



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:15 AM UTC

PDB ID : 4COD / pdb_00004cod
Title : Encoded library technology as a source of hits for the discovery and lead optimization of a potent and selective class of bactericidal direct inhibitors of Mycobacterium tuberculosis InhA
Authors : Encinas, L.; OKeefe, H.; Neu, M.; Convery, M.A.; McDowell, W.; Mendoza-Losana, A.; Pages, L.B.; Castro-Pichel, J.; Evindar, G.
Deposited on : 2014-01-28
Resolution : 2.40 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtrriage (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

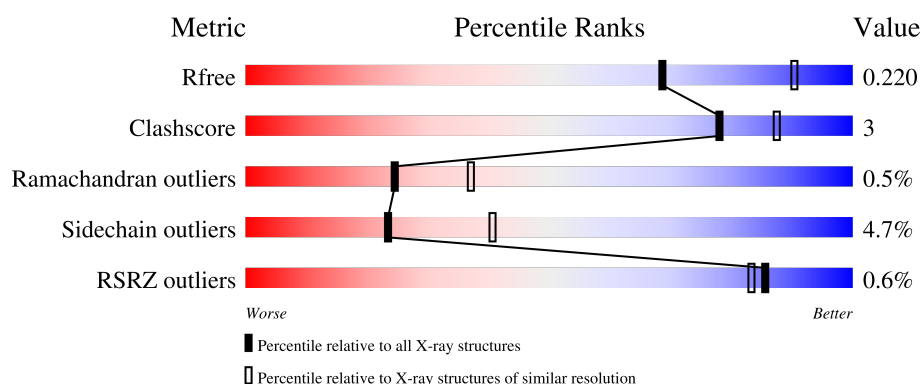
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	B	269	<div> <div>86%</div> <div>12%</div> <div>.</div> </div>
1	D	269	<div> <div>%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>
1	F	269	<div> <div>90%</div> <div>9%</div> </div>
1	H	269	<div> <div>%</div> <div>85%</div> <div>13%</div> <div>.</div> </div>

2 Entry composition [i](#)

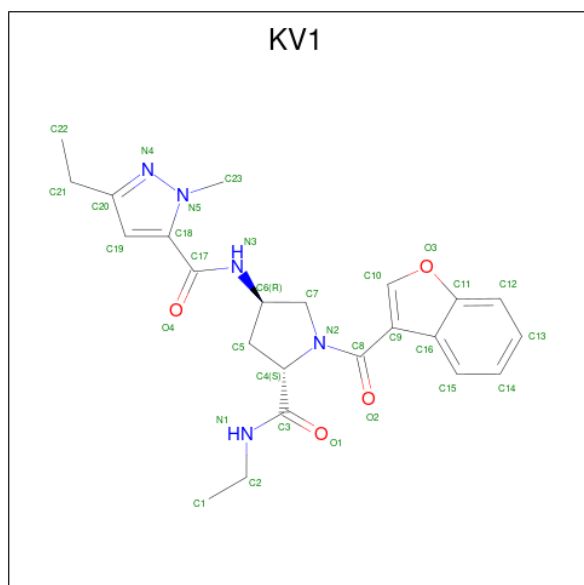
There are 4 unique types of molecules in this entry. The entry contains 8672 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	268	Total	C	N	O	S	0	0	0
			1996	1264	348	374	10			
1	D	268	Total	C	N	O	S	0	0	0
			1996	1264	348	374	10			
1	F	268	Total	C	N	O	S	0	0	0
			1996	1264	348	374	10			
1	H	268	Total	C	N	O	S	0	0	0
			1996	1264	348	374	10			

- Molecule 2 is N-((3R,5S)-1-(benzofuran-3-carbonyl)-5-(ethylcarbamoyl)pyrrolidin-3-yl)-3-ethyl-1-methyl-1H-pyrazole-5-carboxamide (CCD ID: KV1) (formula: C₂₃H₂₇N₅O₄).



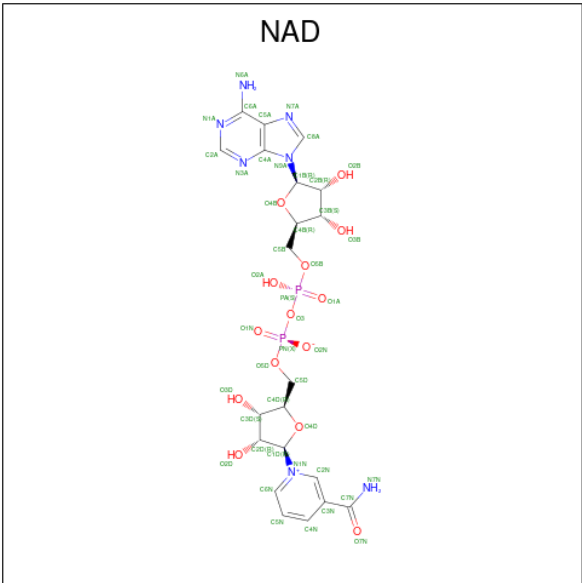
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			32	23	5	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	D	1	Total	C	N	O	0	0
			32	23	5	4		
2	F	1	Total	C	N	O	0	0
			32	23	5	4		
2	H	1	Total	C	N	O	0	0
			32	23	5	4		

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



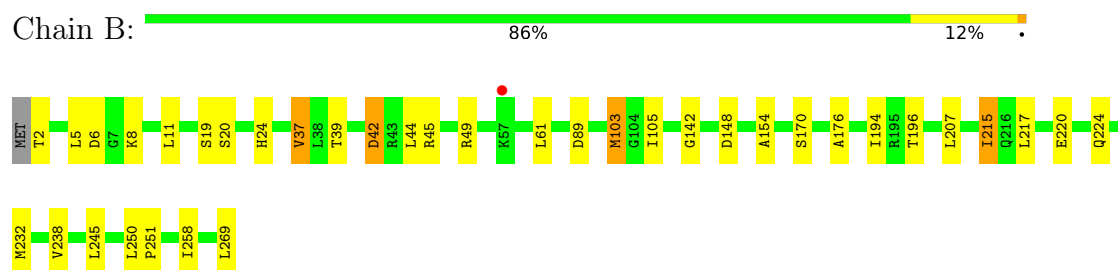
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	76	Total 76	O 76	0	0
4	H	48	Total 48	O 48	0	0

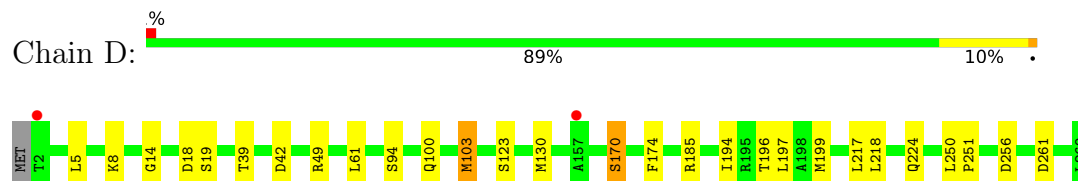
3 Residue-property plots [i](#)

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.

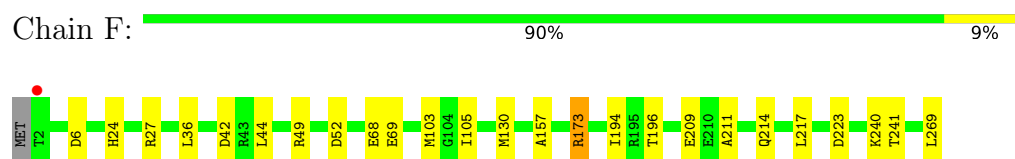
- Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH]



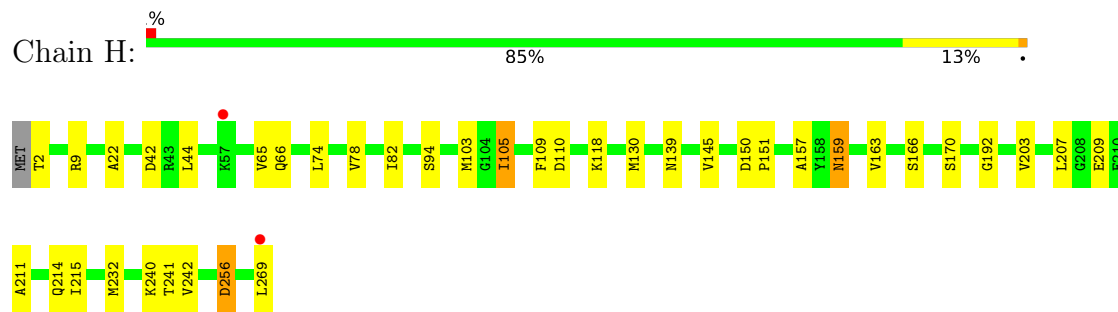
- Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH]



- Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH]



- Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH]



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	100.18Å 102.35Å 179.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.14 – 2.40 35.14 – 2.40	Depositor EDS
% Data completeness (in resolution range)	71.2 (35.14-2.40) 71.2 (35.14-2.40)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.40Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.170 , 0.206 0.183 , 0.220	Depositor DCC
R_{free} test set	2637 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	55.8	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.025 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8672	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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, KV1

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	B	0.89	0/2034	1.40	9/2761 (0.3%)
1	D	0.88	0/2034	1.41	9/2761 (0.3%)
1	F	0.85	0/2034	1.41	6/2761 (0.2%)
1	H	0.83	0/2034	1.37	4/2761 (0.1%)
All	All	0.86	0/8136	1.40	28/11044 (0.3%)

