



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:40 PM UTC

PDB ID : 2OME / pdb_00002ome
Title : Crystal structure of human CTBP2 dehydrogenase complexed with NAD(H)
Authors : Pilka, E.S.; Guo, K.; Rojkova, A.; Debreczeni, J.E.; Kavanagh, K.L.; von Delft, F.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.; Sundstrom, M.; Oppermann, U.; Structural Genomics Consortium (SGC)
Deposited on : 2007-01-22
Resolution : 2.80 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:

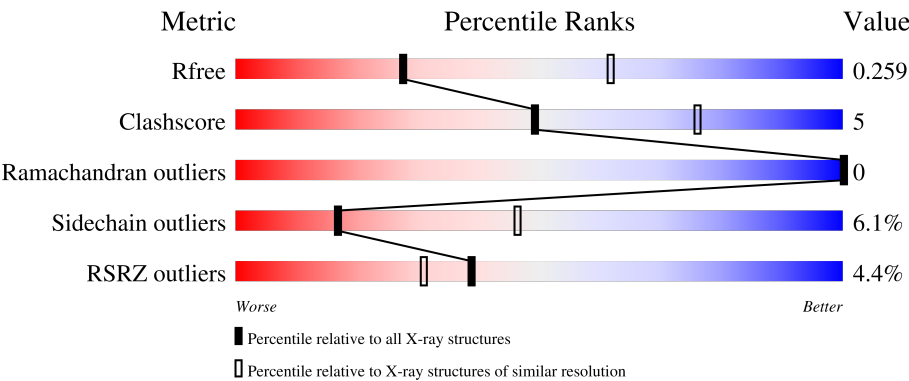
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	336	% 85%12%..
1	B	336	6% 85%11%..
1	C	336	% 83%14%..
1	D	336	13% 80%15%..

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Mol	Chain	Length	Quality of chain
1	E	336	7% 80% 15% • •
1	F	336	2% 83% 15% •
1	G	336	5% 84% 14% • •
1	H	336	78% 20% • •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20793 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 C-terminal-binding protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	1	0
			2554	1601	458	482	13			
1	B	330	Total	C	N	O	S	0	0	0
			2520	1586	445	476	13			
1	C	330	Total	C	N	O	S	0	1	0
			2561	1607	461	480	13			
1	D	330	Total	C	N	O	S	0	0	0
			2532	1589	455	475	13			
1	E	330	Total	C	N	O	S	0	0	0
			2487	1560	447	467	13			
1	F	330	Total	C	N	O	S	0	2	0
			2551	1599	457	482	13			
1	G	330	Total	C	N	O	S	0	3	0
			2508	1570	449	476	13			
1	H	330	Total	C	N	O	S	0	1	0
			2544	1593	457	481	13			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	SER	-	cloning artifact	UNP P56545
A	30	MET	-	cloning artifact	UNP P56545
B	29	SER	-	cloning artifact	UNP P56545
B	30	MET	-	cloning artifact	UNP P56545
C	29	SER	-	cloning artifact	UNP P56545
C	30	MET	-	cloning artifact	UNP P56545
D	29	SER	-	cloning artifact	UNP P56545
D	30	MET	-	cloning artifact	UNP P56545
E	29	SER	-	cloning artifact	UNP P56545
E	30	MET	-	cloning artifact	UNP P56545
F	29	SER	-	cloning artifact	UNP P56545
F	30	MET	-	cloning artifact	UNP P56545
G	29	SER	-	cloning artifact	UNP P56545

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Chain	Residue	Modelled	Actual	Comment	Reference
G	30	MET	-	cloning artifact	UNP P56545
H	29	SER	-	cloning artifact	UNP P56545
H	30	MET	-	cloning artifact	UNP P56545

- # NAD

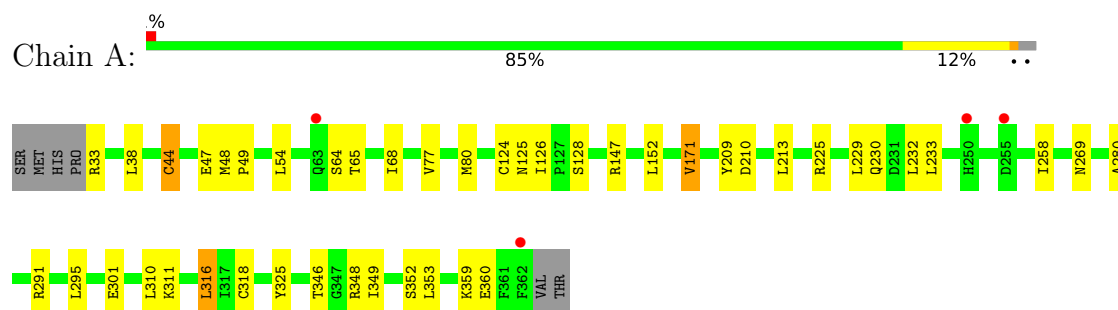
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	28	Total 28	O 28	0	0
3	B	19	Total 19	O 19	0	0
3	C	29	Total 29	O 29	0	0
3	D	23	Total 23	O 23	0	0
3	E	9	Total 9	O 9	0	0
3	F	30	Total 30	O 30	0	0
3	G	17	Total 17	O 17	0	0
3	H	29	Total 29	O 29	0	0

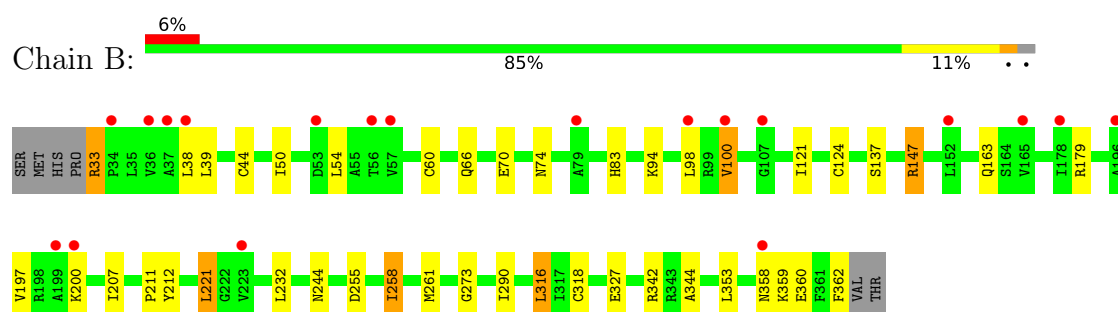
3 Residue-property plots

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

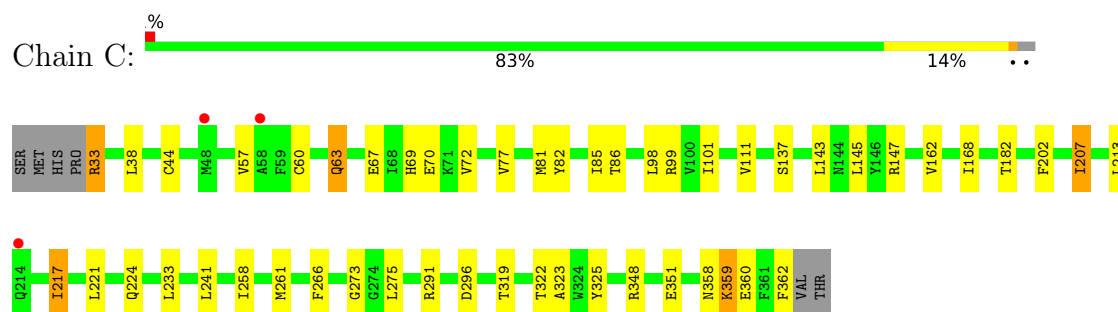
• Molecule 1: C-terminal-binding protein 2



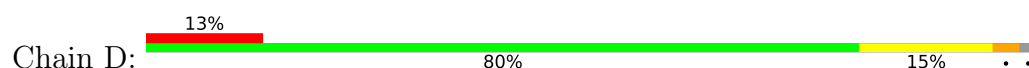
• Molecule 1: C-terminal-binding protein 2

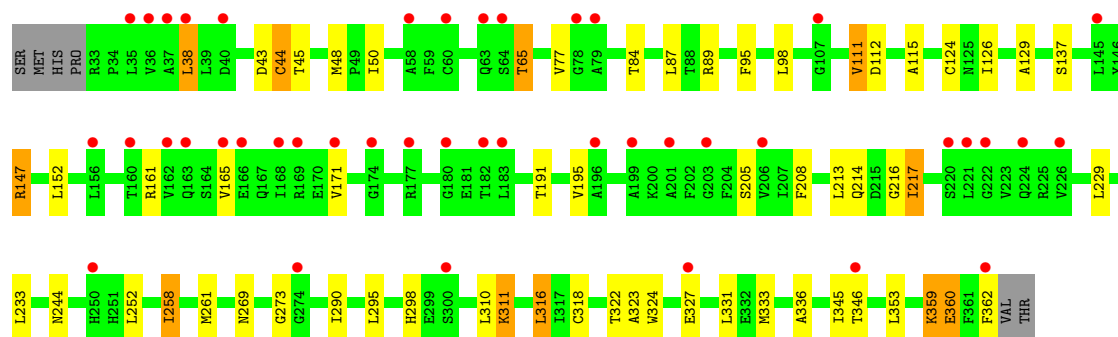


• Molecule 1: C-terminal-binding protein 2

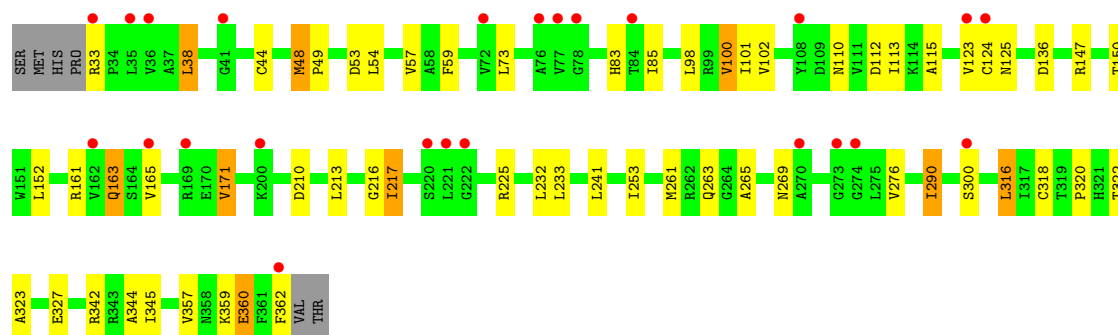
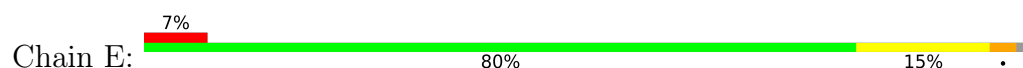


• Molecule 1: C-terminal-binding protein 2

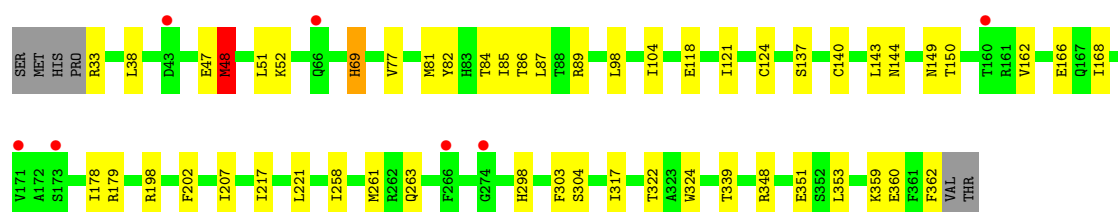
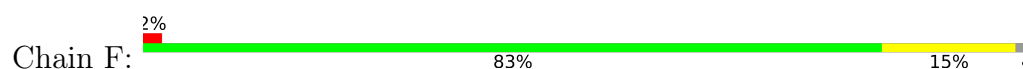




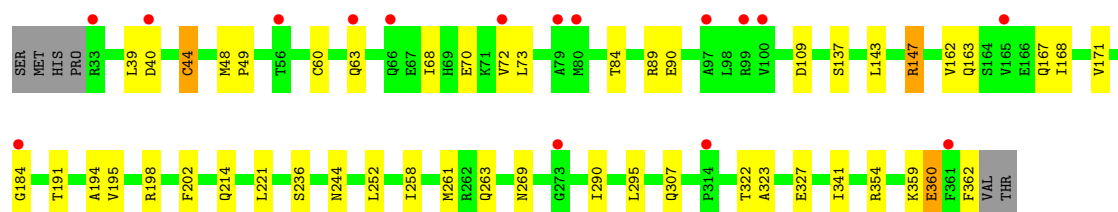
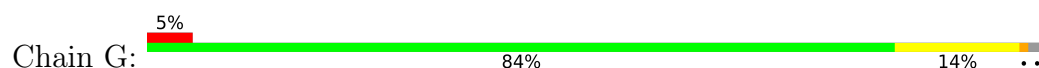
• Molecule 1: C-terminal-binding protein 2



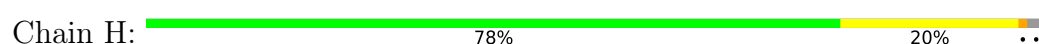
• Molecule 1: C-terminal-binding protein 2

