3
1	E	171	LEU	5.2
1	E	147	ILE	5.2
1	F	171	LEU	5.1
1	B	192	ILE	5.0
1	C	192	ILE	4.8
1	E	192	ILE	4.8
1	F	172	LEU	4.6
1	D	53	LEU	4.6
1	D	172	LEU	4.6
1	F	169	LEU	4.6
1	E	149	THR	4.6
1	A	204	VAL	4.6
1	A	172	LEU	4.5
1	B	3	SER	4.5
1	F	48	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	147	ILE	4.4
1	F	96	VAL	4.3
1	E	191	THR	4.3
1	B	169	LEU	4.3
1	C	169	LEU	4.3
1	D	192	ILE	4.2
1	F	173	GLY	4.1
1	D	167	ALA	4.1
1	C	172	LEU	4.0
1	E	203	THR	4.0
1	D	261	ASN	3.8
1	E	172	LEU	3.8
1	E	170	GLY	3.7
1	F	146	ILE	3.7
1	B	261	ASN	3.7
1	D	171	LEU	3.7
1	F	170	GLY	3.6
1	E	52	SER	3.6
1	A	48	VAL	3.6
1	E	97	VAL	3.6
1	F	148	MET	3.6
1	F	149	THR	3.5
1	B	171	LEU	3.5
1	A	14	VAL	3.5
1	F	73	TYR	3.5
1	B	51	GLY	3.5
1	B	172	LEU	3.4
1	D	191	THR	3.4
1	F	14	VAL	3.4
1	D	203	THR	3.4
1	A	97	VAL	3.4
1	B	167	ALA	3.4
1	E	304	SER	3.3
1	D	97	VAL	3.3
1	D	303	ASP	3.2
1	E	70	VAL	3.2
1	E	124	LEU	3.2
1	E	96	VAL	3.2
1	A	96	VAL	3.2
1	D	202	GLN	3.1
1	E	183	ARG	3.1
1	C	149	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	171	LEU	3.1
1	F	203	THR	3.1
1	B	202	GLN	3.1
1	A	302	ILE	3.1
1	F	192	ILE	3.1
1	E	99	ASN	3.1
1	E	3	SER	3.1
1	D	222	VAL	3.1
1	C	147	ILE	3.1
1	A	203	THR	3.0
1	C	304	SER	3.0
1	E	98	ASN	3.0
1	E	150	SER	3.0
1	A	303	ASP	3.0
1	C	209	LEU	3.0
1	D	208	ASP	3.0
1	F	167	ALA	3.0
1	E	261	ASN	3.0
1	C	100	ALA	3.0
1	A	169	LEU	2.9
1	E	303	ASP	2.9
1	E	296	ILE	2.9
1	E	148	MET	2.9
1	C	13	LEU	2.9
1	E	100	ALA	2.9
1	E	166	ALA	2.9
1	B	191	THR	2.9
1	D	174	LEU	2.9
1	E	48	VAL	2.8
1	B	149	THR	2.8
1	F	15	THR	2.8
1	B	222	VAL	2.8
1	E	222	VAL	2.8
1	B	100	ALA	2.8
1	E	204	VAL	2.8
1	E	71	ALA	2.8
1	A	192	ILE	2.8
1	E	174	LEU	2.8
1	C	193	ALA	2.8
1	B	124	LEU	2.8
1	D	169	LEU	2.8
1	B	219	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	F	175	ALA	2.7
1	F	191	THR	2.7
1	A	222	VAL	2.7
1	D	207	GLU	2.7
1	E	146	ILE	2.7
1	A	13	LEU	2.7
1	F	174	LEU	2.7