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	42	ASP	CA-CB-CG	6.77	119.37	112.60
1	F	223	ASP	CA-CB-CG	6.04	118.64	112.60
1	D	224	GLN	CA-C-N	6.00	128.32	120.28
1	D	224	GLN	C-N-CA	6.00	128.32	120.28
1	B	148	ASP	CA-CB-CG	5.79	118.39	112.60
1	B	37	VAL	N-CA-CB	5.72	119.60	111.82
1	D	197	LEU	CA-C-N	5.54	128.26	120.28
1	D	197	LEU	C-N-CA	5.54	128.26	120.28
1	H	256	ASP	N-CA-C	5.54	118.28	110.14
1	H	109	PHE	CA-CB-CG	5.40	119.20	113.80
1	H	192	GLY	N-CA-C	-5.35	105.76	112.23
1	D	18	ASP	CA-CB-CG	5.31	117.91	112.60
1	F	36	LEU	CA-C-N	5.30	130.36	122.99
1	F	36	LEU	C-N-CA	5.30	130.36	122.99
1	H	110	ASP	CA-CB-CG	5.28	117.88	112.60
1	D	14	GLY	N-CA-C	5.21	121.69	114.92
1	D	261	ASP	CA-CB-CG	5.19	117.79	112.60
1	B	220	GLU	CA-C-N	5.19	125.74	119.98
1	B	220	GLU	C-N-CA	5.19	125.74	119.98
1	B	176	ALA	CA-C-N	5.15	127.45	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	176	ALA	C-N-CA	5.15	127.45	120.44
1	F	52	ASP	CA-CB-CG	5.10	117.70	112.60
1	D	199	MET	CA-C-N	5.07	127.78	120.38
1	D	199	MET	C-N-CA	5.07	127.78	120.38
1	B	224	GLN	CA-C-N	5.02	127.01	120.28
1	B	224	GLN	C-N-CA	5.02	127.01	120.28
1	F	69	GLU	CA-C-N	5.00	126.98	120.28
1	F	69	GLU	C-N-CA	5.00	126.98	120.28

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	B	1996	0	2013	18	0
1	D	1996	0	2013	11	0
1	F	1996	0	2013	9	0
1	H	1996	0	2013	18	0
2	B	32	0	27	2	0
2	D	32	0	27	2	0
2	F	32	0	27	3	0
2	H	32	0	27	3	0
3	B	44	0	26	0	0
3	D	44	0	26	0	0
3	F	44	0	26	0	0
3	H	44	0	26	1	0
4	B	144	0	0	0	0
4	D	116	0	0	0	0
4	F	76	0	0	0	0
4	H	48	0	0	0	0
All	All	8672	0	8264	47	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (47) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:MET:HE1	2:B:1270:KV1:H19	1.35	1.07
1:D:103:MET:HE1	2:D:1270:KV1:H19	1.31	1.06
1:F:103:MET:HE1	2:F:1271:KV1:H19	1.48	0.95
1:D:103:MET:HE1	2:D:1270:KV1:C19	2.02	0.88
1:B:103:MET:HE1	2:B:1270:KV1:C19	2.03	0.87
1:F:103:MET:HE1	2:F:1271:KV1:C19	2.11	0.81
1:H:103:MET:HE1	2:H:1270:KV1:C19	2.28	0.63
1:B:45:ARG:HD2	1:B:49:ARG:HH21	1.65	0.60
1:H:103:MET:HE1	2:H:1270:KV1:H19	1.84	0.59
1:F:24:HIS:HD2	1:F:27:ARG:HH21	1.51	0.58
1:B:154:ALA:HB2	1:F:173:ARG:HB3	1.87	0.56
1:F:157:ALA:HB1	2:F:1271:KV1:H12	1.88	0.56
1:H:74:LEU:O	1:H:78:VAL:HG23	2.09	0.53
1:H:66:GLN:HE22	1:H:118:LYS:HE2	1.74	0.52
1:H:157:ALA:HB1	2:H:1270:KV1:H12	1.91	0.52
1:D:19:SER:O	1:D:196:THR:HG22	2.09	0.52
1:B:2:THR:HG1	1:H:2:THR:N	2.08	0.52
1:B:89:ASP:O	1:B:142:GLY:HA2	2.10	0.51
1:H:105:ILE:HG23	1:H:211:ALA:HB2	1.92	0.51
1:H:22:ALA:HB2	1:H:94:SER:HB3	1.93	0.51
1:B:20:SER:O	1:B:24:HIS:HD2	1.94	0.50
1:B:250:LEU:HD23	1:H:241:THR:HG23	1.93	0.50
1:H:105:ILE:HG12	1:H:207:LEU:HB3	1.94	0.50
1:D:5:LEU:O	1:D:8:LYS:HB2	2.12	0.49
1:D:250:LEU:HD23	1:F:241:THR:HG23	1.96	0.48
1:B:19:SER:O	1:B:196:THR:HG22	2.16	0.46
1:B:5:LEU:O	1:B:8:LYS:HB2	2.15	0.46
1:B:39:THR:HA	1:B:61:LEU:O	2.16	0.45
1:H:145:VAL:HG11	1:H:242:VAL:HG13	1.98	0.45
1:D:170:SER:HB3	1:H:163:VAL:HG22	1.98	0.44
1:B:194:ILE:HD11	1:B:238:VAL:HG21	2.00	0.44
1:F:194:ILE:HG22	1:F:196:THR:HG23	1.99	0.44
1:H:203:VAL:HG22	1:H:215:ILE:HG21	2.01	0.43
1:H:9:ARG:HD3	1:H:82:ILE:HB	2.00	0.43
1:H:150:ASP:HA	1:H:151:PRO:HD3	1.90	0.43
1:D:39:THR:HA	1:D:61:LEU:O	2.19	0.42
1:D:194:ILE:HG22	1:D:196:THR:HG23	2.00	0.42
1:B:269:LEU:HD21	1:D:218:LEU:HD12	2.01	0.42
1:B:215:ILE:HD13	1:B:215:ILE:HA	1.98	0.42
1:F:105:ILE:HD13	1:F:211:ALA:HB2	2.01	0.42
1:B:245:LEU:HD21	1:B:258:ILE:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:251:PRO:HG3	1:F:240:LYS:HD3	2.01	0.41
1:H:65:VAL:HG22	3:H:1271:NAD:N1A	2.36	0.41
1:B:251:PRO:HG3	1:H:240:LYS:HD3	2.02	0.41
1:B:11:LEU:HA	1:B:37:VAL:O	2.21	0.41
1:D:174:PHE:CE1	1:H:159:ASN:HA	2.56	0.41
1:B:105:ILE:HG12	1:B:207:LEU:HD23	2.03	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	B	266/269 (99%)	253 (95%)	12 (4%)	1 (0%)	30	43
1	D	266/269 (99%)	253 (95%)	12 (4%)	1 (0%)	30	43
1	F	266/269 (99%)	254 (96%)	11 (4%)	1 (0%)	30	43
1	H	266/269 (99%)	252 (95%)	12 (4%)	2 (1%)	16	25
All	All	1064/1076 (99%)	1012 (95%)	47 (4%)	5 (0%)	24	37

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	42	ASP
1	B	42	ASP
1	D	42	ASP
1	F	42	ASP
1	H	159	ASN

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	B	204/205 (100%)	197 (97%)	7 (3%)	32	54
1	D	204/205 (100%)	194 (95%)	10 (5%)	22	39
1	F	204/205 (100%)	194 (95%)	10 (5%)	22	39
1	H	204/205 (100%)	193 (95%)	11 (5%)	20	35
All	All	816/820 (100%)	778 (95%)	38 (5%)	23	41

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	6	ASP
1	B	44	LEU
1	B	103	MET
1	B	170	SER
1	B	215	ILE
1	B	217	LEU
1	B	232	MET
1	D	49	ARG
1	D	94	SER
1	D	100	GLN
1	D	103	MET
1	D	123	SER
1	D	130	MET
1	D	170	SER
1	D	185	ARG
1	D	217	LEU
1	D	256	ASP
1	F	6	ASP
1	F	44	LEU
1	F	49	ARG
1	F	68	GLU
1	F	130	MET
1	F	173	ARG
1	F	209	GLU

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Mol	Chain	Res	Type
1	F	214	GLN
1	F	217	LEU
1	F	269	LEU
1	H	44	LEU
1	H	105	ILE
1	H	130	MET
1	H	139	ASN
1	H	166	SER
1	H	170	SER
1	H	209	GLU
1	H	214	GLN
1	H	232	MET
1	H	256	ASP
1	H	269	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	66	GLN
1	B	224	GLN
1	F	24	HIS
1	F	48	GLN
1	F	106	ASN
1	F	139	ASN
1	F	172	ASN
1	H	48	GLN
1	H	66	GLN
1	H	70	HIS
1	H	139	ASN
1	H	216	GLN
1	H	224	GLN
1	H	265	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

8 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	NAD	D	1271	-	46,48,48	1.39	4 (8%)	64,73,73	1.78	11 (17%)
3	NAD	B	1271	-	46,48,48	1.45	8 (17%)	64,73,73	1.87	14 (21%)
2	KV1	H	1270	-	35,35,35	0.85	1 (2%)	41,50,50	1.41	7 (17%)
2	KV1	F	1271	-	35,35,35	0.88	1 (2%)	41,50,50	1.28	3 (7%)
3	NAD	F	1270	-	46,48,48	1.33	8 (17%)	64,73,73	1.63	11 (17%)
3	NAD	H	1271	-	46,48,48	1.37	6 (13%)	64,73,73	1.57	11 (17%)
2	KV1	D	1270	-	35,35,35	1.00	1 (2%)	41,50,50	1.16	3 (7%)
2	KV1	B	1270	-	35,35,35	0.95	1 (2%)	41,50,50	1.28	4 (9%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAD	D	1271	-	-	7/30/62/62	0/5/5/5
3	NAD	B	1271	-	-	9/30/62/62	0/5/5/5
2	KV1	H	1270	-	-	4/25/37/37	0/4/4/4
2	KV1	F	1271	-	-	5/25/37/37	0/4/4/4
3	NAD	F	1270	-	-	16/30/62/62	0/5/5/5
3	NAD	H	1271	-	-	13/30/62/62	0/5/5/5
2	KV1	D	1270	-	-	4/25/37/37	0/4/4/4
2	KV1	B	1270	-	-	3/25/37/37	0/4/4/4