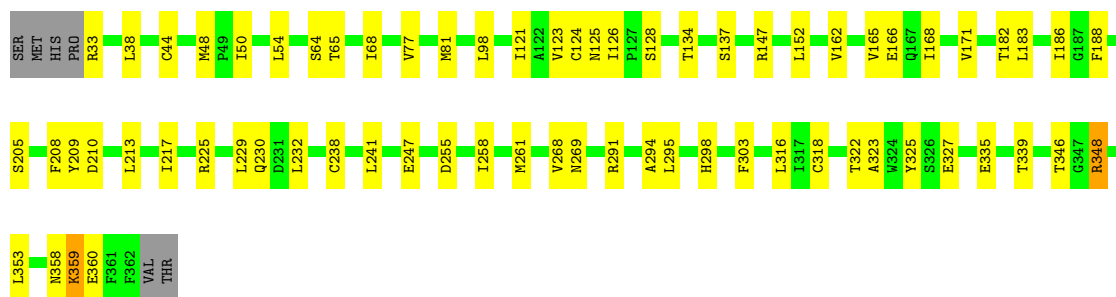


• Molecule 1: C-terminal-binding protein 2



• Molecule 1: C-terminal-binding protein 2





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.75Å 141.57Å 138.22Å 90.00° 98.93° 90.00°	Depositor
Resolution (Å)	43.31 – 2.80 43.31 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.31-2.80) 100.0 (43.31-2.80)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.207 , 0.257 0.213 , 0.259	Depositor DCC
R_{free} test set	4104 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	56.5	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 47.4	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	0.89	EDS
Total number of atoms	20793	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.80% 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	0.86	0/2601	0.91	4/3525 (0.1%)
1	B	0.79	0/2561	0.91	4/3474 (0.1%)
1	C	0.89	0/2609	0.92	2/3533 (0.1%)
1	D	0.78	0/2573	0.89	3/3488 (0.1%)
1	E	0.71	0/2528	0.88	3/3434 (0.1%)
1	F	0.85	3/2603 (0.1%)	0.93	5/3530 (0.1%)
1	G	0.75	0/2558	0.85	1/3472 (0.0%)
1	H	0.82	0/2592	0.90	3/3516 (0.1%)
All	All	0.81	3/20625 (0.0%)	0.90	25/27972 (0.1%)

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	A	0	1
1	B	0	2
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
All	All	0	9

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	48	MET	N-CA	5.97	1.51	1.46
1	F	48	MET	CG-SD	5.80	1.95	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	48	MET	CB-CG	5.49	1.69	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	33	ARG	CA-C-N	-10.46	108.91	119.90
1	B	33	ARG	C-N-CA	-10.46	108.91	119.90
1	A	33	ARG	CA-C-N	8.67	128.74	119.90
1	A	33	ARG	C-N-CA	8.67	128.74	119.90
1	E	33	ARG	CA-C-N	7.81	127.87	119.90
1	E	33	ARG	C-N-CA	7.81	127.87	119.90
1	F	360	GLU	N-CA-C	-7.24	101.61	110.88
1	E	360	GLU	N-CA-C	-7.14	101.75	110.88
1	G	360	GLU	N-CA-C	-6.90	102.04	110.88
1	C	273	GLY	N-CA-C	-6.88	103.31	111.36
1	A	360	GLU	N-CA-C	-6.87	102.08	110.88
1	D	360	GLU	N-CA-C	-6.76	102.23	110.88
1	F	48	MET	N-CA-CB	6.50	118.09	110.42
1	C	360	GLU	N-CA-C	-6.26	102.87	110.88
1	B	360	GLU	N-CA-C	-6.24	102.89	110.88
1	H	360	GLU	N-CA-C	-6.17	102.98	110.88
1	B	273	GLY	N-CA-C	-6.12	104.20	111.36
1	F	33	ARG	CA-C-N	5.84	125.86	119.90
1	F	33	ARG	C-N-CA	5.84	125.86	119.90
1	A	349	ILE	CB-CA-C	-5.68	104.24	110.78
1	D	258	ILE	CB-CA-C	-5.58	104.61	112.14
1	D	65	THR	CB-CA-C	-5.40	101.50	110.68
1	F	48	MET	CB-CG-SD	5.25	128.44	112.70
1	H	33	ARG	CA-C-N	5.25	125.25	119.90
1	H	33	ARG	C-N-CA	5.25	125.25	119.90

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	359	LYS	Peptide
1	B	33	ARG	Peptide
1	B	359	LYS	Peptide
1	C	359	LYS	Peptide
1	D	359	LYS	Peptide
1	E	359	LYS	Peptide
1	F	359	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	G	359	LYS	Peptide
1	H	359	LYS	Peptide