1	B	148	MET	2.7
1	F	204	VAL	2.7
1	A	261	ASN	2.7
1	A	171	LEU	2.7
1	D	150	SER	2.6
1	D	166	ALA	2.6
1	D	259	GLN	2.6
1	F	261	ASN	2.6
1	D	100	ALA	2.6
1	C	155	ILE	2.6
1	A	280	GLU	2.6
1	C	184	LYS	2.6
1	C	51	GLY	2.6
1	D	110	ARG	2.6
1	B	166	ALA	2.6
1	F	166	ALA	2.6
1	F	222	VAL	2.5
1	E	127	SER	2.5
1	C	98	ASN	2.5
1	C	222	VAL	2.5
1	F	98	ASN	2.5
1	A	304	SER	2.5
1	D	25	TYR	2.5
1	B	52	SER	2.5
1	C	168	LYS	2.5
1	E	45	PHE	2.5
1	F	99	ASN	2.5
1	B	225	LEU	2.5
1	B	146	ILE	2.5
1	C	124	LEU	2.5
1	F	13	LEU	2.5
1	D	148	MET	2.5
1	D	194	PRO	2.5
1	A	146	ILE	2.5
1	C	49	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	147	ILE	2.4
1	C	3	SER	2.4
1	F	224	TRP	2.4
1	E	168	LYS	2.4
1	A	25	TYR	2.4
1	B	13	LEU	2.4
1	C	207	GLU	2.4
1	E	173	GLY	2.4
1	A	12	VAL	2.4
1	B	97	VAL	2.4
1	D	14	VAL	2.4
1	E	95	VAL	2.4
1	B	4	PRO	2.4
1	E	193	ALA	2.4
1	F	150	SER	2.4
1	F	300	SER	2.4
1	A	49	GLY	2.4
1	B	174	LEU	2.4
1	D	21	LEU	2.4
1	B	303	ASP	2.4
1	A	109	ALA	2.4
1	A	167	ALA	2.4
1	D	149	THR	2.4
1	D	168	LYS	2.3
1	E	167	ALA	2.3
1	E	226	CYS	2.3
1	C	146	ILE	2.3
1	C	259	GLN	2.3
1	B	207	GLU	2.3
1	E	190	ASN	2.3
1	E	231	GLU	2.3
1	A	223	LEU	2.3
1	B	223	LEU	2.3
1	E	159	PHE	2.3
1	F	189	CYS	2.3
1	F	127	SER	2.3
1	A	26	ALA	2.2
1	B	159	PHE	2.2
1	A	202	GLN	2.2
1	F	95	VAL	2.2
1	F	5	LEU	2.2
1	E	90	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	262	HIS	2.2
1	B	190	ASN	2.2
1	C	15	THR	2.2
1	A	263	PRO	2.2
1	D	170	GLY	2.2
1	E	131	THR	2.2
1	E	106	ARG	2.2
1	E	155	ILE	2.1
1	A	191	THR	2.1
1	B	193	ALA	2.1
1	E	237	PHE	2.1
1	D	193	ALA	2.1
1	A	36	VAL	2.1
1	A	148	MET	2.1
1	F	3	SER	2.1
1	F	45	PHE	2.1
1	C	226	CYS	2.1
1	B	21	LEU	2.1
1	C	170	GLY	2.1
1	C	96	VAL	2.1
1	B	194	PRO	2.1
1	C	175	ALA	2.1
1	C	194	PRO	2.1
1	F	63	ARG	2.1
1	C	281	ASN	2.0
1	D	302	ILE	2.0
1	C	167	ALA	2.0
1	D	99	ASN	2.0
1	B	14	VAL	2.0
1	C	110	ARG	2.0
1	F	190	ASN	2.0
1	E	73	TYR	2.0
1	C	97	VAL	2.0