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1271	NAD	C5A-C4A	5.53	1.49	1.39
3	H	1271	NAD	C5A-C4A	5.19	1.48	1.39
3	B	1271	NAD	C5A-C4A	5.13	1.48	1.39
3	F	1270	NAD	C5A-C4A	4.73	1.47	1.39
2	B	1270	KV1	C10-C9	4.61	1.40	1.35
2	D	1270	KV1	C10-C9	4.28	1.40	1.35
2	F	1271	KV1	C10-C9	4.07	1.40	1.35
2	H	1270	KV1	C10-C9	3.95	1.39	1.35
3	D	1271	NAD	C5A-C6A	3.60	1.51	1.41
3	D	1271	NAD	PN-O3	3.39	1.63	1.59
3	B	1271	NAD	PA-O3	3.25	1.63	1.59
3	B	1271	NAD	PN-O3	2.90	1.62	1.59
3	H	1271	NAD	PA-O3	2.86	1.62	1.59
3	H	1271	NAD	C5A-C6A	2.81	1.48	1.41
3	B	1271	NAD	C5A-C6A	2.78	1.48	1.41
3	F	1270	NAD	PA-O3	2.75	1.62	1.59
3	F	1270	NAD	C2N-N1N	2.69	1.37	1.35
3	D	1271	NAD	C8A-N7A	2.55	1.36	1.31
3	F	1270	NAD	C5A-C6A	2.45	1.47	1.41
3	H	1271	NAD	C8A-N7A	2.41	1.36	1.31
3	H	1271	NAD	PN-O3	2.39	1.62	1.59
3	F	1270	NAD	PN-O3	2.37	1.62	1.59
3	B	1271	NAD	C8A-N7A	2.34	1.36	1.31
3	F	1270	NAD	C5A-N7A	-2.30	1.34	1.39
3	F	1270	NAD	O4D-C1D	2.27	1.43	1.40
3	F	1270	NAD	C8A-N7A	2.12	1.35	1.31
3	H	1271	NAD	C5A-N7A	-2.11	1.35	1.39
3	B	1271	NAD	O4D-C1D	2.05	1.43	1.40
3	B	1271	NAD	C4A-N3A	2.02	1.38	1.34
3	B	1271	NAD	C2N-C3N	2.01	1.42	1.39

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1271	NAD	O4B-C1B-N9A	5.66	118.97	108.09
3	B	1271	NAD	O4B-C1B-N9A	5.40	118.45	108.09
3	D	1271	NAD	C5A-C4A-N3A	-5.33	119.38	126.72
3	H	1271	NAD	C5A-C4A-N3A	-5.22	119.53	126.72
3	F	1270	NAD	C5A-C4A-N3A	-5.19	119.57	126.72
3	B	1271	NAD	C5A-C4A-N3A	-5.04	119.78	126.72
3	B	1271	NAD	N3A-C4A-N9A	4.76	135.26	127.17
3	F	1270	NAD	N3A-C4A-N9A	4.75	135.24	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	1271	NAD	N3A-C4A-N9A	4.61	135.00	127.17
3	D	1271	NAD	C4A-C5A-N7A	-4.43	105.52	110.58
3	B	1271	NAD	N3A-C2A-N1A	-4.42	121.90	128.58
3	D	1271	NAD	N3A-C4A-N9A	4.13	134.19	127.17
3	F	1270	NAD	N3A-C2A-N1A	-3.94	122.61	128.58
3	B	1271	NAD	C2A-N3A-C4A	3.88	121.32	111.83
3	F	1270	NAD	C2A-N3A-C4A	3.67	120.79	111.83
3	H	1271	NAD	N3A-C2A-N1A	-3.56	123.19	128.58
3	F	1270	NAD	C4A-N9A-C8A	3.56	109.48	105.74
3	D	1271	NAD	C2A-N3A-C4A	3.56	120.52	111.83
3	B	1271	NAD	C4A-N9A-C8A	3.54	109.45	105.74
3	H	1271	NAD	C2A-N3A-C4A	3.53	120.45	111.83
2	D	1270	KV1	C20-N4-N5	3.48	107.11	104.48
3	H	1271	NAD	C4A-N9A-C8A	3.47	109.38	105.74
2	B	1270	KV1	O3-C10-C9	-3.33	110.82	112.68
3	D	1271	NAD	C4A-N9A-C8A	3.31	109.21	105.74
2	H	1270	KV1	O3-C11-C16	3.28	113.99	110.53
2	F	1271	KV1	O3-C11-C16	3.23	113.93	110.53
3	H	1271	NAD	C4A-C5A-N7A	-3.23	106.89	110.58
3	D	1271	NAD	C5A-N7A-C8A	3.10	108.33	103.45
2	B	1270	KV1	C11-C16-C9	-3.03	104.04	105.84
2	D	1270	KV1	O3-C11-C16	3.00	113.69	110.53
3	D	1271	NAD	N3A-C2A-N1A	-2.96	124.09	128.58
3	D	1271	NAD	C6A-C5A-N7A	2.94	137.76	132.09
3	B	1271	NAD	C4A-C5A-N7A	-2.94	107.22	110.58
2	B	1270	KV1	C20-N4-N5	2.92	106.68	104.48
3	B	1271	NAD	C3N-C7N-N7N	2.91	121.33	117.74
2	H	1270	KV1	C18-C19-C20	2.83	107.37	105.60
2	B	1270	KV1	O3-C11-C16	2.83	113.51	110.53
3	F	1270	NAD	C4A-C5A-N7A	-2.81	107.37	110.58
2	H	1270	KV1	C20-N4-N5	2.78	106.58	104.48
3	F	1270	NAD	O4B-C1B-N9A	2.77	113.42	108.09
2	F	1271	KV1	C20-N4-N5	2.68	106.51	104.48
3	F	1270	NAD	C5A-N7A-C8A	2.58	107.51	103.45
3	B	1271	NAD	C5A-N7A-C8A	2.58	107.50	103.45
3	H	1271	NAD	C5A-N7A-C8A	2.57	107.49	103.45
2	D	1270	KV1	C11-C16-C9	-2.48	104.36	105.84
3	B	1271	NAD	C2A-N1A-C6A	2.47	122.79	118.73
2	H	1270	KV1	C23-N5-C18	2.47	132.53	129.48
3	F	1270	NAD	N9A-C8A-N7A	-2.45	110.45	113.94
2	F	1271	KV1	C11-C16-C9	-2.43	104.39	105.84
3	D	1271	NAD	N9A-C8A-N7A	-2.42	110.50	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1271	NAD	C6A-C5A-N7A	2.42	136.76	132.09
2	H	1270	KV1	C11-C16-C9	-2.41	104.40	105.84
3	B	1271	NAD	O3-PA-O1A	-2.33	103.69	110.70
3	F	1270	NAD	C2A-N1A-C6A	2.30	122.51	118.73
2	H	1270	KV1	C19-C18-N5	-2.27	105.05	106.64
3	H	1271	NAD	C4D-O4D-C1D	-2.25	107.87	109.92
3	H	1271	NAD	N9A-C8A-N7A	-2.23	110.77	113.94
2	H	1270	KV1	C6-N3-C17	2.21	126.78	123.09
3	H	1271	NAD	C6A-C5A-N7A	2.18	136.30	132.09
3	B	1271	NAD	N9A-C8A-N7A	-2.18	110.85	113.94
3	B	1271	NAD	C5N-C4N-C3N	-2.17	118.23	120.36
3	H	1271	NAD	C2A-N1A-C6A	2.13	122.22	118.73
3	F	1270	NAD	C6A-C5A-N7A	2.05	136.04	132.09
3	D	1271	NAD	C4B-O4B-C1B	-2.04	104.97	109.47

There are no chirality outliers.

All (61) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1270	KV1	O2-C8-C9-C16
2	D	1270	KV1	O2-C8-C9-C16
3	B	1271	NAD	C5B-O5B-PA-O1A
3	B	1271	NAD	C5D-O5D-PN-O3
3	B	1271	NAD	C5D-O5D-PN-O1N
3	B	1271	NAD	C5D-O5D-PN-O2N
3	B	1271	NAD	O4D-C1D-N1N-C2N
3	B	1271	NAD	O4D-C1D-N1N-C6N
3	D	1271	NAD	PN-O3-PA-O5B
3	D	1271	NAD	C5D-O5D-PN-O3
3	D	1271	NAD	C5D-O5D-PN-O1N
3	D	1271	NAD	C5D-O5D-PN-O2N
3	D	1271	NAD	O4D-C1D-N1N-C2N
3	D	1271	NAD	O4D-C1D-N1N-C6N
3	F	1270	NAD	C5B-O5B-PA-O1A
3	F	1270	NAD	C5B-O5B-PA-O3
3	F	1270	NAD	PN-O3-PA-O5B
3	F	1270	NAD	C5D-O5D-PN-O3
3	F	1270	NAD	C5D-O5D-PN-O1N
3	F	1270	NAD	C5D-O5D-PN-O2N
3	F	1270	NAD	O4D-C1D-N1N-C2N
3	F	1270	NAD	O4D-C1D-N1N-C6N
3	H	1271	NAD	C5B-O5B-PA-O1A

