



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:33 AM UTC

PDB ID : 6VR6 / pdb_00006vr6
Title : Structure of ALDH9A1 complexed with NAD⁺ in space group P1
Authors : Wyatt, J.W.; Tanner, J.J.
Deposited on : 2020-02-06
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

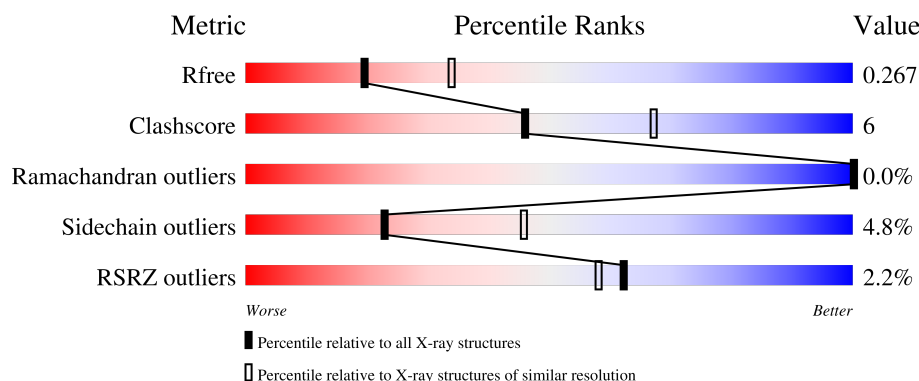
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	493	2% 82% 17% .
1	B	493	2% 82% 16% .
1	C	493	3% 83% 16% .
1	D	493	2% 83% 16% .
1	E	493	2% 83% 17% .

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Mol	Chain	Length	Quality of chain
1	F	493	2% 83% 16%
1	G	493	2% 89% 10%
1	H	493	2% 85% 13%

2 Entry composition

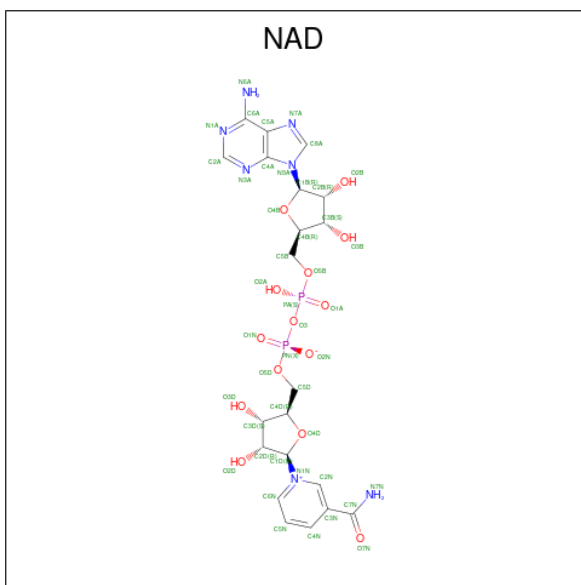
There are 2 unique types of molecules in this entry. The entry contains 29310 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 4-trimethylaminobutyraldehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	492	Total	C	N	O	S	0	0	0
			3670	2327	632	681	30			
1	B	492	Total	C	N	O	S	0	0	0
			3650	2311	620	689	30			
1	C	492	Total	C	N	O	S	0	0	0
			3646	2311	619	686	30			
1	D	493	Total	C	N	O	S	0	0	0
			3646	2309	621	686	30			
1	E	493	Total	C	N	O	S	0	0	0
			3608	2285	616	677	30			
1	F	492	Total	C	N	O	S	0	0	0
			3626	2293	614	689	30			
1	G	493	Total	C	N	O	S	0	0	0
			3633	2302	616	685	30			
1	H	492	Total	C	N	O	S	0	0	0
			3598	2271	614	684	29			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).