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](#)

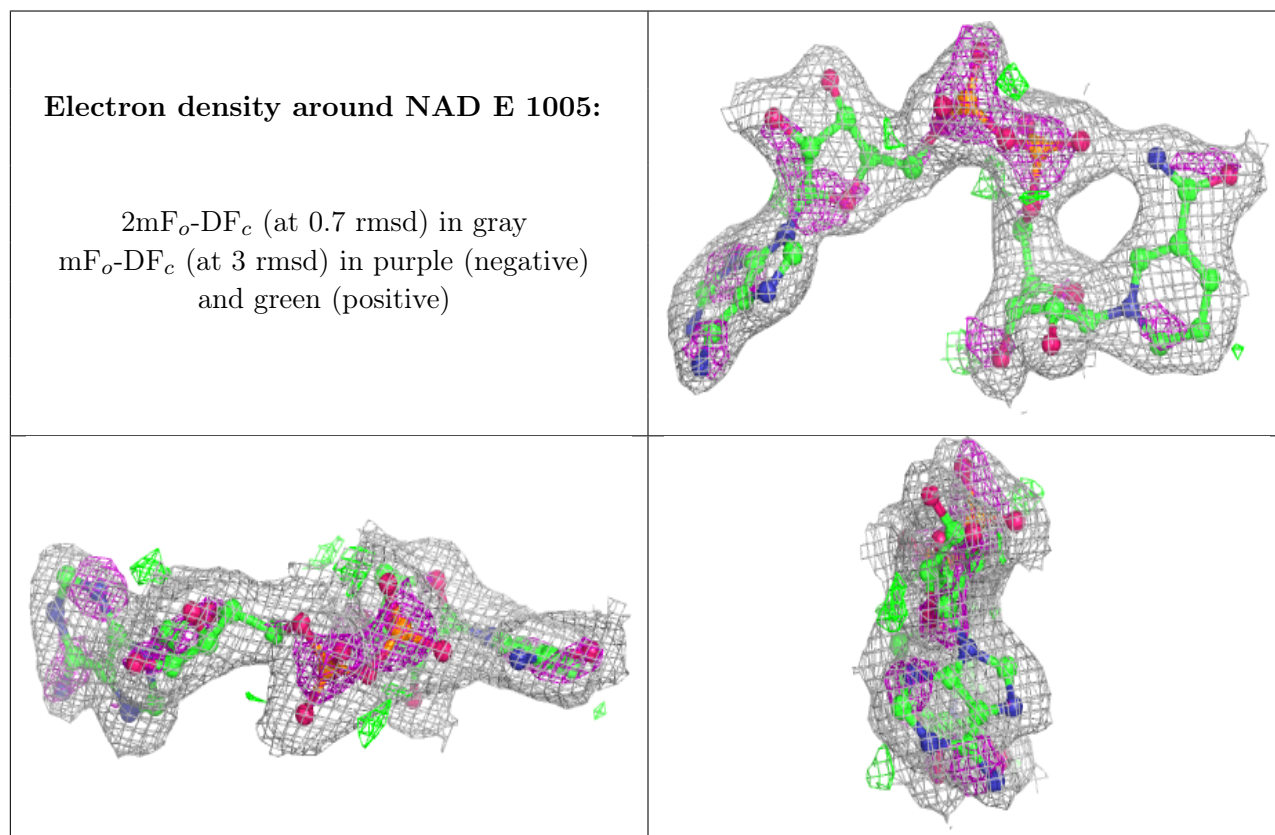
There are no monosaccharides in this entry.

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.

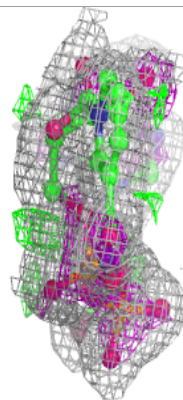
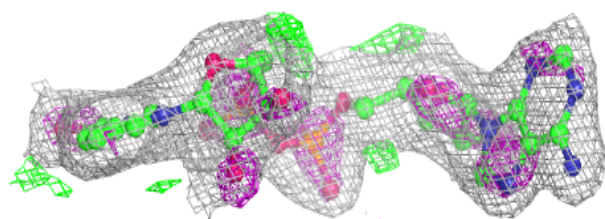
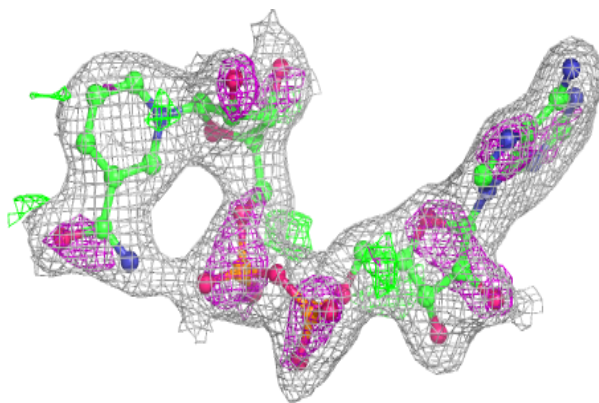
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAD	E	1005	44/44	0.95	0.11	31,37,40,41	0
2	NAD	F	1006	44/44	0.95	0.11	28,34,42,45	0
2	NAD	D	1004	44/44	0.96	0.09	25,30,32,34	0
2	NAD	A	1001	44/44	0.96	0.09	22,27,33,34	0
2	NAD	B	1002	44/44	0.96	0.10	20,28,31,33	0
2	NAD	C	1003	44/44	0.97	0.08	21,27,31,32	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.