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	2554	0	2507	23	0
1	B	2520	0	2464	23	0
1	C	2561	0	2542	26	0
1	D	2532	0	2497	39	0
1	E	2487	0	2403	39	0
1	F	2551	0	2499	28	0
1	G	2508	0	2414	24	0
1	H	2544	0	2491	34	0
2	A	44	0	26	0	0
2	B	44	0	26	1	0
2	C	44	0	26	0	0
2	D	44	0	26	2	0
2	E	44	0	26	0	0
2	F	44	0	26	1	0
2	G	44	0	26	1	0
2	H	44	0	26	0	0
3	A	28	0	0	0	0
3	B	19	0	0	0	0
3	C	29	0	0	1	0
3	D	23	0	0	1	0
3	E	9	0	0	0	0
3	F	30	0	0	0	0
3	G	17	0	0	1	0
3	H	29	0	0	1	0
All	All	20793	0	20025	220	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 (220) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:213:LEU:HD13	1:D:217:ILE:HD12	1.41	1.01
1:F:81:MET:CE	1:F:85:ILE:HG23	1.93	0.98
1:F:81:MET:HE3	1:F:85:ILE:HG23	1.44	0.96
1:F:81:MET:HE3	1:F:85:ILE:CG2	1.99	0.92
1:D:261:MET:HE1	1:D:290:ILE:HD11	1.55	0.89
1:C:81:MET:CE	1:C:111:VAL:HG22	2.03	0.87
1:H:124:CYS:SG	1:H:353:LEU:HD13	2.15	0.86
1:C:81:MET:HE1	1:C:111:VAL:HG22	1.60	0.84
1:H:98:LEU:HD23	1:H:121:ILE:HD13	1.59	0.84
1:D:213:LEU:CD1	1:D:217:ILE:HD12	2.11	0.80
1:H:213:LEU:HD13	1:H:217:ILE:HD12	1.64	0.79
1:H:258:ILE:HA	1:H:261:MET:HE3	1.66	0.74
1:E:44:CYS:SG	1:E:59:PHE:HB3	2.28	0.72
1:D:261:MET:CE	1:D:290:ILE:HD11	2.20	0.71
1:B:261:MET:HE1	1:B:290:ILE:HD11	1.71	0.71
1:C:81:MET:CE	1:C:111:VAL:CG2	2.69	0.70
1:D:229:LEU:HD22	1:D:252:LEU:HD11	1.72	0.70
1:G:147:ARG:NH2	1:H:325:TYR:O	2.24	0.69
1:F:98:LEU:HD23	1:F:121:ILE:HD13	1.73	0.69
1:B:261:MET:CE	1:B:290:ILE:HD11	2.25	0.67
1:E:232:LEU:C	1:E:232:LEU:HD23	2.22	0.65
1:B:258:ILE:HA	1:B:261:MET:HE2	1.79	0.65
1:G:40:ASP:OD2	1:G:84:THR:OG1	2.14	0.63
1:C:63:GLN:NE2	1:C:67:GLU:OE2	2.31	0.63
1:A:310:LEU:HD13	1:A:316:LEU:HD11	1.81	0.61
1:E:113:ILE:HG22	1:E:123:VAL:HG11	1.82	0.61
1:H:54:LEU:HD11	1:H:346:THR:HG23	1.81	0.61
1:G:162:VAL:HG22	1:G:171:VAL:HG21	1.81	0.60
1:G:70:GLU:HA	1:G:73:LEU:HD12	1.83	0.60
1:C:82:TYR:CG	1:D:165:VAL:HG21	2.36	0.60
1:F:258:ILE:HG12	1:F:261:MET:HE3	1.84	0.60
1:E:150:THR:HG23	1:F:150:THR:HG23	1.84	0.60
1:F:298:HIS:CD2	1:F:303:PHE:CD1	2.91	0.58
1:E:261:MET:HE2	1:E:290:ILE:HD11	1.85	0.58
1:E:83:HIS:HA	1:E:110:ASN:ND2	2.19	0.58
1:E:98:LEU:HD21	1:E:101:ILE:HG12	1.87	0.57
1:A:124:CYS:SG	1:A:353:LEU:HD13	2.45	0.57
1:C:325:TYR:O	1:D:147:ARG:NH2	2.37	0.57
1:A:209:TYR:HB3	1:A:232:LEU:HD13	1.86	0.57
1:B:124:CYS:SG	1:B:353:LEU:HD13	2.45	0.57
1:H:44:CYS:SG	1:H:48:MET:CE	2.93	0.56
1:H:152:LEU:HD23	1:H:171:VAL:HG12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:112:ASP:OD2	1:D:115:ALA:HB2	2.06	0.56
1:B:70:GLU:O	1:B:74:ASN:ND2	2.39	0.56
1:B:258:ILE:HG23	1:B:261:MET:HE3	1.88	0.55
1:E:152:LEU:CD2	1:E:171:VAL:HG13	2.37	0.55
1:A:125:ASN:O	1:A:126:ILE:HD13	2.07	0.55
1:D:258:ILE:HA	1:D:261:MET:HE2	1.88	0.55
1:G:137:SER:OG	1:H:147:ARG:HD3	2.07	0.55
1:G:162:VAL:CG2	1:G:171:VAL:HG21	2.37	0.54
1:F:124:CYS:SG	1:F:353:LEU:HD13	2.46	0.54
1:H:348:ARG:HA	3:H:903:HOH:O	2.07	0.54
1:A:38:LEU:HD23	1:A:38:LEU:C	2.32	0.54
1:C:241:LEU:HD22	1:C:275:LEU:HD13	1.89	0.54
1:G:44:CYS:O	1:G:44:CYS:SG	2.65	0.54
1:C:60:CYS:SG	1:C:72:VAL:HG21	2.47	0.54
1:H:123:VAL:HG23	1:H:358:ASN:ND2	2.22	0.54
1:E:165:VAL:HG21	1:F:82:TYR:CG	2.43	0.53
1:D:213:LEU:HD13	1:D:217:ILE:CD1	2.27	0.53
1:H:54:LEU:HD11	1:H:346:THR:CG2	2.37	0.53
1:C:33:ARG:N	3:C:909:HOH:O	2.41	0.53
1:B:100:VAL:HG11	1:B:344:ALA:HB1	1.89	0.53
1:D:87:LEU:HD12	1:D:111:VAL:HG22	1.90	0.53
1:C:143:LEU:HD11	1:C:202:PHE:CE2	2.45	0.52
1:E:163:GLN:HE21	1:E:163:GLN:C	2.18	0.52
1:D:269:ASN:HB3	1:D:295:LEU:HD22	1.91	0.52
1:E:112:ASP:OD2	1:E:115:ALA:HB2	2.10	0.52
1:E:152:LEU:HD22	1:E:171:VAL:CG1	2.40	0.52
1:E:44:CYS:HB3	1:E:48:MET:HE3	1.92	0.52
1:G:184:GLY:HA3	1:G:236:SER:OG	2.10	0.52
1:H:134:THR:HG23	1:H:323:ALA:HB1	1.92	0.52
1:E:261:MET:CE	1:E:290:ILE:HD11	2.40	0.52
1:A:44:CYS:SG	1:A:48:MET:HE2	2.50	0.51
1:F:86:THR:O	1:F:87:LEU:HD23	2.10	0.51
1:B:100:VAL:HG11	1:B:344:ALA:CB	2.40	0.51
1:A:258:ILE:HD12	1:A:280:ALA:HB1	1.93	0.51
1:E:38:LEU:C	1:E:38:LEU:CD2	2.84	0.51
1:D:316:LEU:HD22	1:D:318:CYS:SG	2.51	0.51
1:B:221:LEU:HD23	1:B:221:LEU:N	2.25	0.51
1:D:311:LYS:O	3:D:909:HOH:O	2.19	0.51
1:G:167:GLN:O	1:G:171:VAL:HG23	2.11	0.50
1:F:221:LEU:HD21	1:G:221:LEU:HD21	1.93	0.50
1:A:47:GLU:HG2	1:A:80:MET:HE1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:136:ASP:OD2	1:F:178:ILE:HD12	2.11	0.50
1:H:165:VAL:HA	1:H:168:ILE:HD12	1.94	0.50
1:A:229:LEU:O	1:A:233:LEU:HG	2.12	0.50
1:D:124:CYS:SG	1:D:353:LEU:HD13	2.51	0.50
1:E:102:VAL:HG22	1:E:124:CYS:HB2	1.94	0.50
1:F:143:LEU:HD11	1:F:202:PHE:CE2	2.47	0.50
1:F:217:ILE:HG22	1:F:221:LEU:CD1	2.42	0.50
1:C:147:ARG:HD3	1:D:137:SER:OG	2.12	0.49
1:F:217:ILE:HG22	1:F:221:LEU:HD12	1.95	0.49
1:C:182:THR:HG21	1:C:207:ILE:HD13	1.94	0.49
1:G:48:MET:N	1:G:49:PRO:HD2	2.28	0.49
1:H:44:CYS:SG	1:H:48:MET:HE2	2.53	0.49
1:E:152:LEU:CD2	1:E:171:VAL:CG1	2.91	0.48
1:B:98:LEU:HD23	1:B:121:ILE:HD13	1.94	0.48
1:C:296:ASP:OD1	1:C:319:THR:OG1	2.25	0.48
1:D:244:ASN:HA	2:D:901:NAD:O3D	2.13	0.48
1:A:152:LEU:CD2	1:A:171:VAL:CG1	2.91	0.48
1:A:210:ASP:O	1:A:225:ARG:NH2	2.46	0.48
1:F:348:ARG:HG3	1:F:351:GLU:HB2	1.96	0.48
1:E:125:ASN:ND2	1:E:357:VAL:HG11	2.28	0.48
1:H:50:ILE:HD11	1:H:335:GLU:HG2	1.96	0.47
1:F:47:GLU:O	1:F:51:LEU:HD12	2.14	0.47
1:G:143:LEU:HD11	1:G:202:PHE:CE2	2.49	0.47
1:H:162:VAL:HG22	1:H:171:VAL:HG21	1.96	0.47
1:H:152:LEU:CD2	1:H:171:VAL:HG12	2.43	0.47
1:B:54:LEU:HD12	1:B:342:ARG:NH1	2.29	0.47
1:D:126:ILE:HD12	1:D:336:ALA:CB	2.44	0.47
1:E:48:MET:HE2	1:E:57:VAL:HB	1.97	0.47
1:E:125:ASN:ND2	1:E:357:VAL:CG1	2.78	0.47
1:C:162:VAL:HG12	1:C:168:ILE:HG13	1.97	0.47
1:C:217:ILE:CG2	1:C:221:LEU:HD12	2.45	0.47
1:E:320:PRO:HD2	1:E:322:THR:HG23	1.97	0.47
1:D:152:LEU:CD2	1:D:171:VAL:HG12	2.44	0.46
1:E:83:HIS:HA	1:E:110:ASN:HD21	1.80	0.46
1:B:244:ASN:HA	2:B:901:NAD:O3D	2.15	0.46
1:H:65:THR:HA	1:H:68:ILE:HD12	1.97	0.46
1:E:54:LEU:HD11	1:E:342:ARG:NE	2.31	0.46
1:G:307:GLN:HA	3:G:917:HOH:O	2.16	0.46
1:A:65:THR:HA	1:A:68:ILE:HD12	1.96	0.46
1:D:126:ILE:HD12	1:D:336:ALA:HB1	1.98	0.46
1:A:325:TYR:O	1:B:147:ARG:NH2	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:320:PRO:HD2	1:E:322:THR:CG2	2.45	0.46
1:B:258:ILE:HG23	1:B:261:MET:CE	2.45	0.46
1:D:43:ASP:OD2	1:D:45:THR:HG23	2.16	0.46
1:E:261:MET:HE3	1:E:265:ALA:HB3	1.97	0.46
1:F:89:ARG:NH2	1:F:118:GLU:OE1	2.48	0.46
1:F:198:ARG:NH1	1:F:198:ARG:HG3	2.31	0.46
1:C:182:THR:CG2	1:C:207:ILE:HD13	2.45	0.46
1:G:60:CYS:SG	1:G:72:VAL:HG21	2.56	0.46
1:H:210:ASP:CG	1:H:213:LEU:HG	2.40	0.46
1:D:233:LEU:HD22	1:D:261:MET:CG	2.46	0.46
1:E:261:MET:HE2	1:E:290:ILE:CD1	2.46	0.45
1:H:268:VAL:HG22	1:H:294:ALA:HB3	1.98	0.45
1:A:269:ASN:HB3	1:A:295:LEU:HD22	1.98	0.45
1:D:38:LEU:HD12	1:D:44:CYS:HB2	1.98	0.45
1:E:152:LEU:HD13	1:F:322:THR:HG21	1.98	0.45
1:G:261:MET:CE	1:G:290:ILE:HD11	2.46	0.45
1:A:147:ARG:HD3	1:B:137:SER:OG	2.17	0.45
1:B:211:PRO:HG2	1:B:212:TYR:CE1	2.52	0.44
1:D:95:PHE:CG	1:D:98:LEU:HD22	2.52	0.44
1:D:95:PHE:CD2	1:D:98:LEU:HD22	2.52	0.44
1:E:253:ILE:HB	1:E:276:VAL:HG22	2.00	0.44
1:H:38:LEU:C	1:H:38:LEU:HD23	2.42	0.44
1:D:310:LEU:HD13	1:D:316:LEU:HD11	1.99	0.44
1:B:200:LYS:NZ	1:B:221:LEU:O	2.50	0.44
1:E:316:LEU:HD22	1:E:318:CYS:SG	2.57	0.44
1:E:213:LEU:HD22	1:E:217:ILE:HD12	1.99	0.44
1:B:50:ILE:O	1:B:342:ARG:NH1	2.51	0.44
1:E:233:LEU:HD22	1:E:261:MET:HG2	1.99	0.44
1:B:83:HIS:CD2	1:B:83:HIS:C	2.96	0.44
1:C:233:LEU:HD22	1:C:261:MET:HG2	1.99	0.44
1:A:128:SER:HB2	1:D:216:GLY:HA2	2.00	0.43
1:D:191:THR:O	1:D:195:VAL:HG23	2.17	0.43
1:A:48:MET:HB3	1:A:49:PRO:HD3	2.00	0.43
1:C:98:LEU:HD21	1:C:101:ILE:CG1	2.48	0.43
1:E:100:VAL:HG11	1:E:344:ALA:HB1	2.00	0.43
1:G:269:ASN:HB3	1:G:295:LEU:HD22	1.99	0.43
1:G:168:ILE:HG23	1:H:322:THR:HG22	2.01	0.43
1:H:186:ILE:HD13	1:H:229:LEU:CD1	2.48	0.43
1:D:208:PHE:CD1	1:D:208:PHE:C	2.97	0.43
1:D:310:LEU:O	1:D:311:LYS:C	2.62	0.43
1:D:324:TRP:HB3	2:D:901:NAD:H4N	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:PRO:HG2	1:B:212:TYR:CD1	2.54	0.43
1:D:44:CYS:SG	1:D:48:MET:HG3	2.58	0.43
1:D:129:ALA:HB3	1:D:333:MET:HE2	2.00	0.43
1:A:44:CYS:SG	1:A:44:CYS:O	2.77	0.43
1:F:221:LEU:HD21	1:G:221:LEU:CD2	2.49	0.43
1:C:77:VAL:HG13	1:C:99:ARG:HG3	2.01	0.43
1:C:98:LEU:HD21	1:C:101:ILE:HG12	2.00	0.43
1:E:216:GLY:HA2	1:H:128:SER:HB2	2.01	0.42
1:A:210:ASP:CG	1:A:213:LEU:HG	2.44	0.42
1:C:207:ILE:HG22	1:C:224:GLN:HB2	2.01	0.42
1:D:295:LEU:O	1:D:318:CYS:HA	2.19	0.42
1:H:241:LEU:HD12	1:H:269:ASN:CG	2.43	0.42
1:B:39:LEU:O	1:B:60:CYS:HB2	2.19	0.42
1:G:341:ILE:HD13	1:G:341:ILE:HA	1.92	0.42
1:A:295:LEU:O	1:A:318:CYS:HA	2.20	0.42
1:D:89:ARG:NH1	1:D:115:ALA:HB2	2.34	0.42
1:H:210:ASP:O	1:H:225:ARG:NH2	2.49	0.42
1:F:162:VAL:HG12	1:F:168:ILE:HG13	2.02	0.42
1:G:194:ALA:O	1:G:198:ARG:HD2	2.19	0.42
1:H:298:HIS:CD2	1:H:303:PHE:CD1	3.08	0.42
1:B:358:ASN:O	1:B:358:ASN:CG	2.62	0.42
1:C:145:LEU:HD13	1:C:266:PHE:HB3	2.01	0.42
1:C:322:THR:O	1:C:323:ALA:C	2.62	0.42
1:F:198:ARG:HG3	1:F:198:ARG:HH11	1.84	0.42
1:F:48:MET:O	1:F:52:LYS:N	2.53	0.42
1:F:324:TRP:HB3	2:F:901:NAD:H4N	2.01	0.42
1:F:140:CYS:O	1:F:144:ASN:ND2	2.52	0.42
1:D:50:ILE:O	1:D:50:ILE:HG22	2.20	0.41
1:C:44:CYS:SG	1:C:57:VAL:HG12	2.60	0.41
1:H:183:LEU:HD12	1:H:238:CYS:O	2.20	0.41
1:C:348:ARG:HB2	1:C:351:GLU:OE1	2.20	0.41
1:E:48:MET:N	1:E:49:PRO:HD2	2.35	0.41
1:F:82:TYR:CZ	1:F:104:ILE:HD13	2.55	0.41
1:G:244:ASN:HA	2:G:901:NAD:O3D	2.21	0.41
1:B:316:LEU:HD22	1:B:318:CYS:SG	2.60	0.41
1:D:233:LEU:HD22	1:D:261:MET:HG3	2.02	0.41
1:D:322:THR:O	1:D:323:ALA:C	2.61	0.41
1:E:210:ASP:O	1:E:225:ARG:NH2	2.53	0.41
1:C:358:ASN:O	1:C:358:ASN:CG	2.63	0.41
1:D:273:GLY:HA3	1:D:298:HIS:C	2.46	0.41
1:G:191:THR:O	1:G:195:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:209:TYR:HB3	1:H:232:LEU:HD13	2.03	0.41
1:E:241:LEU:HD12	1:E:269:ASN:HB2	2.03	0.41
1:E:322:THR:O	1:E:323:ALA:C	2.63	0.41
1:H:166:GLU:OE1	1:H:166:GLU:N	2.54	0.41
1:A:54:LEU:HD11	1:A:346:THR:CG2	2.51	0.41
1:A:310:LEU:O	1:A:311:LYS:C	2.64	0.41
1:E:232:LEU:C	1:E:232:LEU:CD2	2.91	0.40
1:H:295:LEU:O	1:H:318:CYS:HA	2.21	0.40
1:A:152:LEU:CD2	1:A:171:VAL:HG13	2.51	0.40
1:G:39:LEU:HD22	1:G:68:ILE:CD1	2.52	0.40
1:G:322:THR:O	1:G:323:ALA:C	2.65	0.40
1:H:125:ASN:O	1:H:126:ILE:HD13	2.22	0.40
1:H:188:PHE:HB2	1:H:208:PHE:CD1	2.57	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	329/336 (98%)	315 (96%)	14 (4%)	0	100	100
1	B	328/336 (98%)	315 (96%)	13 (4%)	0	100	100
1	C	329/336 (98%)	316 (96%)	13 (4%)	0	100	100
1	D	328/336 (98%)	314 (96%)	14 (4%)	0	100	100
1	E	328/336 (98%)	314 (96%)	14 (4%)	0	100	100
1	F	330/336 (98%)	317 (96%)	13 (4%)	0	100	100
1	G	331/336 (98%)	315 (95%)	16 (5%)	0	100	100
1	H	329/336 (98%)	312 (95%)	17 (5%)	0	100	100
All	All	2632/2688 (98%)	2518 (96%)	114 (4%)	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	261/276 (95%)	251 (96%)	10 (4%)	29	64
1	B	254/276 (92%)	237 (93%)	17 (7%)	15	42
1	C	267/276 (97%)	251 (94%)	16 (6%)	17	47
1	D	259/276 (94%)	239 (92%)	20 (8%)	12	36
1	E	247/276 (90%)	228 (92%)	19 (8%)	12	36
1	F	263/276 (95%)	247 (94%)	16 (6%)	17	46
1	G	252/276 (91%)	237 (94%)	15 (6%)	17	47
1	H	262/276 (95%)	247 (94%)	15 (6%)	18	49
All	All	2065/2208 (94%)	1937 (94%)	128 (6%)	17	45

All (128) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	CYS
1	A	64	SER
1	A	77	VAL
1	A	171	VAL
1	A	230	GLN
1	A	291	ARG
1	A	301	GLU
1	A	316	LEU
1	A	348	ARG
1	A	352	SER
1	B	38	LEU
1	B	44	CYS
1	B	66	GLN
1	B	94	LYS
1	B	100	VAL
1	B	147	ARG

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Mol	Chain	Res	Type
1	B	163	GLN
1	B	179	ARG
1	B	197	VAL
1	B	207	ILE
1	B	221	LEU
1	B	232	LEU
1	B	255	ASP
1	B	258	ILE
1	B	316	LEU
1	B	327	GLU
1	B	362	PHE
1	C	33	ARG
1	C	38	LEU
1	C	63	GLN
1	C	69[A]	HIS
1	C	69[B]	HIS
1	C	70	GLU
1	C	85	ILE
1	C	86	THR
1	C	137	SER
1	C	207	ILE
1	C	213	LEU
1	C	217	ILE
1	C	258	ILE
1	C	291	ARG
1	C	359	LYS
1	C	362	PHE
1	D	38	LEU
1	D	44	CYS
1	D	65	THR
1	D	77	VAL
1	D	84	THR
1	D	111	VAL
1	D	147	ARG
1	D	161	ARG
1	D	205	SER
1	D	214	GLN
1	D	217	ILE
1	D	311	LYS
1	D	316	LEU
1	D	327	GLU
1	D	331	LEU

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Mol	Chain	Res	Type
1	D	345	ILE
1	D	346	THR
1	D	359	LYS
1	D	360	GLU
1	D	362	PHE
1	E	38	LEU
1	E	48	MET
1	E	53	ASP
1	E	73	LEU
1	E	85	ILE
1	E	100	VAL
1	E	147	ARG
1	E	161	ARG
1	E	163	GLN
1	E	171	VAL
1	E	217	ILE
1	E	263	GLN
1	E	290	ILE
1	E	300	SER
1	E	316	LEU
1	E	327	GLU
1	E	345	ILE
1	E	360	GLU
1	E	362	PHE
1	F	38	LEU
1	F	48	MET
1	F	69[A]	HIS
1	F	69[B]	HIS
1	F	77	VAL
1	F	84	THR
1	F	137	SER
1	F	149	ASN
1	F	166	GLU
1	F	179	ARG
1	F	207	ILE
1	F	263	GLN
1	F	304	SER
1	F	317	ILE
1	F	339	THR
1	F	362	PHE
1	G	44	CYS
1	G	63	GLN

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Mol	Chain	Res	Type
1	G	89	ARG
1	G	90	GLU
1	G	109	ASP
1	G	147	ARG
1	G	163	GLN
1	G	214	GLN
1	G	252	LEU
1	G	258	ILE
1	G	263	GLN
1	G	327	GLU
1	G	354	ARG
1	G	360	GLU
1	G	362	PHE
1	H	64	SER
1	H	77	VAL
1	H	81	MET
1	H	137	SER
1	H	182	THR
1	H	205	SER
1	H	230	GLN
1	H	247	GLU
1	H	255	ASP
1	H	291	ARG
1	H	316	LEU
1	H	327	GLU
1	H	339	THR
1	H	348	ARG
1	H	359	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	ASN
1	A	260	GLN
1	A	263	GLN
1	A	355	ASN
1	B	63	GLN
1	B	74	ASN
1	B	149	ASN
1	B	260	GLN
1	B	315	ASN
1	B	328	GLN