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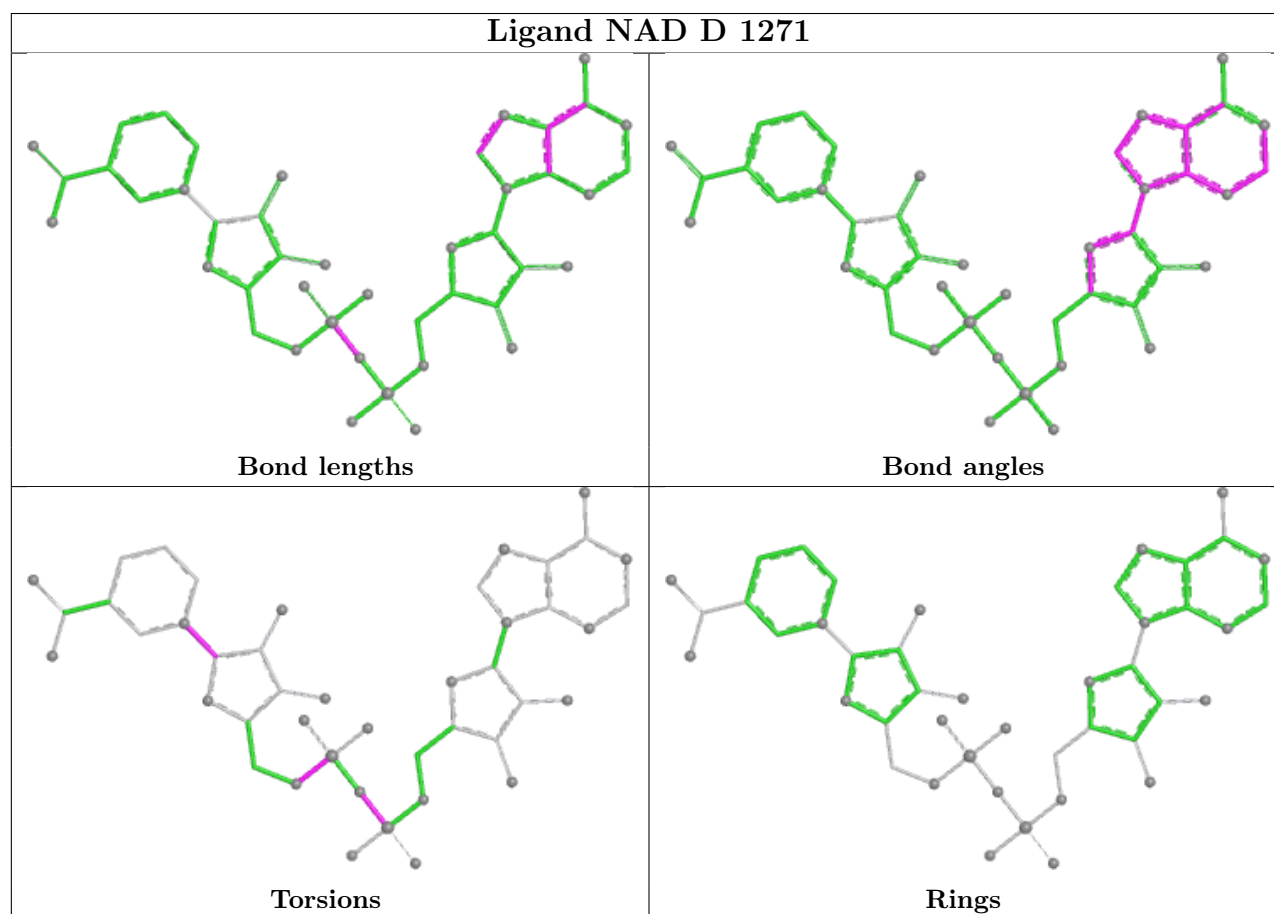
Mol	Chain	Res	Type	Atoms
3	H	1271	NAD	C5B-O5B-PA-O3
3	H	1271	NAD	PN-O3-PA-O5B
3	H	1271	NAD	C5D-O5D-PN-O3
3	H	1271	NAD	C5D-O5D-PN-O1N
3	H	1271	NAD	C5D-O5D-PN-O2N
3	H	1271	NAD	O4D-C1D-N1N-C2N
3	H	1271	NAD	O4D-C1D-N1N-C6N
3	F	1270	NAD	C4N-C3N-C7N-N7N
3	F	1270	NAD	C2N-C3N-C7N-O7N
3	F	1270	NAD	C4N-C3N-C7N-O7N
3	F	1270	NAD	C2N-C3N-C7N-N7N
2	F	1271	KV1	O2-C8-C9-C16
2	F	1271	KV1	N4-C20-C21-C22
2	H	1270	KV1	N4-C20-C21-C22
2	B	1270	KV1	C19-C20-C21-C22
2	D	1270	KV1	C19-C20-C21-C22
2	F	1271	KV1	C19-C20-C21-C22
2	H	1270	KV1	C19-C20-C21-C22
2	F	1271	KV1	O1-C3-N1-C2
2	H	1270	KV1	O2-C8-C9-C16
3	F	1270	NAD	C5B-O5B-PA-O2A
3	H	1271	NAD	C5B-O5B-PA-O2A
3	B	1271	NAD	PN-O3-PA-O1A
3	D	1271	NAD	C2D-C1D-N1N-C6N
3	F	1270	NAD	C2D-C1D-N1N-C2N
3	F	1270	NAD	C2D-C1D-N1N-C6N
3	B	1271	NAD	PN-O3-PA-O5B
3	H	1271	NAD	C4N-C3N-C7N-N7N
2	H	1270	KV1	O1-C3-N1-C2
3	H	1271	NAD	C4N-C3N-C7N-O7N
2	F	1271	KV1	C4-C3-N1-C2
2	D	1270	KV1	O4-C17-N3-C6
2	B	1270	KV1	N4-C20-C21-C22
2	D	1270	KV1	N4-C20-C21-C22
3	H	1271	NAD	O4B-C4B-C5B-O5B
3	B	1271	NAD	O4B-C4B-C5B-O5B
3	F	1270	NAD	O4B-C4B-C5B-O5B
3	H	1271	NAD	C2N-C3N-C7N-N7N

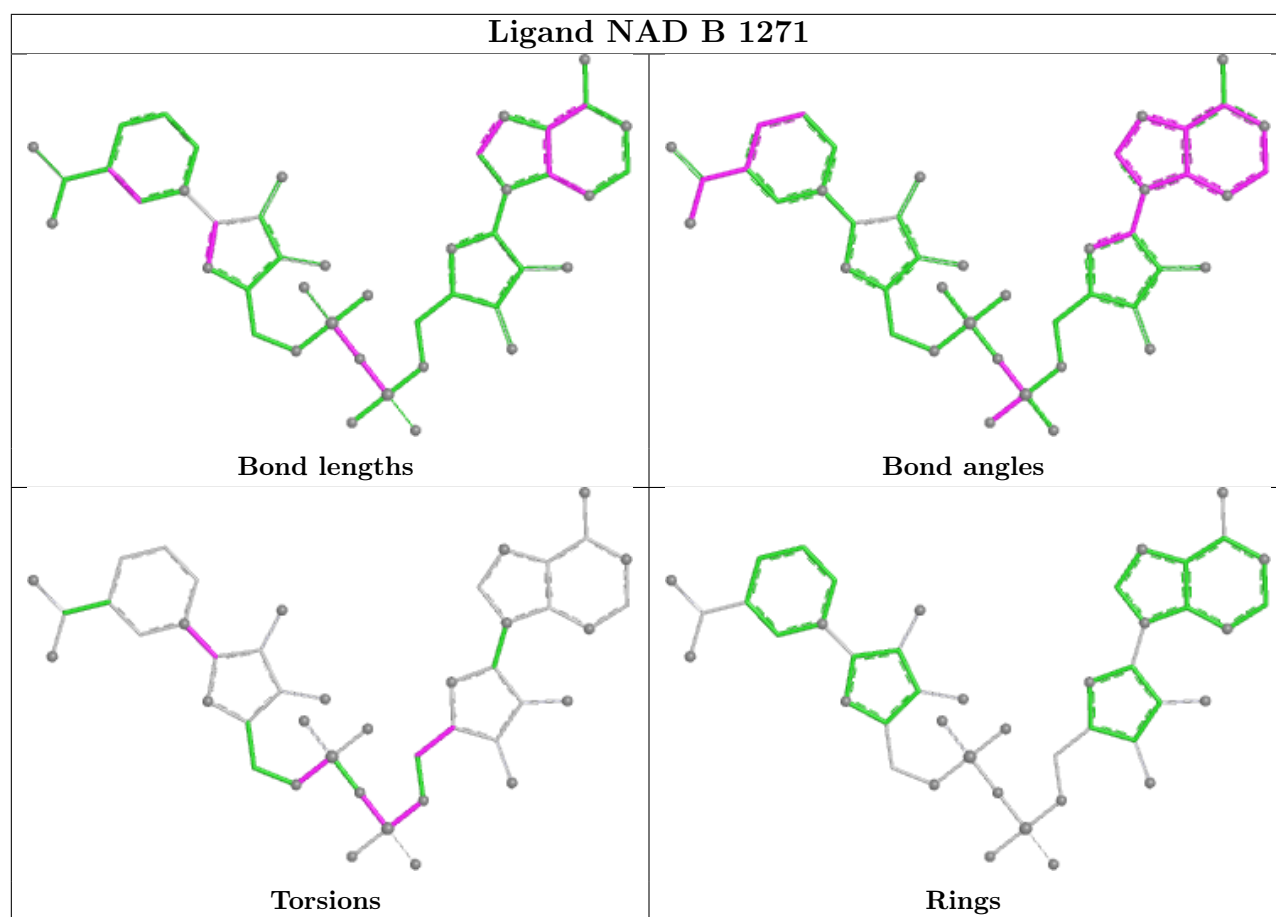
There are no ring outliers.