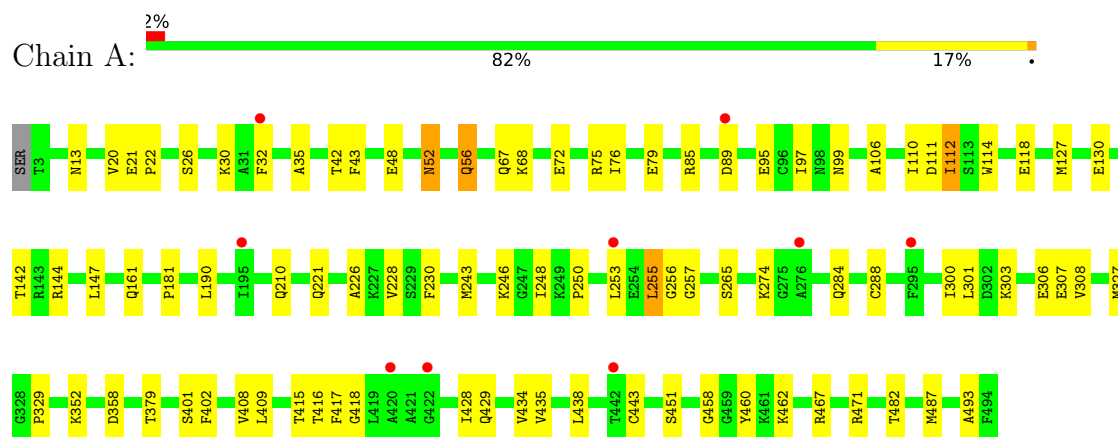


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	B	1	Total 27	C 10	N 5	O 10	P 2	0	0
2	C	1	Total 27	C 10	N 5	O 10	P 2	0	0
2	D	1	Total 27	C 10	N 5	O 10	P 2	0	0
2	E	1	Total 27	C 10	N 5	O 10	P 2	0	0
2	F	1	Total 27	C 10	N 5	O 10	P 2	0	0
2	G	1	Total 27	C 10	N 5	O 10	P 2	0	0
2	H	1	Total 27	C 10	N 5	O 10	P 2	0	0

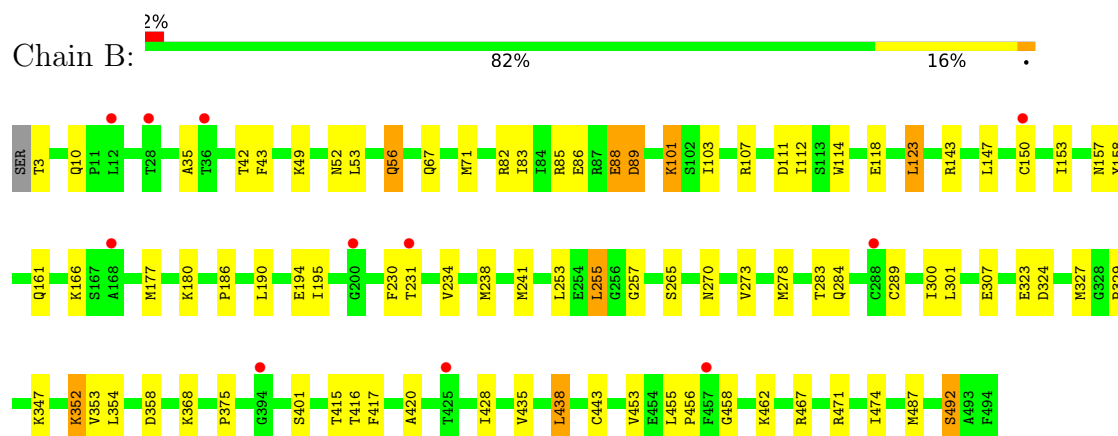
3 Residue-property plots [i](#)

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.

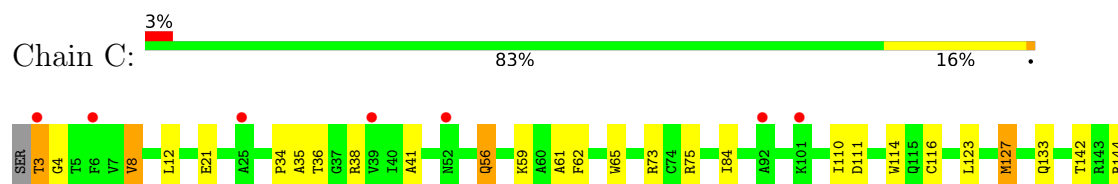
- Molecule 1: 4-trimethylaminobutyraldehyde dehydrogenase