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Mol	Chain	Res	Type
1	C	63	GLN
1	C	141	HIS
1	C	230	GLN
1	C	263	GLN
1	D	141	HIS
1	D	149	ASN
1	D	230	GLN
1	D	355	ASN
1	E	125	ASN
1	E	163	GLN
1	E	283	GLN
1	E	307	GLN
1	E	355	ASN
1	F	74	ASN
1	F	154	GLN
1	F	260	GLN
1	F	315	ASN
1	G	83	HIS
1	G	251	HIS
1	G	263	GLN
1	G	283	GLN
1	G	307	GLN
1	G	355	ASN
1	H	149	ASN
1	H	230	GLN
1	H	283	GLN
1	H	315	ASN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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
2	NAD	B	901	-	46,48,48	1.65	5 (10%)	64,73,73	1.72	15 (23%)
2	NAD	G	901	-	46,48,48	1.78	5 (10%)	64,73,73	1.47	10 (15%)
2	NAD	E	901	-	46,48,48	1.80	5 (10%)	64,73,73	1.87	12 (18%)
2	NAD	C	901	-	46,48,48	1.80	6 (13%)	64,73,73	1.79	15 (23%)
2	NAD	F	901	-	46,48,48	1.68	5 (10%)	64,73,73	1.94	15 (23%)
2	NAD	D	901	-	46,48,48	1.82	6 (13%)	64,73,73	1.76	10 (15%)
2	NAD	H	901	-	46,48,48	1.55	6 (13%)	64,73,73	1.65	11 (17%)
2	NAD	A	901	-	46,48,48	1.52	4 (8%)	64,73,73	1.62	14 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	B	901	-	-	12/30/62/62	0/5/5/5
2	NAD	G	901	-	-	7/30/62/62	0/5/5/5
2	NAD	E	901	-	-	10/30/62/62	0/5/5/5
2	NAD	C	901	-	-	6/30/62/62	0/5/5/5
2	NAD	F	901	-	-	4/30/62/62	0/5/5/5
2	NAD	D	901	-	-	3/30/62/62	0/5/5/5
2	NAD	H	901	-	-	7/30/62/62	0/5/5/5
2	NAD	A	901	-	-	7/30/62/62	0/5/5/5

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	901	NAD	O7N-C7N	9.79	1.42	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	901	NAD	O7N-C7N	9.10	1.41	1.24
2	G	901	NAD	O7N-C7N	8.73	1.40	1.24
2	C	901	NAD	O7N-C7N	8.70	1.40	1.24
2	F	901	NAD	O7N-C7N	8.23	1.39	1.24
2	B	901	NAD	O7N-C7N	8.17	1.39	1.24
2	A	901	NAD	O7N-C7N	7.61	1.38	1.24
2	H	901	NAD	O7N-C7N	7.23	1.37	1.24
2	G	901	NAD	C2A-N1A	3.62	1.40	1.33
2	B	901	NAD	C2A-N1A	3.39	1.39	1.33
2	C	901	NAD	C2A-N3A	3.31	1.39	1.33
2	D	901	NAD	C2A-N3A	3.30	1.39	1.33
2	G	901	NAD	C5A-N7A	-3.24	1.33	1.39
2	F	901	NAD	C2A-N3A	3.20	1.39	1.33
2	B	901	NAD	C2A-N3A	3.15	1.39	1.33
2	E	901	NAD	C2A-N3A	3.06	1.39	1.33
2	D	901	NAD	PN-O3	3.00	1.62	1.59
2	E	901	NAD	C5A-N7A	-2.93	1.33	1.39
2	G	901	NAD	C2A-N3A	2.91	1.39	1.33
2	D	901	NAD	C2A-N1A	2.90	1.39	1.33
2	H	901	NAD	C2A-N3A	2.87	1.39	1.33
2	C	901	NAD	C2A-N1A	2.87	1.39	1.33
2	F	901	NAD	C5A-N7A	-2.82	1.33	1.39
2	D	901	NAD	C5A-N7A	-2.72	1.34	1.39
2	F	901	NAD	C2A-N1A	2.71	1.38	1.33
2	B	901	NAD	C5A-N7A	-2.69	1.34	1.39
2	A	901	NAD	C2A-N1A	2.69	1.38	1.33
2	D	901	NAD	C8A-N7A	2.63	1.36	1.31
2	A	901	NAD	C5A-N7A	-2.61	1.34	1.39
2	C	901	NAD	C5A-N7A	-2.56	1.34	1.39
2	C	901	NAD	O4D-C4D	-2.56	1.39	1.45
2	H	901	NAD	C2A-N1A	2.54	1.38	1.33
2	E	901	NAD	C8A-N7A	2.51	1.36	1.31
2	E	901	NAD	C2A-N1A	2.51	1.38	1.33
2	H	901	NAD	O4D-C4D	-2.26	1.40	1.45
2	H	901	NAD	C8A-N7A	2.24	1.36	1.31
2	G	901	NAD	C8A-N7A	2.23	1.36	1.31
2	A	901	NAD	C2A-N3A	2.17	1.37	1.33
2	F	901	NAD	O4D-C4D	-2.17	1.40	1.45
2	H	901	NAD	C5A-N7A	-2.15	1.35	1.39
2	B	901	NAD	C8A-N7A	2.08	1.35	1.31
2	C	901	NAD	C3N-C7N	-2.06	1.47	1.50

All (102) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	901	NAD	C5A-C4A-N3A	-5.51	119.14	126.72
2	F	901	NAD	N3A-C2A-N1A	-5.42	120.38	128.58
2	F	901	NAD	C5A-C4A-N3A	-5.35	119.35	126.72
2	B	901	NAD	C5A-C4A-N3A	-5.21	119.54	126.72
2	D	901	NAD	N3A-C2A-N1A	-5.08	120.90	128.58
2	H	901	NAD	N3A-C2A-N1A	-5.02	120.98	128.58
2	E	901	NAD	N3A-C2A-N1A	-4.97	121.07	128.58
2	C	901	NAD	N3A-C2A-N1A	-4.95	121.09	128.58
2	D	901	NAD	C5A-C4A-N3A	-4.93	119.92	126.72
2	E	901	NAD	C5A-C4A-N3A	-4.87	120.02	126.72
2	B	901	NAD	N3A-C2A-N1A	-4.86	121.22	128.58
2	A	901	NAD	N3A-C2A-N1A	-4.67	121.52	128.58
2	D	901	NAD	N9A-C8A-N7A	-4.66	107.32	113.94
2	G	901	NAD	N3A-C2A-N1A	-4.64	121.56	128.58
2	D	901	NAD	C5A-N7A-C8A	4.58	110.65	103.45
2	E	901	NAD	N9A-C8A-N7A	-4.55	107.49	113.94
2	E	901	NAD	O2A-PA-O3	4.48	119.38	107.27
2	A	901	NAD	C5A-C4A-N3A	-4.40	120.65	126.72
2	H	901	NAD	N9A-C8A-N7A	-4.30	107.84	113.94
2	F	901	NAD	N3A-C4A-N9A	4.24	134.38	127.17
2	E	901	NAD	C5A-N7A-C8A	4.24	110.11	103.45
2	F	901	NAD	N9A-C8A-N7A	-4.23	107.93	113.94
2	H	901	NAD	C5A-C4A-N3A	-4.17	120.98	126.72
2	C	901	NAD	N3A-C4A-N9A	4.16	134.25	127.17
2	C	901	NAD	O4B-C1B-N9A	4.04	115.85	108.09
2	F	901	NAD	C2A-N3A-C4A	3.99	121.56	111.83
2	D	901	NAD	C4A-C5A-N7A	-3.83	106.21	110.58
2	E	901	NAD	C4A-C5A-N7A	-3.82	106.21	110.58
2	B	901	NAD	O2A-PA-O3	3.81	117.57	107.27
2	F	901	NAD	C3N-C7N-N7N	3.81	122.43	117.74
2	A	901	NAD	C5A-N7A-C8A	3.77	109.38	103.45
2	F	901	NAD	C5A-N7A-C8A	3.76	109.37	103.45
2	G	901	NAD	C5A-C4A-N3A	-3.72	121.59	126.72
2	E	901	NAD	O3-PN-O1N	-3.68	99.62	110.70
2	D	901	NAD	O2A-PA-O3	3.67	117.20	107.27
2	H	901	NAD	C5A-N7A-C8A	3.63	109.15	103.45
2	G	901	NAD	C4D-O4D-C1D	-3.59	106.63	109.92
2	C	901	NAD	C2A-N3A-C4A	3.59	120.59	111.83
2	B	901	NAD	N3A-C4A-N9A	3.59	133.27	127.17
2	F	901	NAD	C4D-O4D-C1D	-3.51	106.71	109.92
2	A	901	NAD	N9A-C8A-N7A	-3.50	108.97	113.94
2	E	901	NAD	C2A-N3A-C4A	3.38	120.08	111.83
2	A	901	NAD	C4A-C5A-N7A	-3.34	106.76	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	901	NAD	C5A-C6A-N6A	-3.31	115.09	123.29
2	F	901	NAD	O7N-C7N-C3N	-3.29	115.58	119.60
2	D	901	NAD	C2A-N3A-C4A	3.28	119.85	111.83
2	B	901	NAD	C2A-N3A-C4A	3.28	119.84	111.83
2	G	901	NAD	N3A-C4A-N9A	3.20	132.61	127.17
2	B	901	NAD	N9A-C8A-N7A	-3.16	109.46	113.94
2	H	901	NAD	C2A-N3A-C4A	3.15	119.51	111.83
2	A	901	NAD	C2A-N3A-C4A	3.09	119.38	111.83
2	C	901	NAD	N9A-C8A-N7A	-3.08	109.56	113.94
2	E	901	NAD	C5A-C4A-N9A	3.04	109.12	105.81
2	B	901	NAD	C5A-N7A-C8A	2.95	108.09	103.45
2	B	901	NAD	O4B-C1B-N9A	2.89	113.64	108.09
2	H	901	NAD	C3N-C7N-N7N	2.87	121.27	117.74
2	A	901	NAD	O2A-PA-O3	2.87	115.02	107.27
2	H	901	NAD	C4A-C5A-N7A	-2.85	107.33	110.58
2	A	901	NAD	C2N-C3N-C4N	2.83	121.56	118.26
2	G	901	NAD	N6A-C6A-N1A	2.80	124.62	118.38
2	D	901	NAD	N3A-C4A-N9A	2.75	131.85	127.17
2	F	901	NAD	C4A-N9A-C8A	2.72	108.59	105.74
2	B	901	NAD	O2N-PN-O3	-2.69	100.00	107.27
2	C	901	NAD	C5A-N7A-C8A	2.66	107.63	103.45
2	C	901	NAD	C6A-C5A-C4A	2.64	120.78	117.18
2	B	901	NAD	O7N-C7N-C3N	-2.57	116.46	119.60
2	B	901	NAD	C6A-C5A-C4A	2.56	120.67	117.18
2	F	901	NAD	C6A-C5A-C4A	2.54	120.65	117.18
2	A	901	NAD	C5A-C4A-N9A	2.54	108.58	105.81
2	H	901	NAD	C2N-C3N-C4N	2.53	121.21	118.26
2	C	901	NAD	C5A-C6A-N6A	-2.52	117.04	123.29
2	A	901	NAD	C3N-C7N-N7N	2.48	120.80	117.74
2	D	901	NAD	C6A-C5A-C4A	2.47	120.55	117.18
2	G	901	NAD	N9A-C8A-N7A	-2.47	110.43	113.94
2	F	901	NAD	O4B-C1B-C2B	-2.46	101.34	106.62
2	E	901	NAD	C3N-C7N-N7N	2.42	120.72	117.74
2	F	901	NAD	C4A-C5A-N7A	-2.40	107.84	110.58
2	G	901	NAD	C2A-N3A-C4A	2.38	117.65	111.83
2	C	901	NAD	O5B-PA-O1A	-2.38	99.51	108.94
2	C	901	NAD	O3D-C3D-C2D	-2.34	104.31	111.82
2	A	901	NAD	C5N-C4N-C3N	-2.32	118.08	120.36
2	G	901	NAD	O2N-PN-O1N	2.26	122.95	112.44
2	C	901	NAD	O4B-C4B-C3B	2.22	109.56	105.15
2	H	901	NAD	C4A-N9A-C1B	-2.22	121.44	126.63
2	E	901	NAD	O5D-C5D-C4D	2.19	116.46	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	901	NAD	C5A-C4A-N9A	2.19	108.20	105.81
2	F	901	NAD	O2N-PN-O1N	2.19	122.63	112.44
2	H	901	NAD	C5A-C4A-N9A	2.17	108.18	105.81
2	E	901	NAD	N3A-C4A-N9A	2.17	130.85	127.17
2	C	901	NAD	C5B-C4B-C3B	-2.16	107.43	115.21
2	G	901	NAD	C6A-C5A-C4A	2.16	120.12	117.18
2	H	901	NAD	N3A-C4A-N9A	2.14	130.80	127.17
2	C	901	NAD	O2A-PA-O3	2.13	113.02	107.27
2	A	901	NAD	N3A-C4A-N9A	2.11	130.75	127.17
2	A	901	NAD	C6A-C5A-C4A	2.10	120.05	117.18
2	B	901	NAD	C5A-C6A-N6A	-2.09	118.10	123.29
2	A	901	NAD	O4B-C1B-C2B	-2.08	102.17	106.62
2	B	901	NAD	C2N-C3N-C4N	2.08	120.67	118.26
2	B	901	NAD	O2N-PN-O1N	2.07	122.06	112.44
2	F	901	NAD	C5A-C6A-N6A	-2.07	118.17	123.29
2	B	901	NAD	O3D-C3D-C2D	-2.03	105.30	111.82
2	C	901	NAD	C2N-C3N-C4N	2.01	120.59	118.26

There are no chirality outliers.