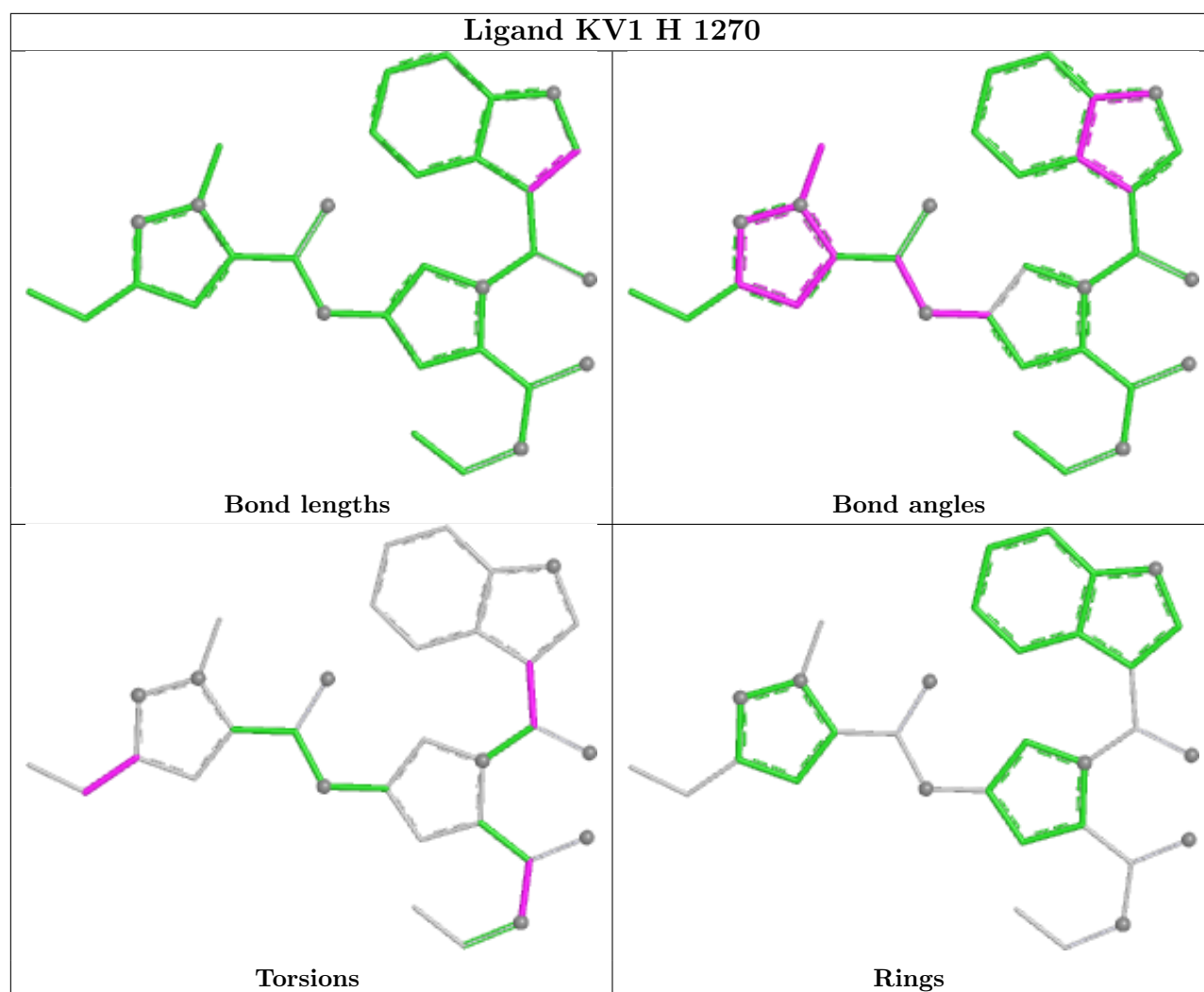
5 monomers are involved in 11 short contacts:

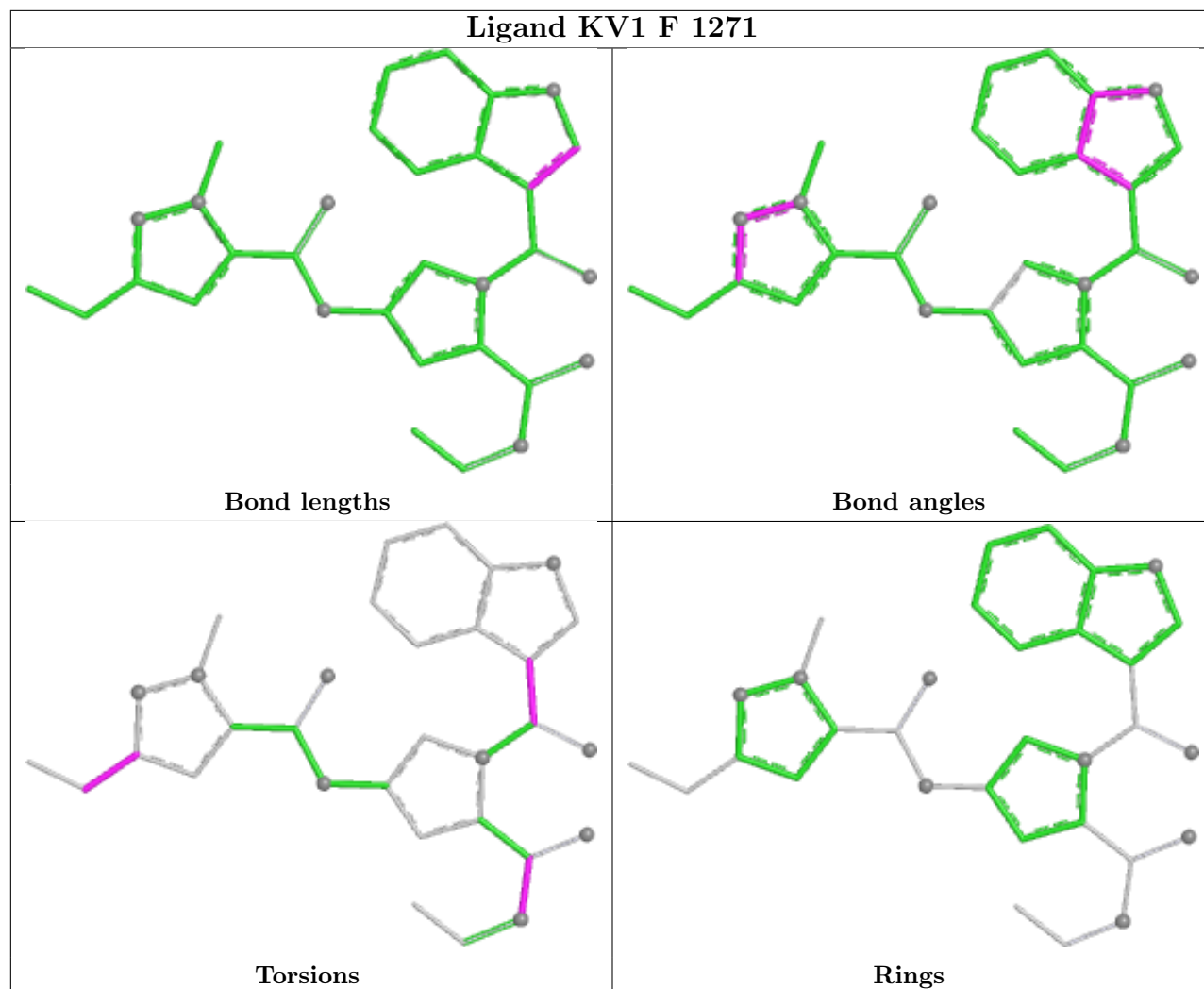
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	1270	KV1	3	0
2	F	1271	KV1	3	0
3	H	1271	NAD	1	0
2	D	1270	KV1	2	0
2	B	1270	KV1	2	0

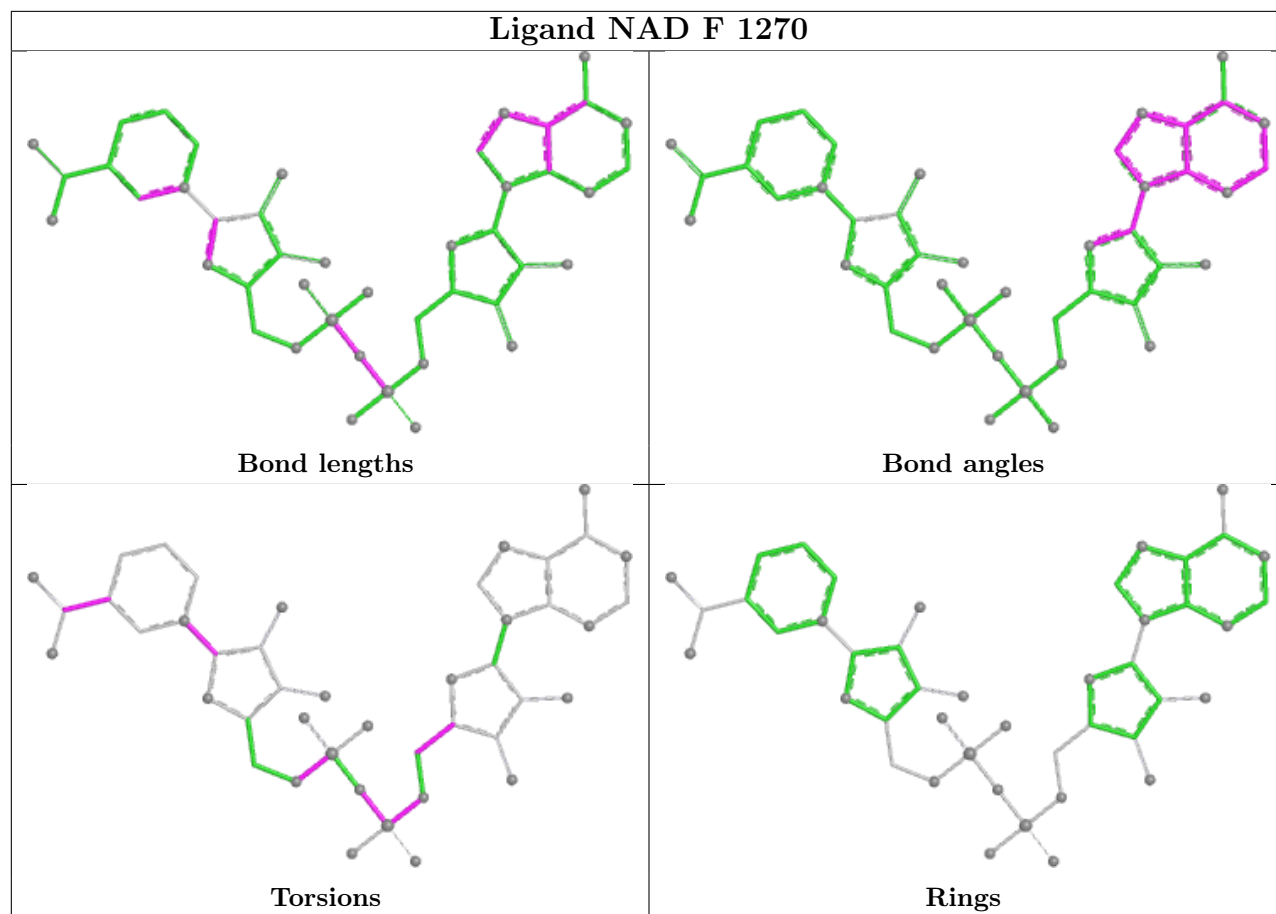
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