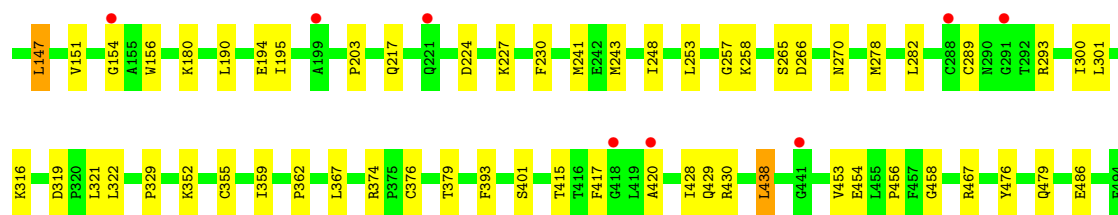


- Molecule 1: 4-trimethylaminobutyraldehyde dehydrogenase

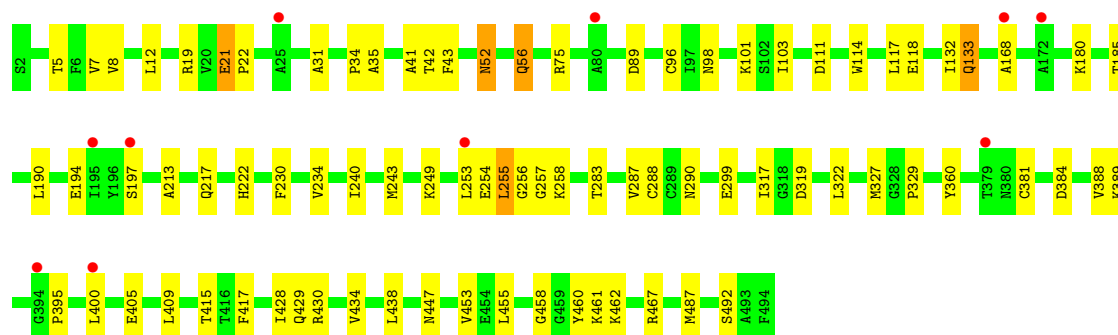
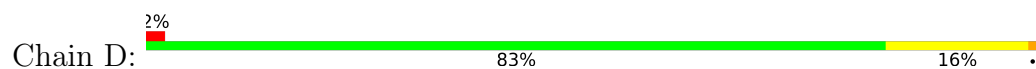


- Molecule 1: 4-trimethylaminobutyraldehyde dehydrogenase

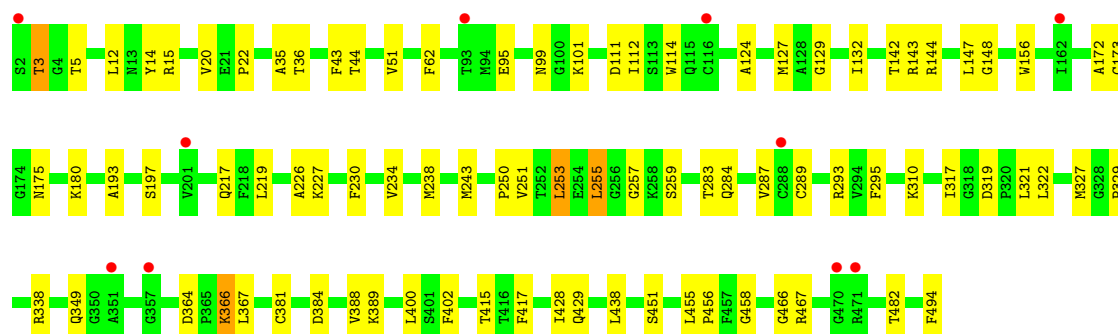
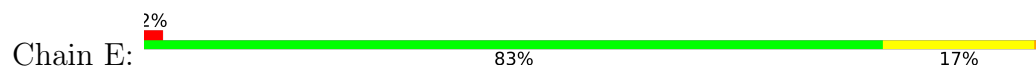