All (56) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	NAD	C5D-O5D-PN-O1N
2	A	901	NAD	O4D-C1D-N1N-C6N
2	B	901	NAD	C5D-O5D-PN-O1N
2	B	901	NAD	O4D-C1D-N1N-C6N
2	C	901	NAD	O4D-C1D-N1N-C2N
2	C	901	NAD	O4D-C1D-N1N-C6N
2	C	901	NAD	C2D-C1D-N1N-C2N
2	D	901	NAD	O4D-C1D-N1N-C6N
2	E	901	NAD	C5B-O5B-PA-O1A
2	E	901	NAD	C5B-O5B-PA-O2A
2	E	901	NAD	O4D-C1D-N1N-C2N
2	E	901	NAD	O4D-C1D-N1N-C6N
2	E	901	NAD	C2D-C1D-N1N-C2N
2	E	901	NAD	C2D-C1D-N1N-C6N
2	F	901	NAD	O4D-C1D-N1N-C2N
2	F	901	NAD	O4D-C1D-N1N-C6N
2	G	901	NAD	O4D-C1D-N1N-C6N
2	H	901	NAD	O4D-C1D-N1N-C6N
2	B	901	NAD	C2N-C3N-C7N-O7N
2	E	901	NAD	O4B-C4B-C5B-O5B

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Mol	Chain	Res	Type	Atoms
2	B	901	NAD	C4N-C3N-C7N-O7N
2	B	901	NAD	O4B-C4B-C5B-O5B
2	G	901	NAD	O4B-C4B-C5B-O5B
2	B	901	NAD	C4N-C3N-C7N-N7N
2	B	901	NAD	C3B-C4B-C5B-O5B
2	C	901	NAD	O4B-C4B-C5B-O5B
2	G	901	NAD	C3B-C4B-C5B-O5B
2	B	901	NAD	C2N-C3N-C7N-N7N
2	C	901	NAD	C3B-C4B-C5B-O5B
2	E	901	NAD	C3B-C4B-C5B-O5B
2	G	901	NAD	O4D-C4D-C5D-O5D
2	A	901	NAD	C5B-O5B-PA-O1A
2	A	901	NAD	C5D-O5D-PN-O3
2	B	901	NAD	C5D-O5D-PN-O3
2	B	901	NAD	C5D-O5D-PN-O2N
2	E	901	NAD	C5B-O5B-PA-O3
2	G	901	NAD	C5D-O5D-PN-O1N
2	H	901	NAD	C5D-O5D-PN-O1N
2	H	901	NAD	PN-O3-PA-O1A
2	H	901	NAD	PN-O3-PA-O2A
2	C	901	NAD	C2D-C1D-N1N-C6N
2	H	901	NAD	O4B-C4B-C5B-O5B
2	A	901	NAD	O4D-C1D-N1N-C2N
2	B	901	NAD	O4D-C1D-N1N-C2N
2	D	901	NAD	O4D-C1D-N1N-C2N
2	G	901	NAD	O4D-C1D-N1N-C2N
2	H	901	NAD	O4D-C1D-N1N-C2N
2	A	901	NAD	PN-O3-PA-O1A
2	B	901	NAD	C2B-C1B-N9A-C8A
2	A	901	NAD	PN-O3-PA-O2A
2	E	901	NAD	PN-O3-PA-O2A
2	D	901	NAD	O4B-C4B-C5B-O5B
2	F	901	NAD	O4B-C4B-C5B-O5B
2	F	901	NAD	C2B-C1B-N9A-C8A
2	H	901	NAD	C2B-C1B-N9A-C8A
2	G	901	NAD	PA-O3-PN-O2N

There are no ring outliers.

4 monomers are involved in 5 short contacts:

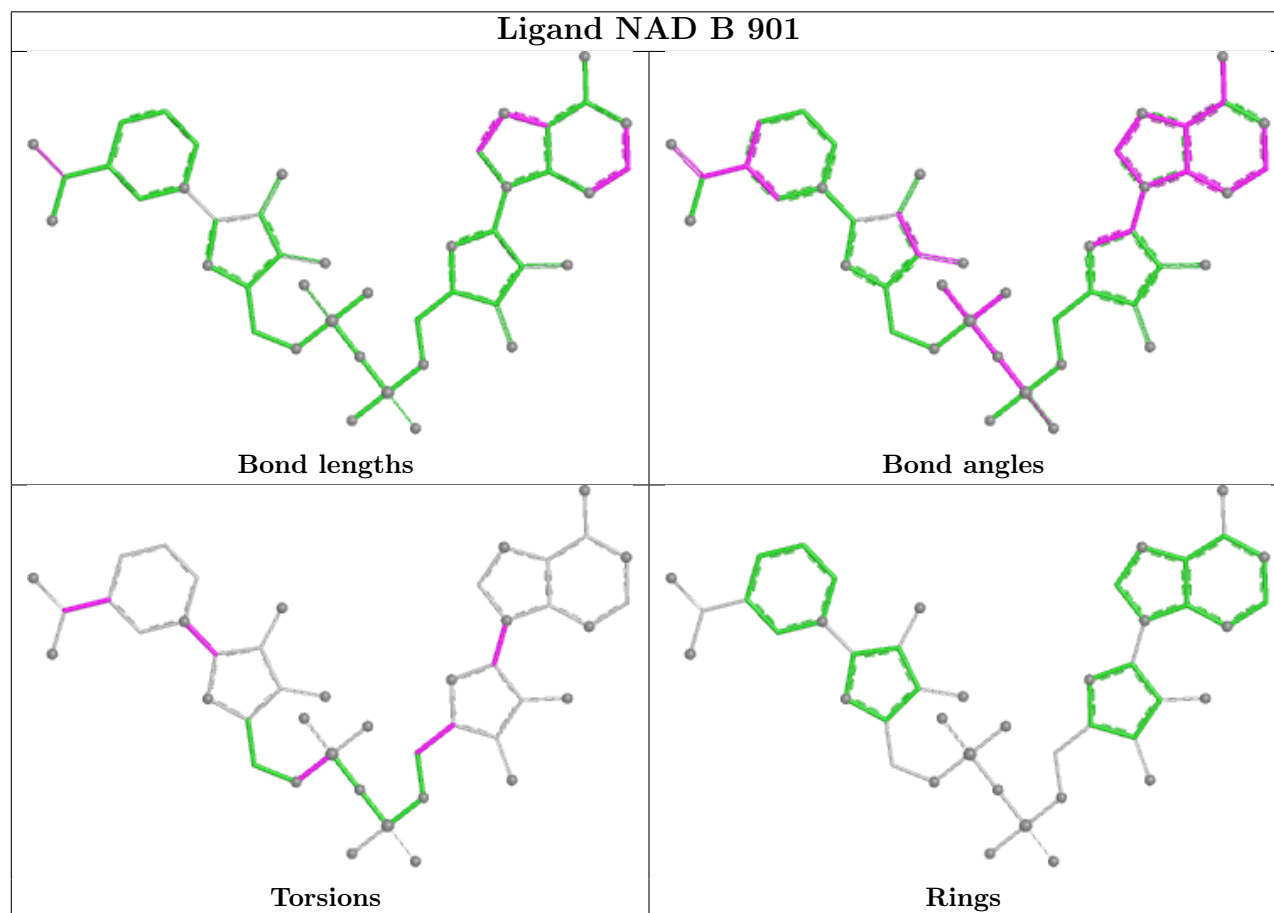
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	NAD	1	0

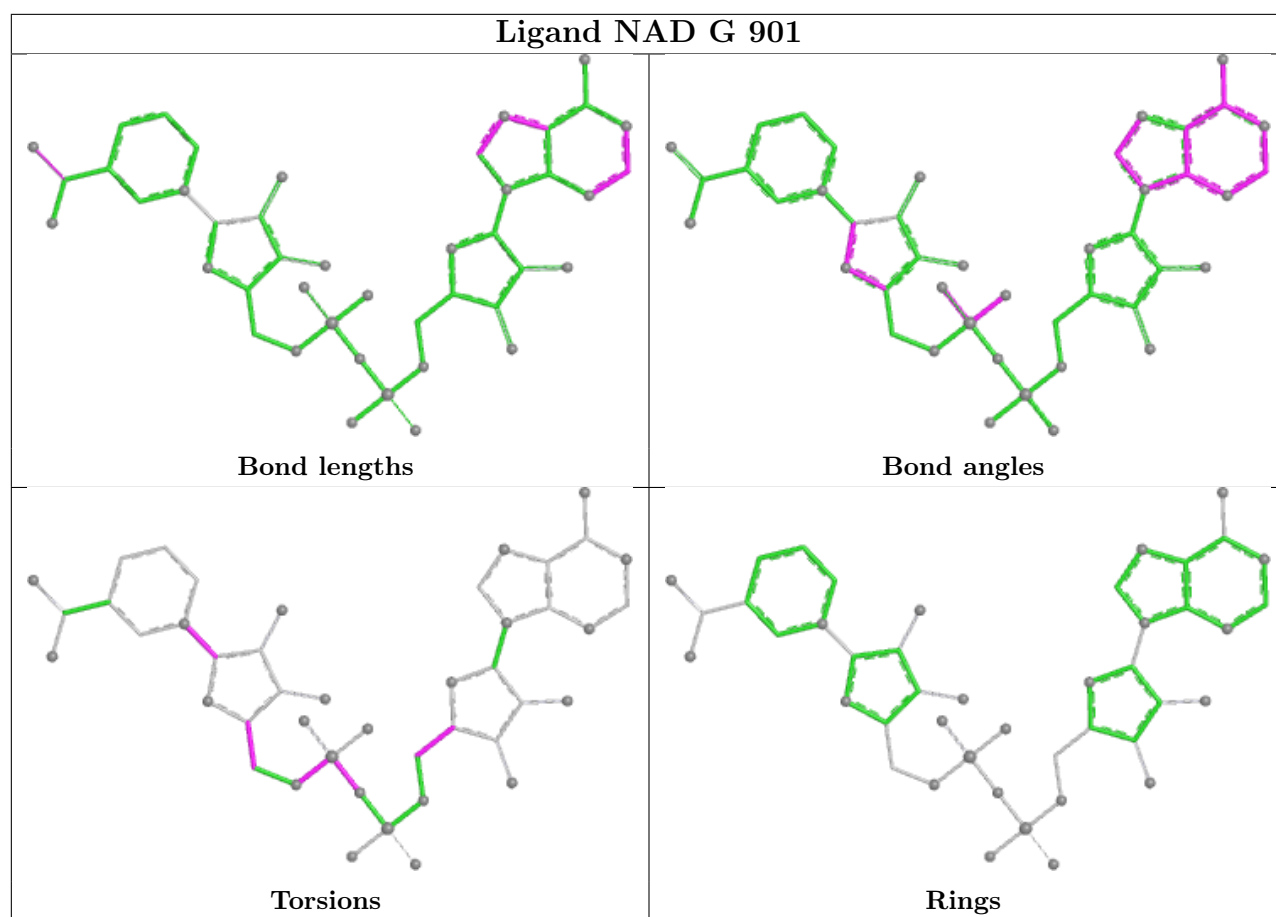
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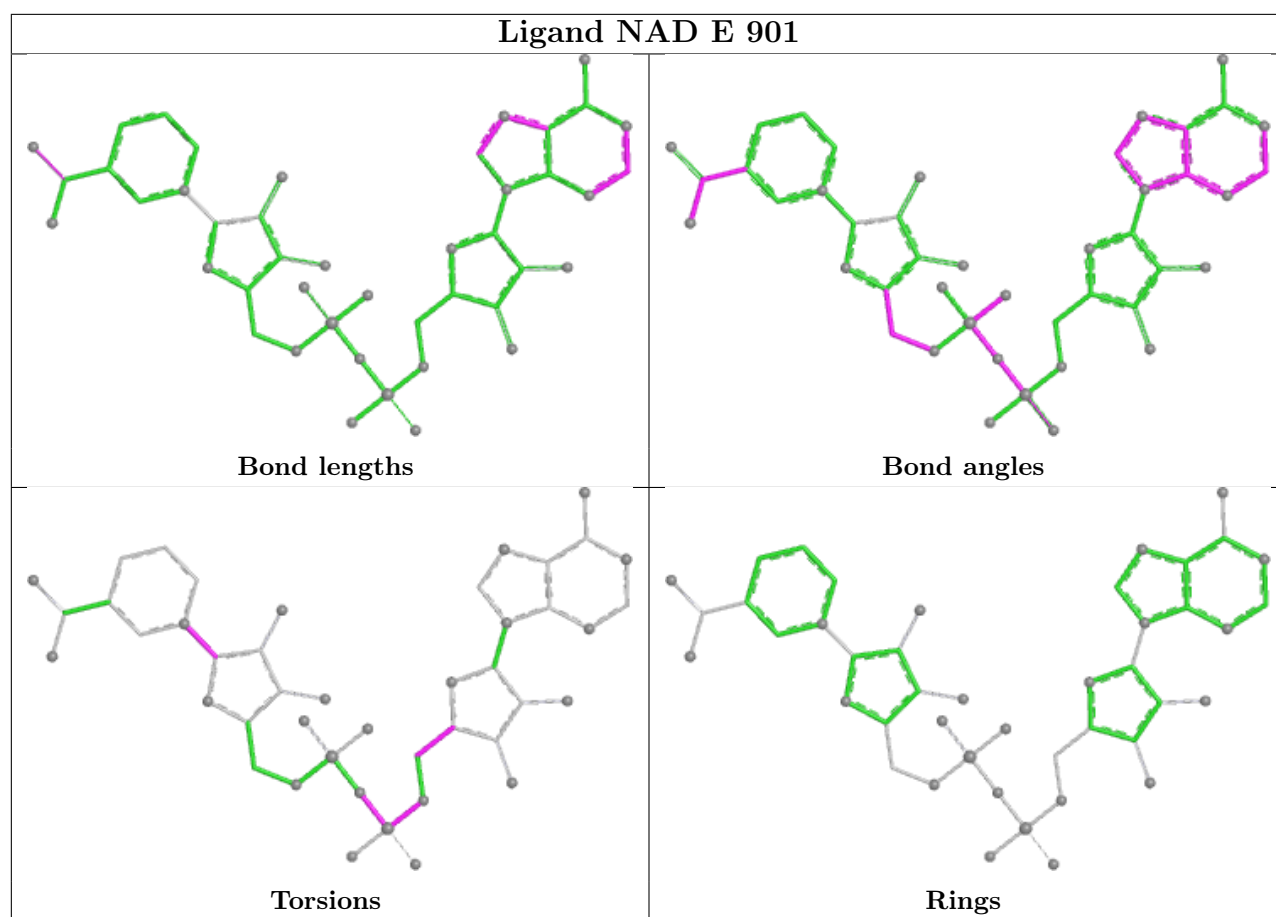
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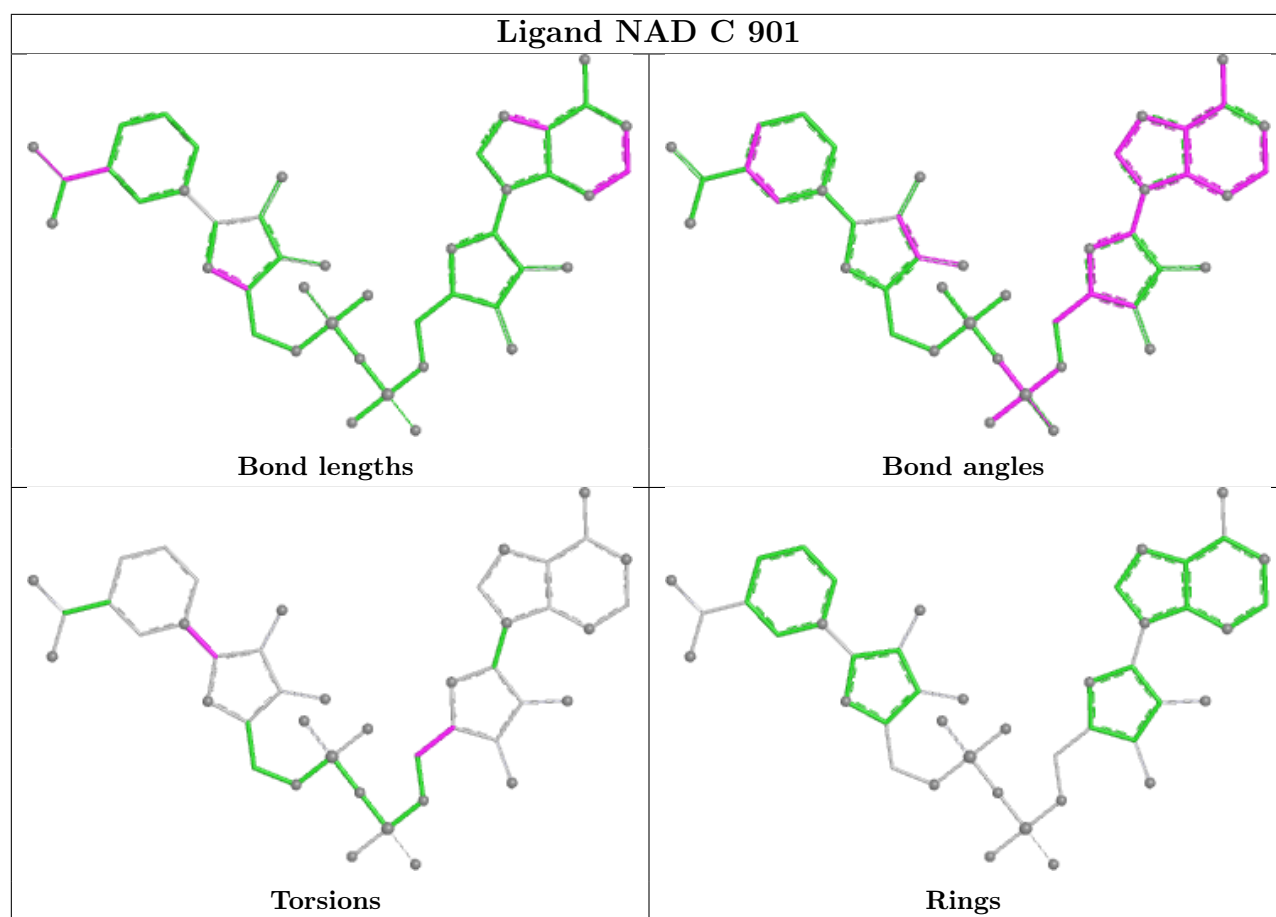
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	901	NAD	1	0
2	F	901	NAD	1	0
2	D	901	NAD	2	0