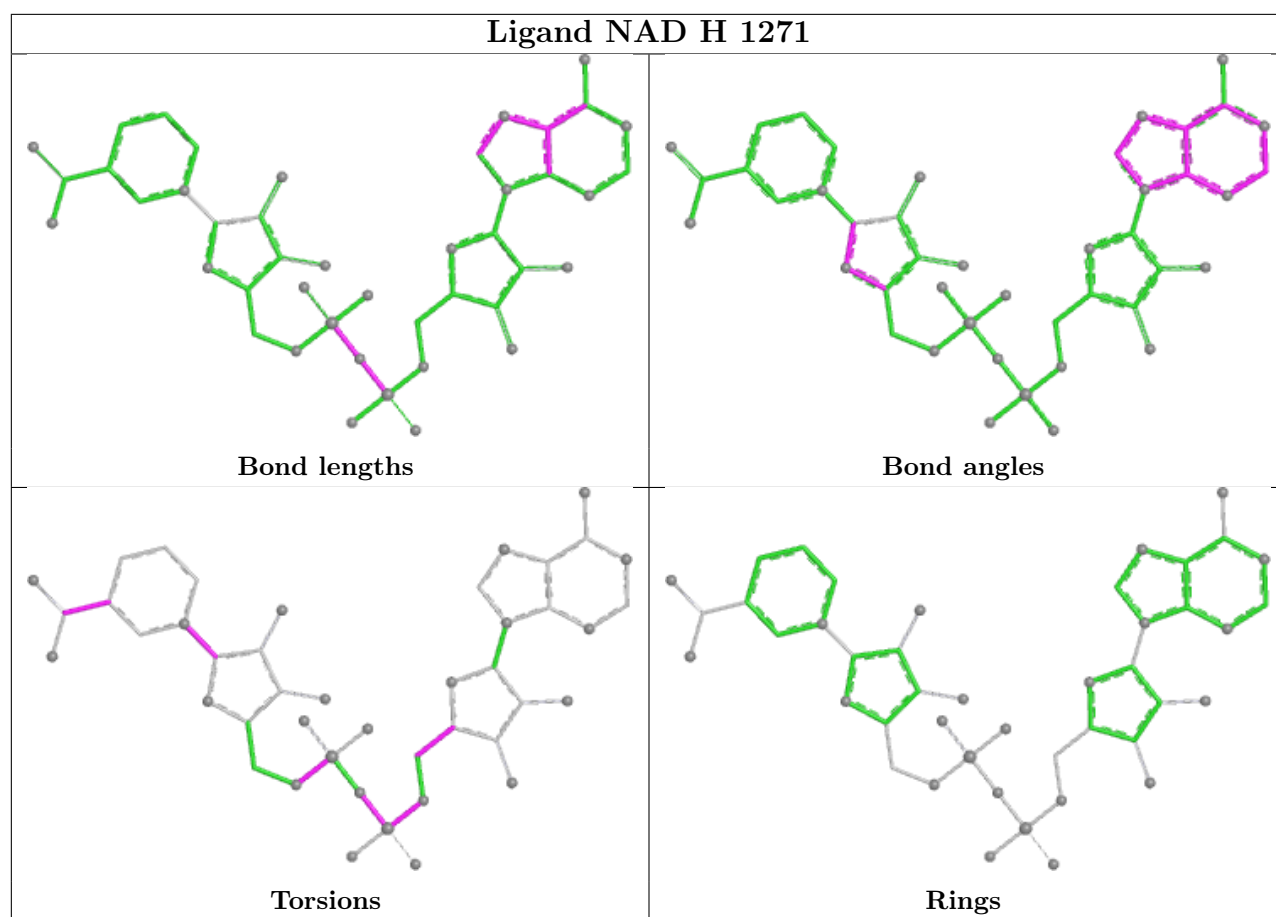


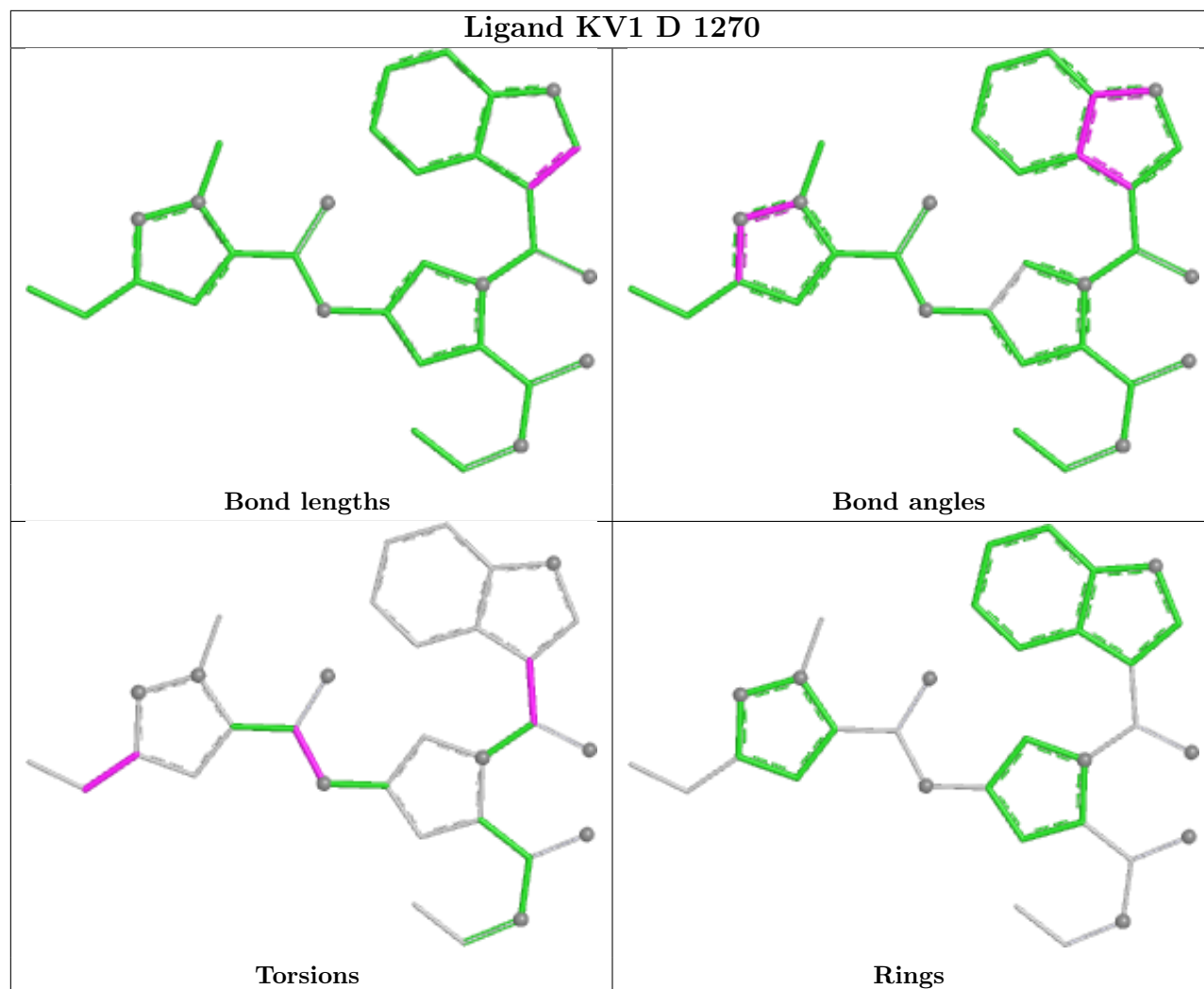


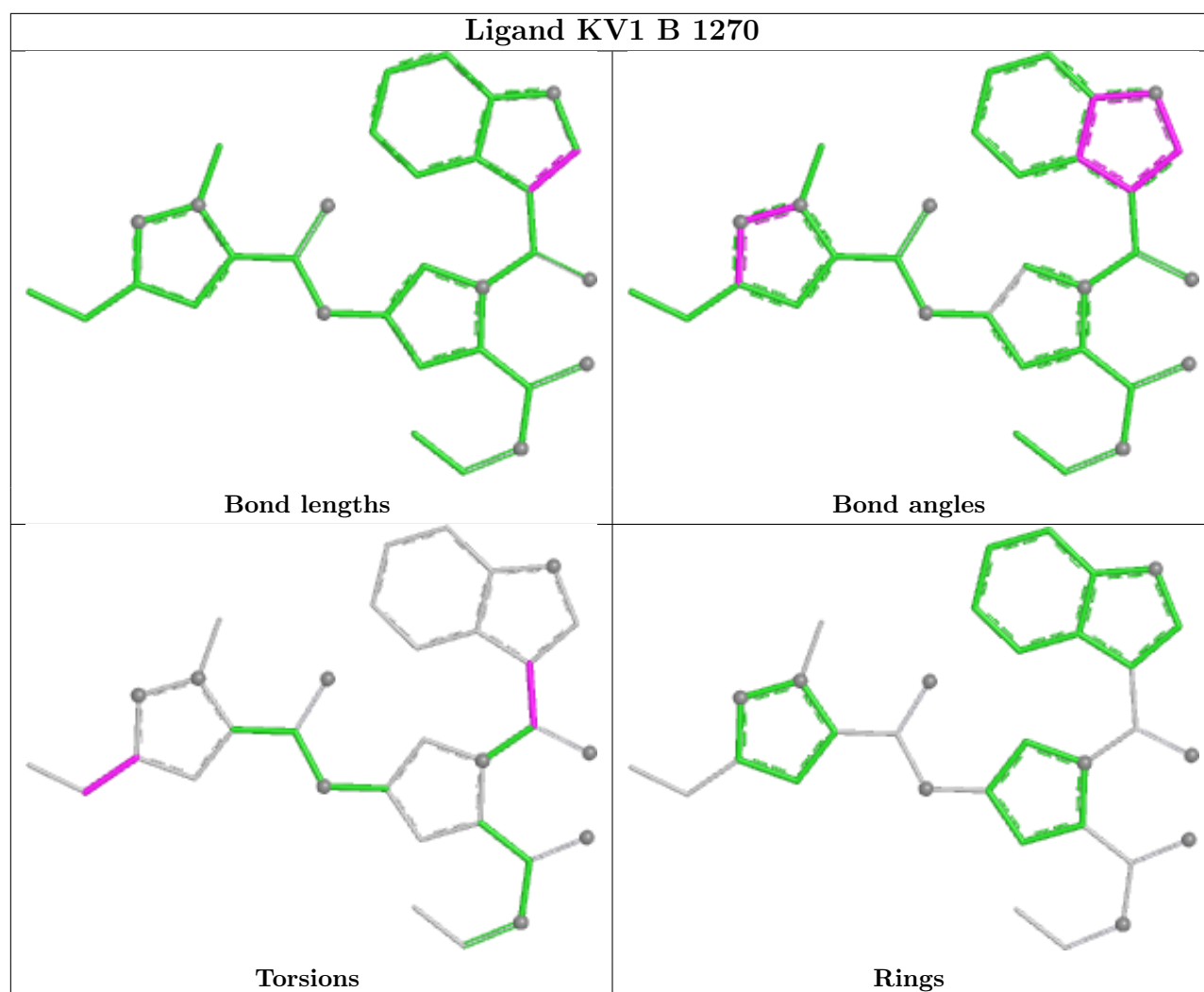












5.7 Other polymers [i](#)

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	B	268/269 (99%)	-0.35	1 (0%) 88 86	42, 55, 79, 95	0
1	D	268/269 (99%)	-0.22	2 (0%) 84 81	44, 61, 83, 96	0
1	F	268/269 (99%)	-0.17	1 (0%) 88 86	45, 63, 84, 104	0
1	H	268/269 (99%)	-0.06	2 (0%) 84 81	48, 66, 87, 111	0
All	All	1072/1076 (99%)	-0.20	6 (0%) 85 83	42, 61, 85, 111	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	2	THR	2.6
1	H	57	LYS	2.5
1	H	269	LEU	2.3
1	D	2	THR	2.3
1	D	157	ALA	2.2
1	B	57	LYS	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.