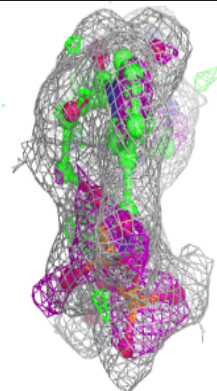
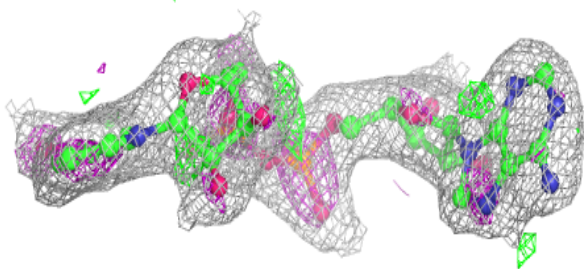
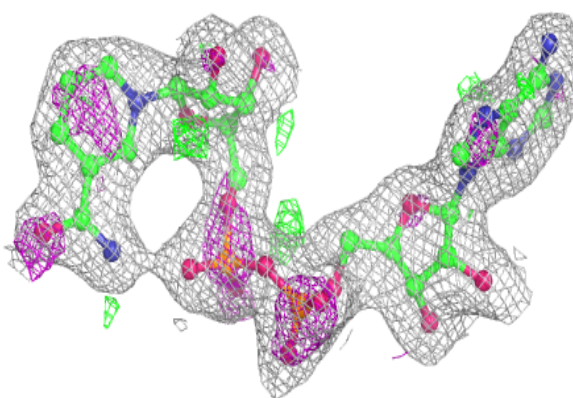


Electron density around NAD F 1006:

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

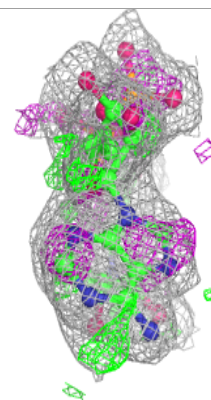
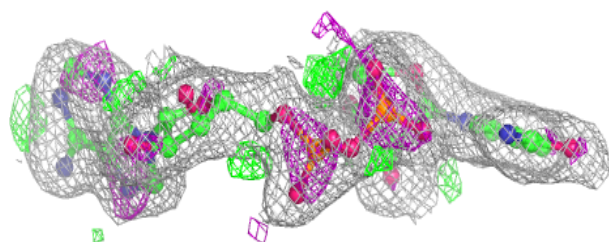
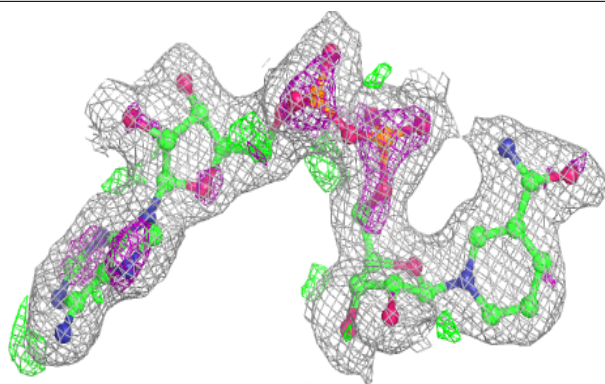
**Electron density around NAD D 1004:**

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

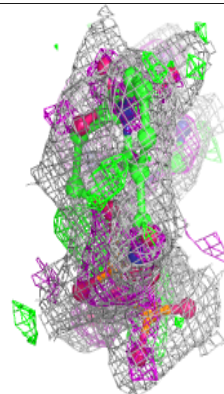
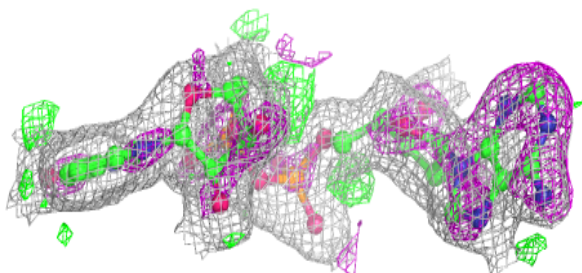
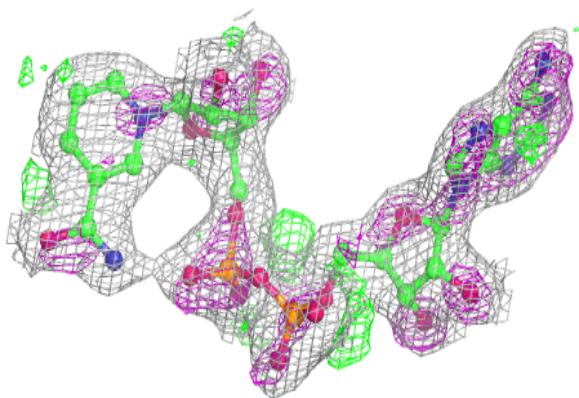