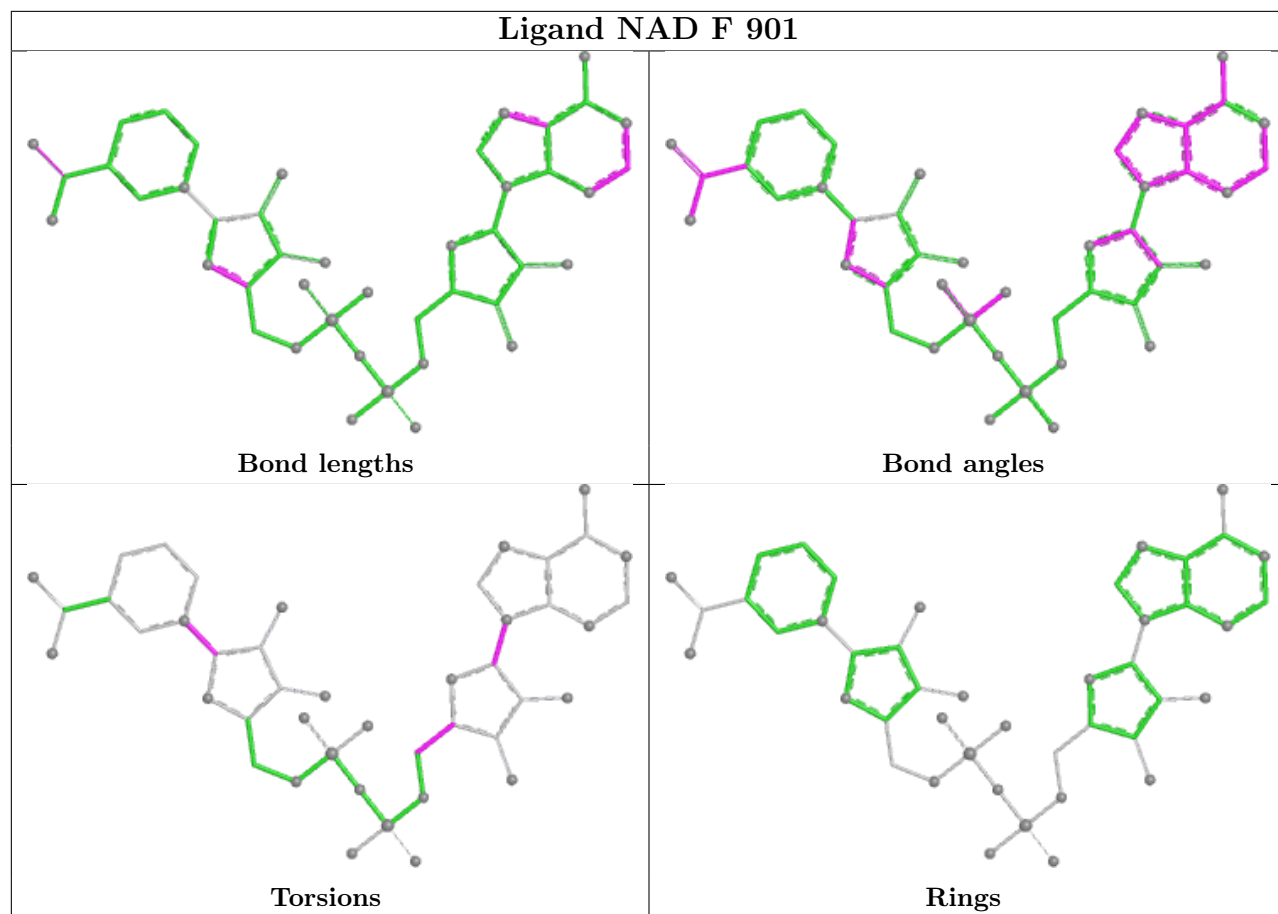
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