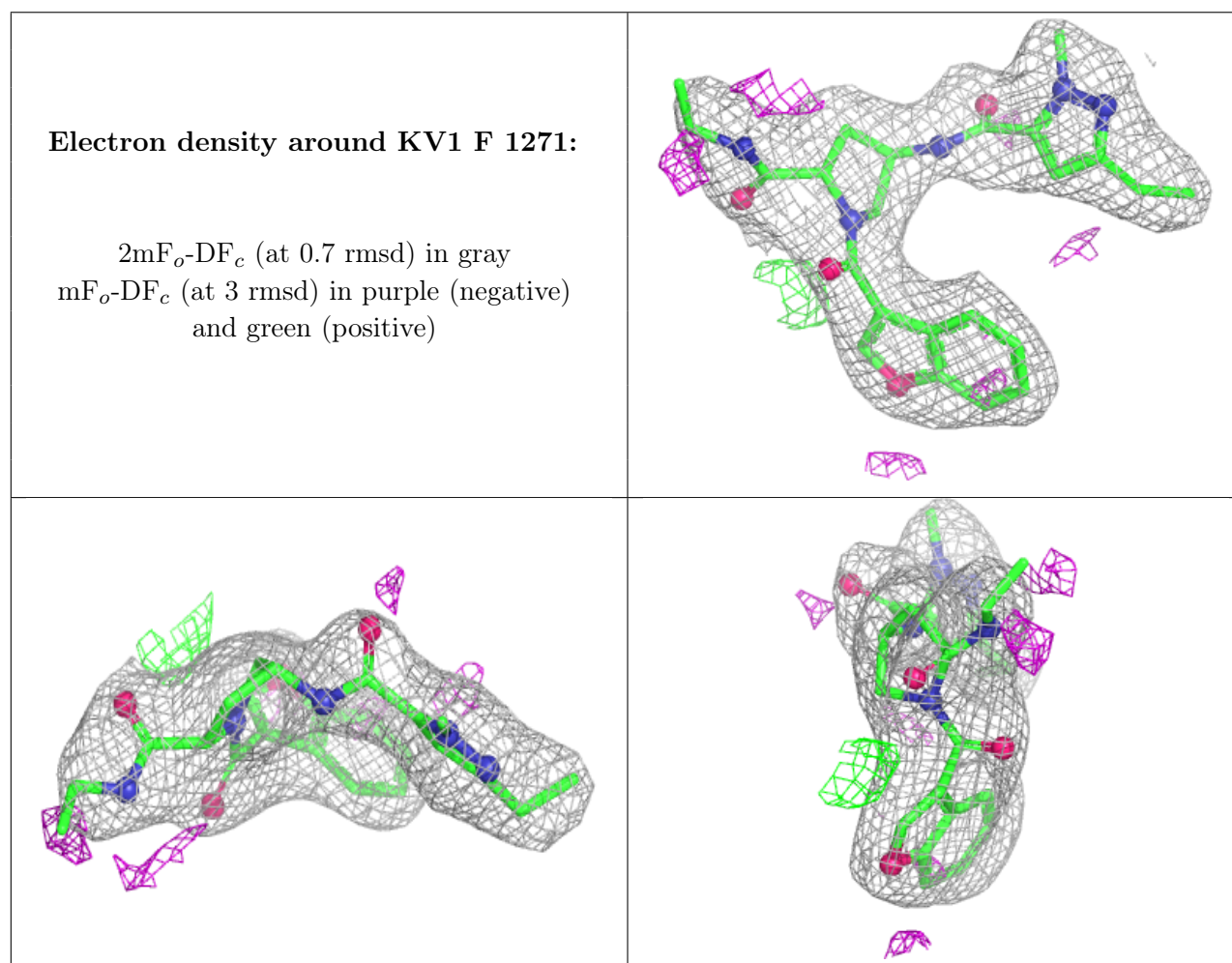
6.4 Ligands [i](#)

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.

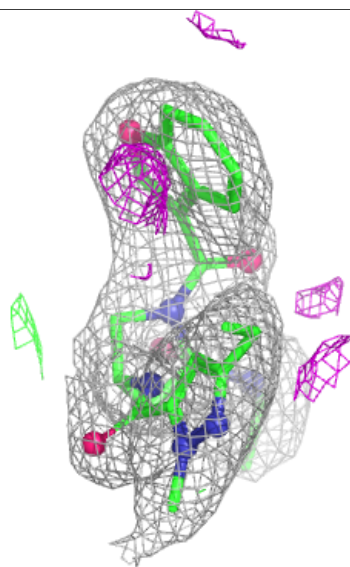
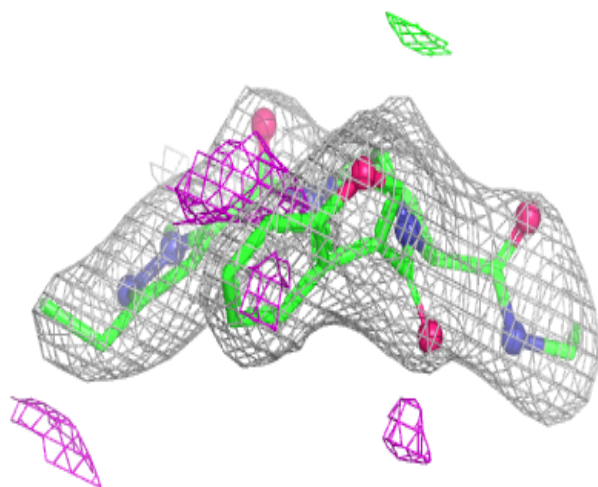
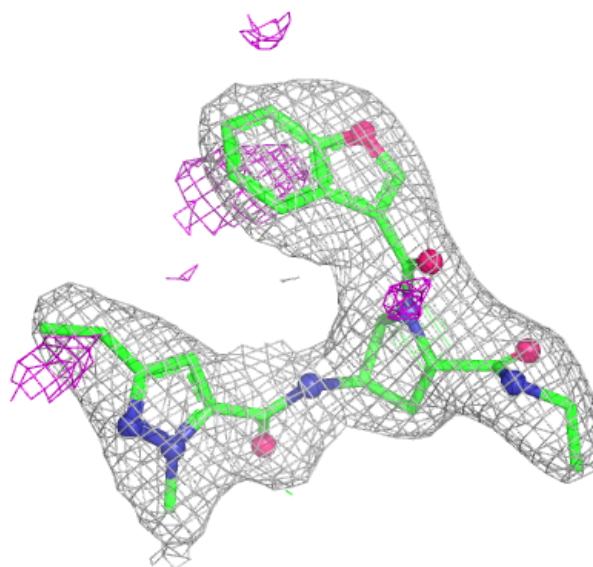
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	KV1	F	1271	32/32	0.95	0.09	51,60,68,71	0
2	KV1	H	1270	32/32	0.95	0.09	53,67,73,73	0
2	KV1	D	1270	32/32	0.96	0.08	47,56,61,65	0
3	NAD	H	1271	44/44	0.96	0.08	64,71,78,83	0
3	NAD	D	1271	44/44	0.97	0.07	51,56,62,67	0
3	NAD	F	1270	44/44	0.97	0.06	54,67,70,72	0
2	KV1	B	1270	32/32	0.97	0.07	38,46,49,50	0
3	NAD	B	1271	44/44	0.98	0.06	41,50,57,60	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.