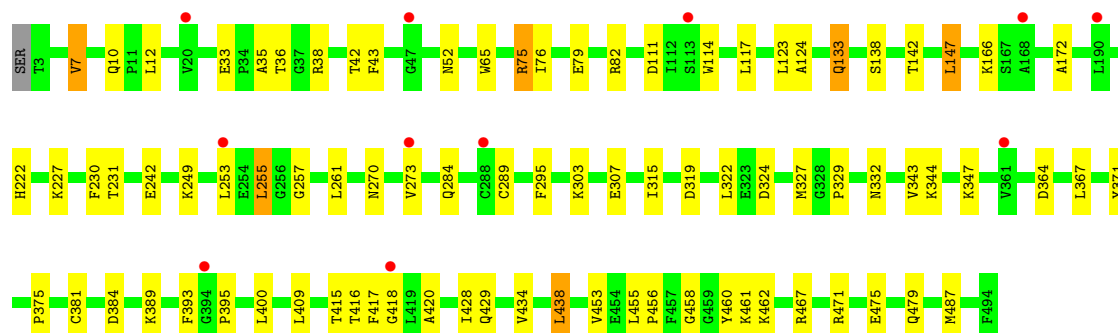
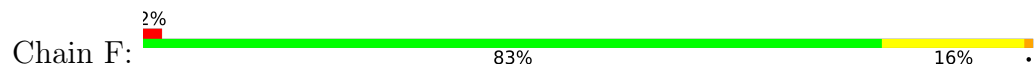
• Molecule 1: 4-trimethylaminobutyraldehyde dehydrogenase



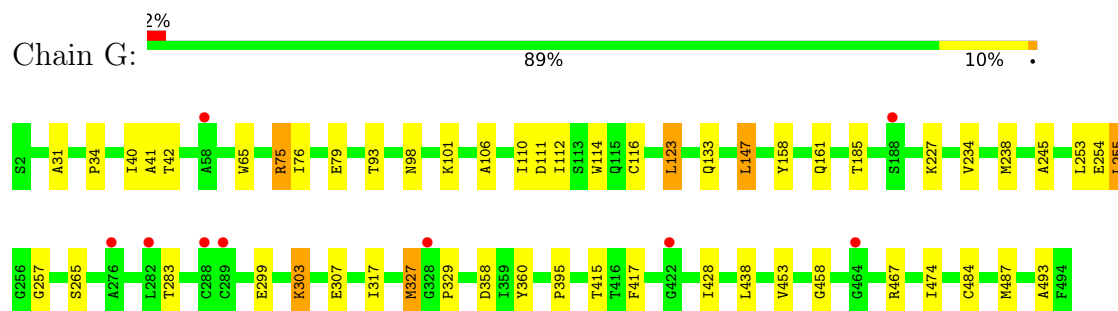
• Molecule 1: 4-trimethylaminobutyraldehyde dehydrogenase



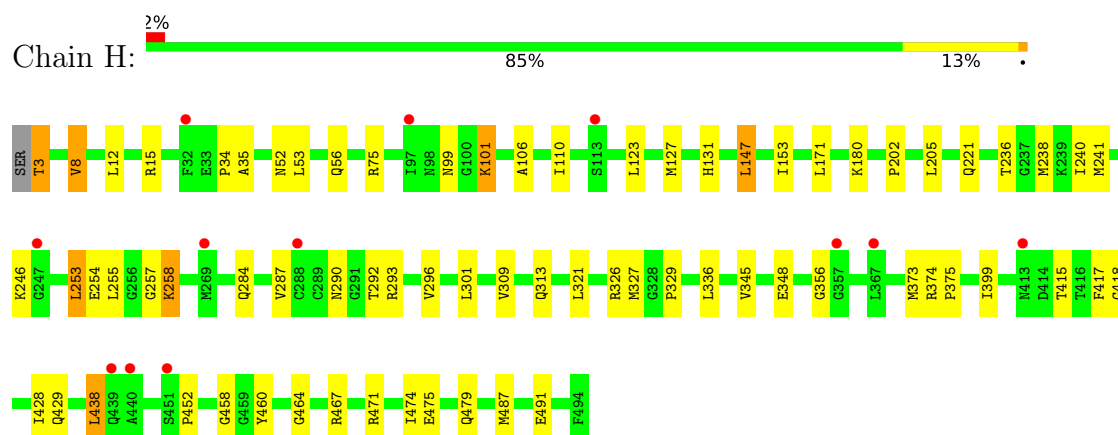
• Molecule 1: 4-trimethylaminobutyraldehyde dehydrogenase