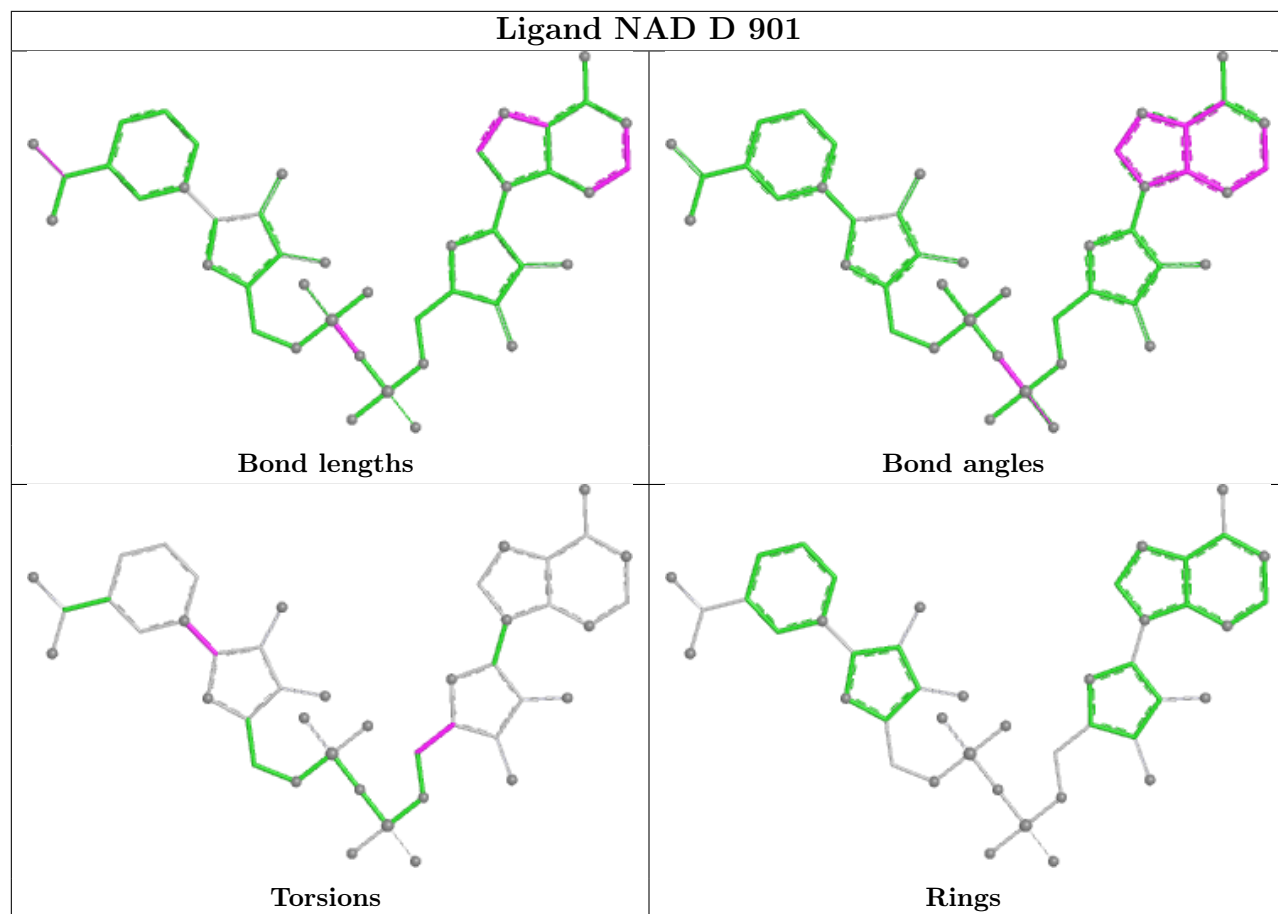


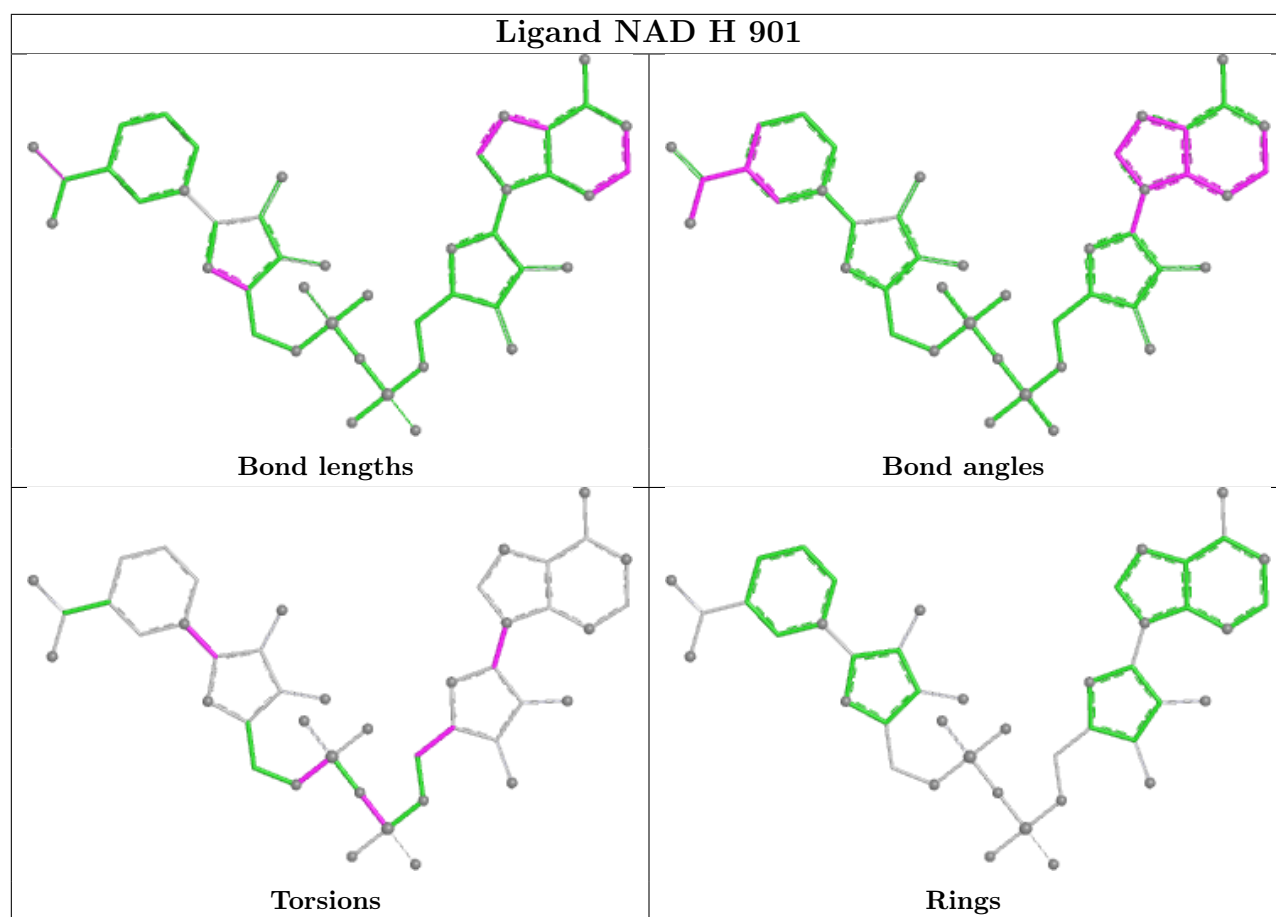


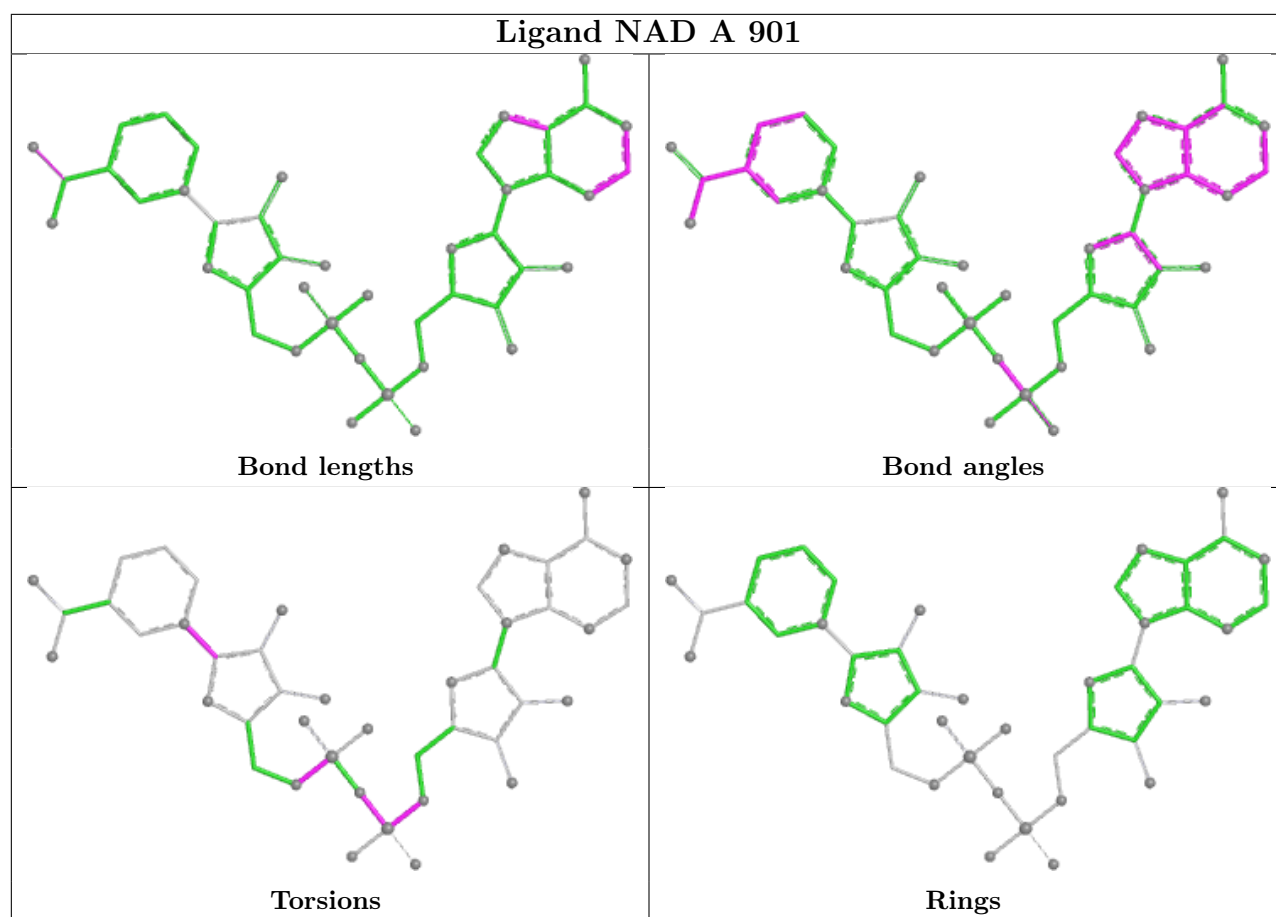












5.7 Other polymers [i](#)

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

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	330/336 (98%)	0.32	4 (1%) 76 68	34, 49, 52, 57	1 (0%)
1	B	330/336 (98%)	0.66	19 (5%) 29 22	46, 49, 52, 57	0
1	C	330/336 (98%)	0.20	3 (0%) 81 74	31, 49, 52, 56	1 (0%)
1	D	330/336 (98%)	1.10	43 (13%) 7 6	46, 49, 51, 56	0
1	E	330/336 (98%)	0.90	24 (7%) 21 15	47, 49, 51, 54	0
1	F	330/336 (98%)	0.56	7 (2%) 63 54	30, 49, 52, 56	2 (0%)
1	G	330/336 (98%)	0.81	16 (4%) 35 28	24, 49, 51, 56	3 (0%)
1	H	330/336 (98%)	0.34	0 100 100	33, 49, 51, 56	1 (0%)
All	All	2640/2688 (98%)	0.61	116 (4%) 39 31	24, 49, 52, 57	8 (0%)

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	79	ALA	5.1
1	E	77	VAL	4.1
1	E	300	SER	3.8
1	G	33	ARG	3.7
1	D	79	ALA	3.7
1	E	362	PHE	3.6
1	E	274	GLY	3.5
1	D	274	GLY	3.4
1	B	165	VAL	3.3
1	G	99	ARG	3.2
1	D	166	GLU	3.0
1	D	177	ARG	2.9
1	D	168	ILE	2.9
1	D	220	SER	2.9
1	D	362	PHE	2.9
1	E	35	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	G	80	MET	2.9
1	D	300	SER	2.9
1	B	178	ILE	2.9
1	D	37	ALA	2.8
1	D	221	LEU	2.8
1	D	222	GLY	2.8
1	E	36	VAL	2.8
1	D	180	GLY	2.8
1	E	165	VAL	2.8
1	G	100	VAL	2.8
1	C	48	MET	2.8
1	E	41	GLY	2.8
1	D	182	THR	2.7
1	G	273[A]	GLY	2.7
1	D	165	VAL	2.7
1	B	34	PRO	2.6
1	D	40	ASP	2.6
1	G	314	PRO	2.6
1	D	224	GLN	2.6
1	E	220	SER	2.5
1	D	174	GLY	2.5
1	B	57	VAL	2.5
1	D	199	ALA	2.5
1	B	358	ASN	2.5
1	G	72	VAL	2.5
1	C	58	ALA	2.5
1	B	200	LYS	2.5
1	D	206	VAL	2.4
1	E	78	GLY	2.4
1	B	53	ASP	2.4
1	B	223	VAL	2.4
1	D	107	GLY	2.4
1	E	84	THR	2.4
1	D	36	VAL	2.4
1	D	162	VAL	2.4
1	D	346	THR	2.4
1	B	38	LEU	2.4
1	D	169	ARG	2.3
1	G	165	VAL	2.3
1	B	196	ALA	2.3
1	D	58	ALA	2.3
1	A	63	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	38	LEU	2.3
1	F	171	VAL	2.3
1	D	203	GLY	2.3
1	A	255	ASP	2.3
1	G	63	GLN	2.3
1	B	36	VAL	2.3
1	E	222	GLY	2.3
1	G	184	GLY	2.3
1	G	361	PHE	2.3
1	D	250	HIS	2.3
1	E	33	ARG	2.3
1	G	56	THR	2.3
1	G	97	ALA	2.2
1	D	226	VAL	2.2
1	E	273	GLY	2.2
1	D	60	CYS	2.2
1	F	160	THR	2.2
1	B	107	GLY	2.2
1	B	79	ALA	2.2
1	B	152	LEU	2.2
1	B	199	ALA	2.2
1	D	327	GLU	2.2
1	G	40	ASP	2.2
1	D	156	LEU	2.2
1	E	72	VAL	2.2
1	B	56	THR	2.2
1	D	78	GLY	2.2
1	A	362	PHE	2.2
1	D	183	LEU	2.1
1	F	266	PHE	2.1
1	E	270	ALA	2.1
1	D	163	GLN	2.1
1	A	250	HIS	2.1
1	B	37	ALA	2.1
1	E	76	ALA	2.1
1	C	214	GLN	2.1
1	D	171	VAL	2.1
1	E	123	VAL	2.1
1	D	160	THR	2.1
1	E	124	CYS	2.1
1	G	66	GLN	2.1
1	E	169	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	108	TYR	2.1
1	E	200	LYS	2.0
1	E	162	VAL	2.0
1	D	35	LEU	2.0
1	D	145	LEU	2.0
1	E	221	LEU	2.0
1	F	274	GLY	2.0
1	D	196	ALA	2.0
1	D	63	GLN	2.0
1	D	64	SER	2.0
1	F	66	GLN	2.0
1	F	173	SER	2.0
1	B	98	LEU	2.0
1	D	201	ALA	2.0
1	F	43	ASP	2.0
1	B	100	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 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.

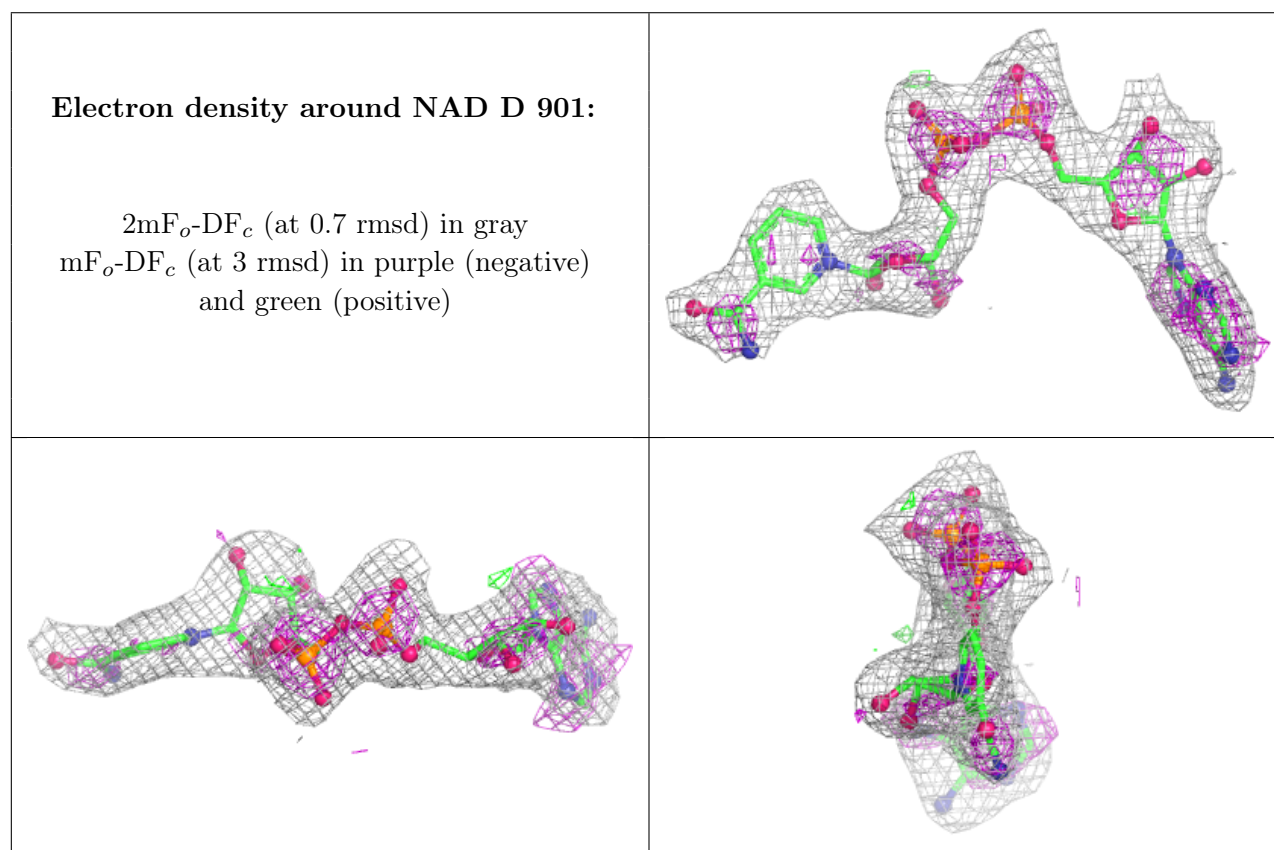
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAD	D	901	44/44	0.91	0.11	35,40,48,49	0
2	NAD	E	901	44/44	0.91	0.11	37,41,56,59	0
2	NAD	G	901	44/44	0.91	0.12	35,41,46,50	0
2	NAD	F	901	44/44	0.92	0.11	27,34,38,41	0
2	NAD	A	901	44/44	0.94	0.11	25,33,34,40	0
2	NAD	B	901	44/44	0.94	0.11	24,35,42,46	0
2	NAD	H	901	44/44	0.94	0.11	30,35,38,40	0