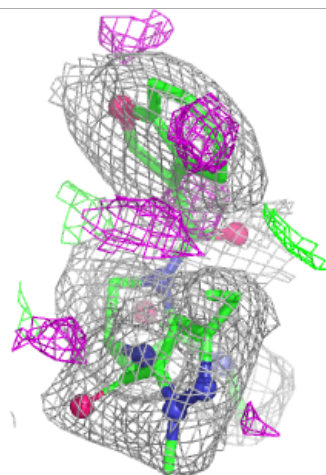
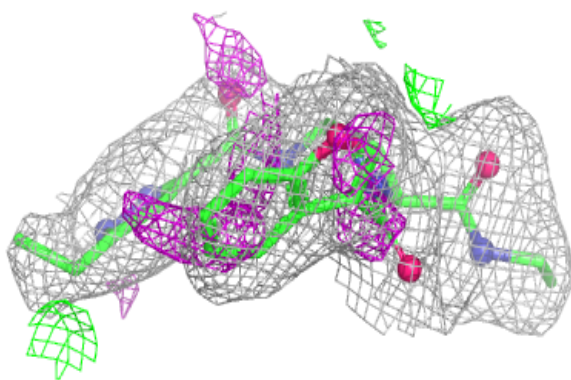
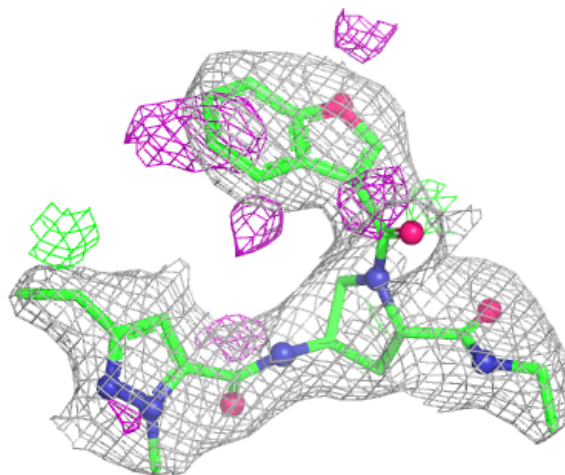
Electron density around KV1 H 1270:

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



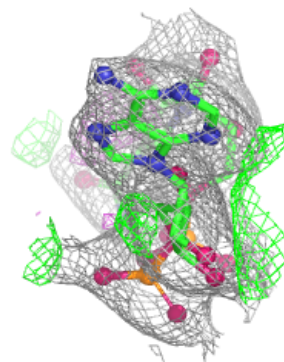
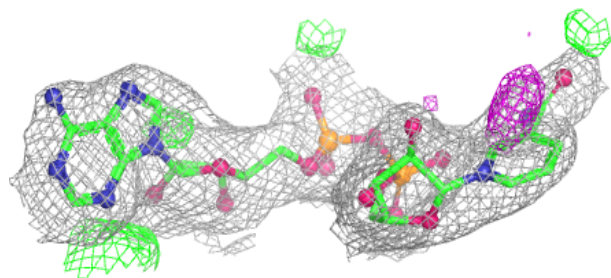
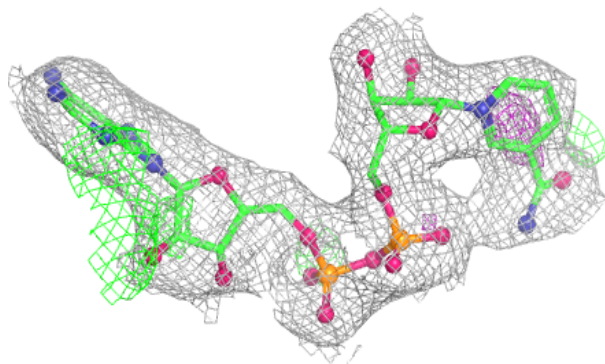
Electron density around KV1 D 1270:

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

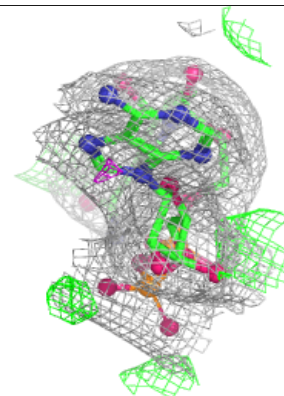
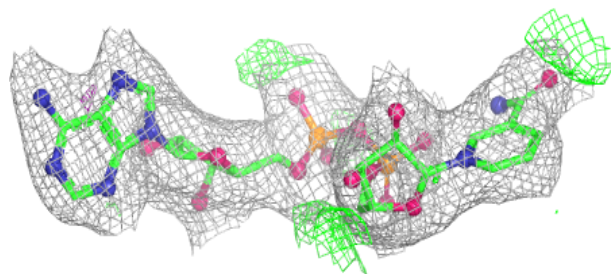
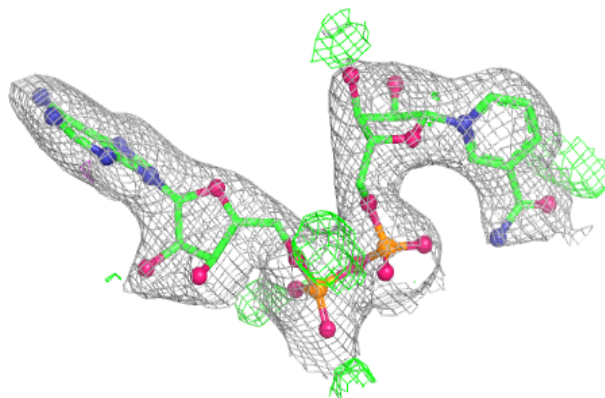


Electron density around NAD H 1271:

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

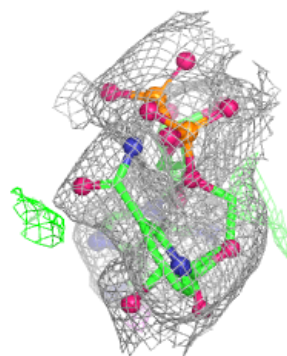
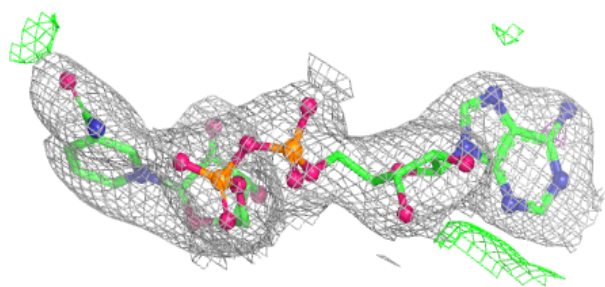
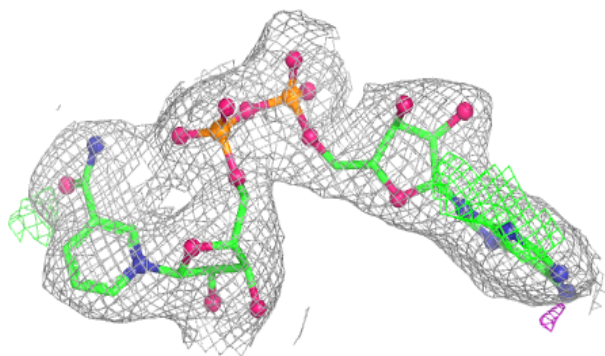
**Electron density around NAD D 1271:**

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



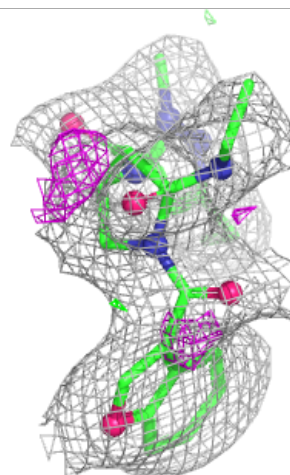
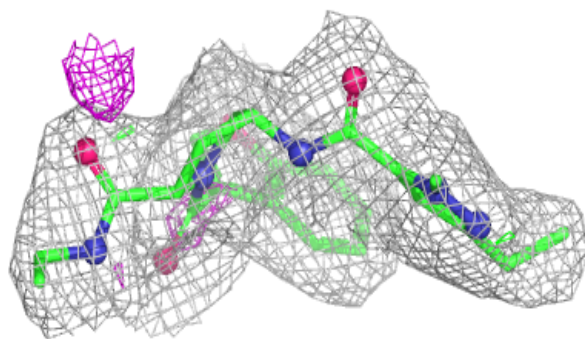
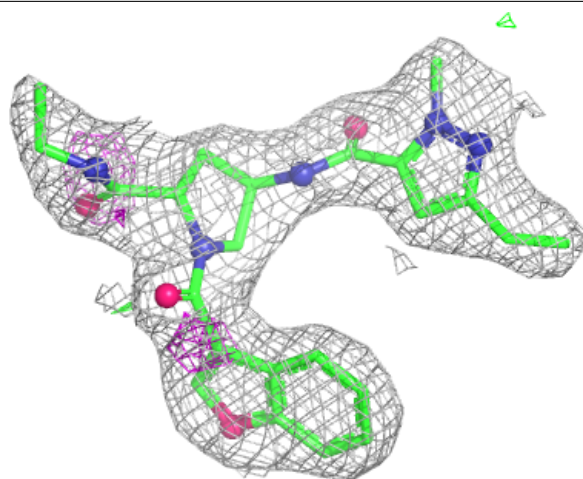
Electron density around NAD F 1270:

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



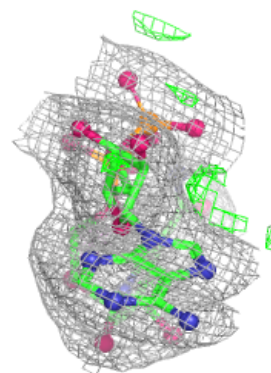
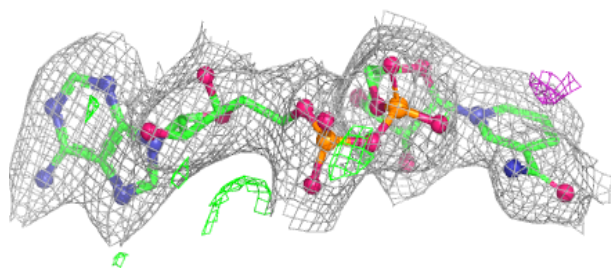
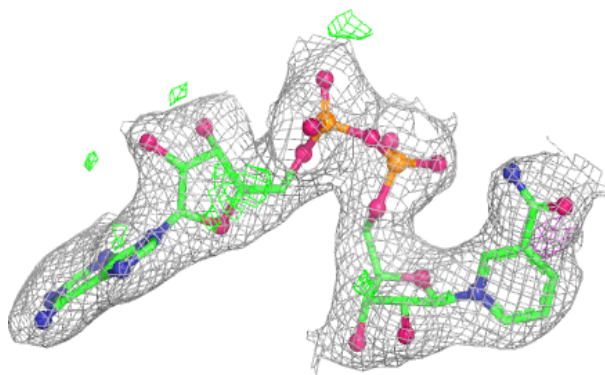
Electron density around KV1 B 1270:

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



Electron density around NAD B 1271:

$2mF_o-DF_c$ (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.