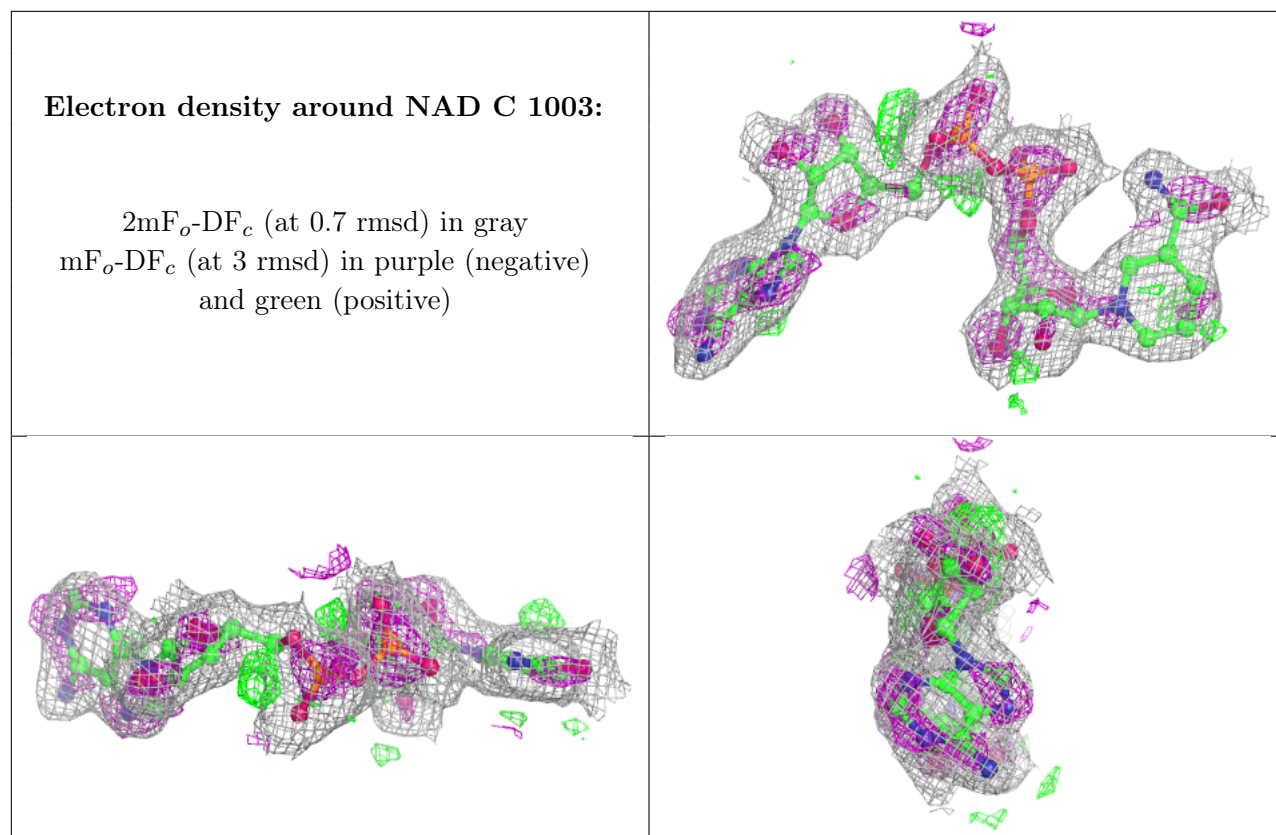
Electron density around NAD A 1001:

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

**Electron density around NAD B 1002:**

$2mF_o-DF_c$ (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.