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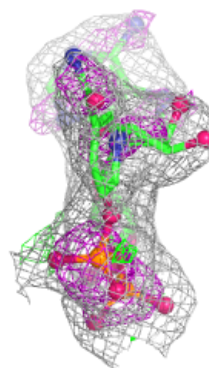
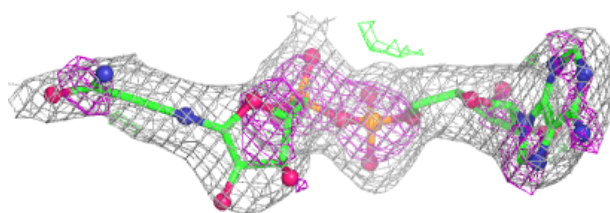
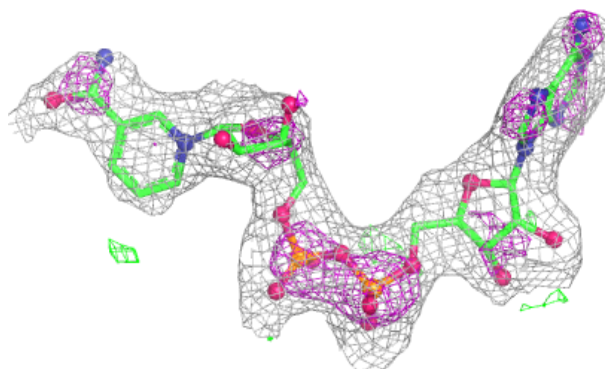
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAD	C	901	44/44	0.95	0.09	20,27,31,33	0

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.

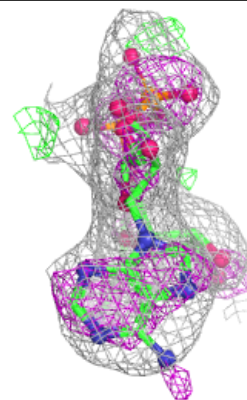
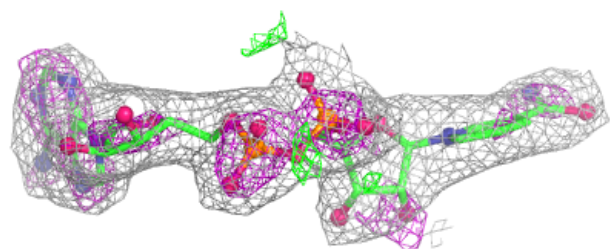
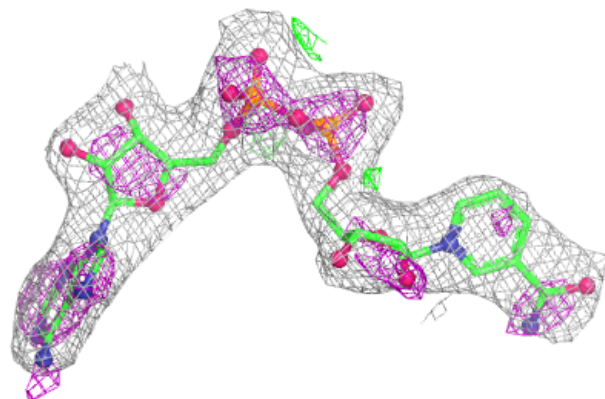


Electron density around NAD E 901:

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

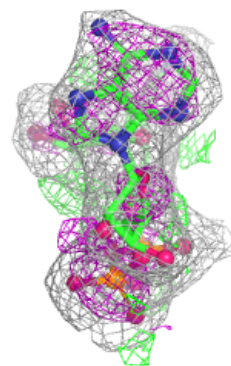
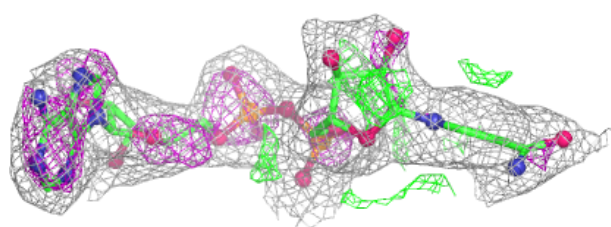
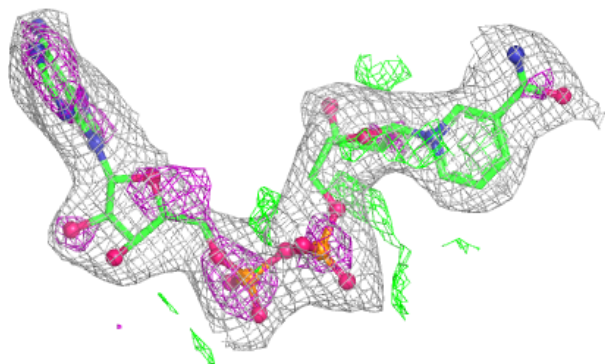
**Electron density around NAD G 901:**

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

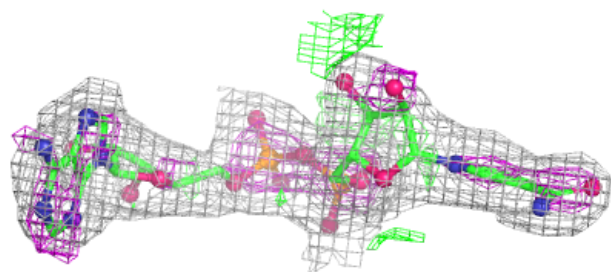
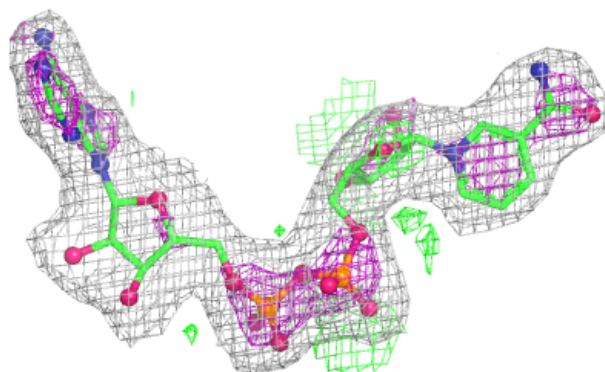


Electron density around NAD F 901:

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

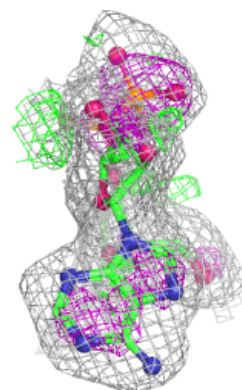
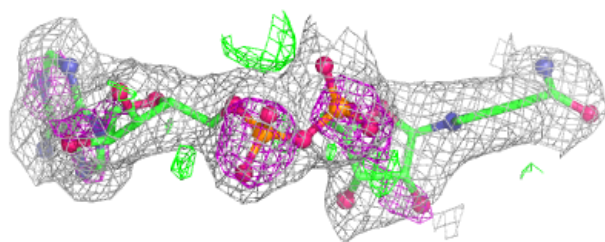
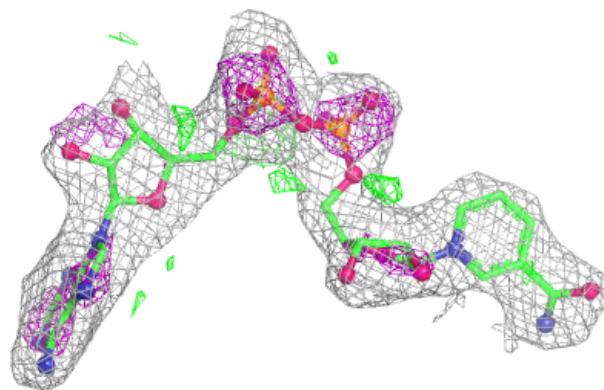
**Electron density around NAD A 901:**

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

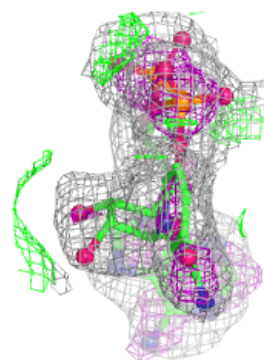
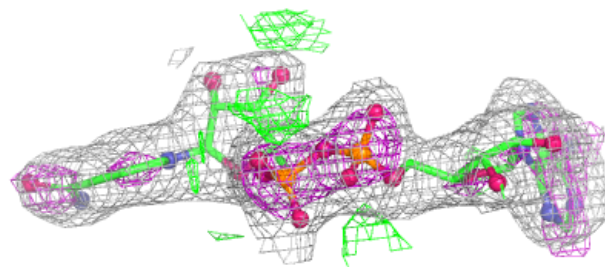
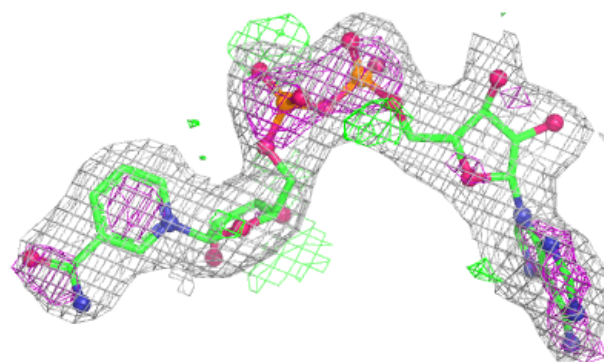


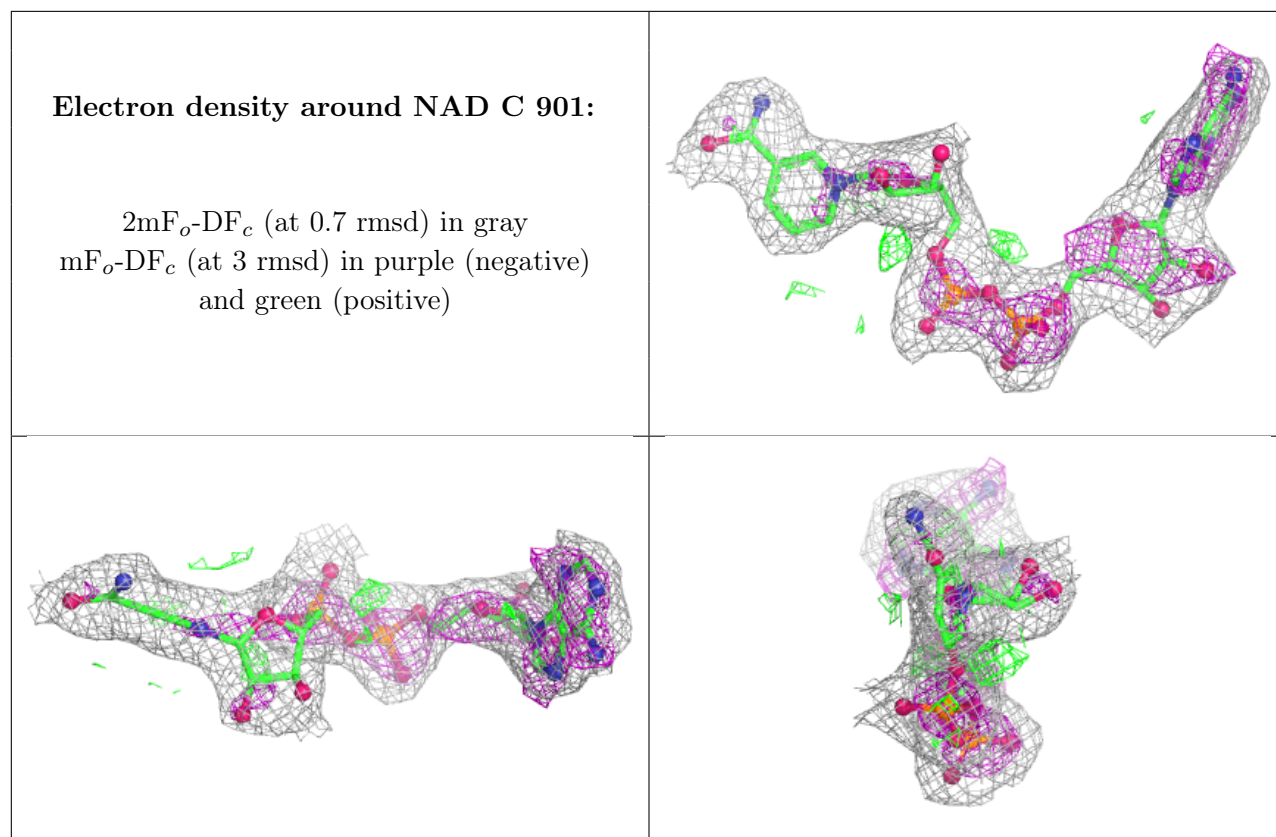
Electron density around NAD B 901:

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

**Electron density around NAD H 901:**

$2mF_o-DF_c$ (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.