- Molecule 1: 4-trimethylaminobutyraldehyde dehydrogenase



- Molecule 1: 4-trimethylaminobutyraldehyde dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	82.78Å 90.30Å 145.24Å 89.37° 84.04° 73.87°	Depositor
Resolution (Å)	79.09 – 2.50 79.09 – 2.50	Depositor EDS
% Data completeness (in resolution range)	76.7 (79.09-2.50) 76.7 (79.09-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.14	Depositor
R, R_{free}	0.213 , 0.269 0.213 , 0.267	Depositor DCC
R_{free} test set	2135 reflections (1.54%)	wwPDB-VP
Wilson B-factor (Å ²)	36.3	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 30.3	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	0.92	EDS
Total number of atoms	29310	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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	0.12	0/3743	0.35	0/5078
1	B	0.11	0/3723	0.34	0/5052
1	C	0.11	0/3720	0.36	0/5052
1	D	0.12	0/3720	0.33	0/5054
1	E	0.12	0/3682	0.35	0/5003
1	F	0.12	0/3699	0.34	0/5026
1	G	0.12	0/3707	0.34	0/5037
1	H	0.12	0/3671	0.35	0/4994
All	All	0.12	0/29665	0.34	0/40296

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3670	0	3603	50	0
1	B	3650	0	3541	53	0
1	C	3646	0	3522	55	0
1	D	3646	0	3525	46	0
1	E	3608	0	3438	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3626	0	3471	50	0
1	G	3633	0	3492	29	0
1	H	3598	0	3406	41	0
2	A	44	0	26	0	0
2	B	27	0	12	0	0
2	C	27	0	12	3	0
2	D	27	0	12	2	0
2	E	27	0	12	1	0
2	F	27	0	12	0	0
2	G	27	0	12	0	0
2	H	27	0	12	0	0
All	All	29310	0	28108	333	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (333) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:GLY:HA2	1:A:288:CYS:HB2	1.66	0.75
1:F:416:THR:HB	1:F:462:LYS:HD2	1.71	0.73
1:D:222:HIS:O	1:D:249:LYS:NZ	2.21	0.72
1:E:15:ARG:HG2	1:E:20:VAL:HG11	1.71	0.72
1:F:222:HIS:O	1:F:249:LYS:NZ	2.23	0.71
1:B:347:LYS:HE2	1:B:353:VAL:HG21	1.72	0.71
1:G:327:MET:HE1	1:G:395:PRO:HG3	1.74	0.69
1:G:238:MET:HE3	1:H:246:LYS:HA	1.75	0.67
1:A:30:LYS:HG2	1:A:42:THR:HG22	1.76	0.67
1:B:143:ARG:NH2	1:D:133:GLN:OE1	2.26	0.67
1:D:256:GLY:HA2	1:D:288:CYS:HB2	1.77	0.67
1:C:359:ILE:O	1:C:374:ARG:NH1	2.28	0.67
1:F:166:LYS:NZ	1:F:231:THR:OG1	2.29	0.66
1:H:3:THR:HB	1:H:321:LEU:HD12	1.78	0.66
1:H:327:MET:HE1	1:H:375:PRO:HB3	1.76	0.66
1:F:65:TRP:HZ3	1:F:76:ILE:HD12	1.59	0.66
1:F:303:LYS:NZ	1:F:307:GLU:OE2	2.26	0.64
1:C:59:LYS:HA	1:C:62:PHE:HB3	1.78	0.64
1:D:52:ASN:ND2	1:D:56:GLN:OE1	2.31	0.64
1:C:116:CYS:HA	1:C:453:VAL:HG21	1.79	0.63
1:A:428:ILE:HA	1:C:428:ILE:HB	1.81	0.63
1:A:284:GLN:HG3	1:A:327:MET:HG3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:147:LEU:HD23	1:E:227:LYS:HB2	1.81	0.62
1:F:75:ARG:NH1	1:F:79:GLU:OE2	2.32	0.62
1:C:3:THR:HB	1:C:321:LEU:HD12	1.80	0.62
1:C:319:ASP:HB3	1:C:322:LEU:HG	1.82	0.61
1:B:273:VAL:HG11	1:B:307:GLU:HG3	1.82	0.61
1:B:103:ILE:HG13	1:B:107:ARG:HE	1.65	0.60
1:D:117:LEU:HD12	1:D:168:ALA:HB2	1.84	0.60
1:G:116:CYS:HA	1:G:453:VAL:HG11	1.83	0.60
1:E:384:ASP:HA	1:E:389:LYS:HE3	1.84	0.59
1:D:217:GLN:HG2	1:D:243:MET:SD	2.43	0.59
1:B:301:LEU:HD22	1:B:401:SER:HB2	1.83	0.59
1:E:456:PRO:HB2	1:E:467:ARG:HD2	1.84	0.58
1:F:384:ASP:HA	1:F:389:LYS:HE3	1.83	0.58
1:C:3:THR:O	1:C:3:THR:OG1	2.22	0.57
1:E:284:GLN:HA	1:E:327:MET:HE2	1.86	0.57
1:D:319:ASP:HB3	1:D:322:LEU:HG	1.87	0.56
1:H:147:LEU:HD12	1:H:479:GLN:NE2	2.22	0.55
1:A:246:LYS:HA	1:B:238:MET:HE3	1.87	0.55
1:B:230:PHE:HB3	1:B:253:LEU:HD23	1.89	0.55
1:C:147:LEU:HD12	1:C:479:GLN:NE2	2.21	0.55
1:C:270:ASN:ND2	1:F:270:ASN:OD1	2.35	0.55
1:G:31:ALA:HB3	1:G:41:ALA:HB3	1.89	0.55
1:E:428:ILE:HA	1:H:428:ILE:HB	1.88	0.55
1:A:274:LYS:HD2	1:B:492:SER:HB3	1.89	0.54
1:A:181:PRO:HG2	1:A:210:GLN:HE22	1.71	0.54
1:H:8:VAL:HG21	1:H:12:LEU:HD11	1.89	0.54
1:B:101:LYS:NZ	1:B:157:ASN:O	2.30	0.54
1:A:482:THR:OG1	1:B:456:PRO:O	2.17	0.53
1:D:180:LYS:HZ3	2:D:501:NAD:H1B	1.73	0.53
1:F:364:ASP:HB3	1:F:367:LEU:HD13	1.90	0.53
1:G:34:PRO:HB2	1:G:329:PRO:HG2	1.90	0.53
1:E:284:GLN:HG3	1:E:327:MET:HG3	1.91	0.53
1:A:111:ASP:HA	1:A:114:TRP:NE1	2.24	0.53
1:F:458:GLY:HA3	1:F:467:ARG:HD3	1.89	0.53
1:C:352:LYS:HB3	1:C:379:THR:HG22	1.90	0.53
1:F:35:ALA:HA	1:F:329:PRO:HG3	1.91	0.53
1:G:253:LEU:HB3	1:G:255:LEU:HD13	1.90	0.53
1:H:236:THR:O	1:H:240:ILE:HD12	2.09	0.52
1:F:12:LEU:HD12	1:F:43:PHE:HB3	1.90	0.52
1:E:257:GLY:HA2	1:E:417:PHE:CD1	2.45	0.52
1:B:166:LYS:NZ	1:B:231:THR:OG1	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:458:GLY:HA3	1:H:467:ARG:HD3	1.92	0.52
1:H:202:PRO:HD2	1:H:205:LEU:HD22	1.91	0.52
1:A:409:LEU:HD21	1:A:434:VAL:HG13	1.92	0.52
1:C:248:ILE:HG13	1:D:462:LYS:HG3	1.92	0.51
1:H:34:PRO:HB2	1:H:329:PRO:HG2	1.92	0.51
1:C:34:PRO:HB2	1:C:329:PRO:HG2	1.93	0.51
1:A:458:GLY:HA3	1:A:467:ARG:HD3	1.92	0.51
1:C:111:ASP:HA	1:C:114:TRP:NE1	2.26	0.51
1:A:226:ALA:O	1:A:250:PRO:HD2	2.11	0.51
1:A:13:ASN:ND2	1:A:22:PRO:HD3	2.25	0.51
1:B:428:ILE:HA	1:D:428:ILE:HB	1.93	0.51
1:E:180:LYS:HE2	2:E:1001:NAD:H1B	1.93	0.51
1:C:12:LEU:HA	1:C:190:LEU:HD21	1.92	0.51
1:D:234:VAL:HG22	1:D:255:LEU:HB3	1.93	0.51
1:G:257:GLY:HA2	1:G:417:PHE:CD1	2.46	0.51
1:F:253:LEU:HB3	1:F:255:LEU:HD13	1.92	0.51
1:H:257:GLY:HA2	1:H:417:PHE:CD1	2.46	0.51
1:F:147:LEU:HD12	1:F:479:GLN:NE2	2.26	0.50
1:A:106:ALA:O	1:A:110:ILE:HG12	2.11	0.50
1:D:21:GLU:HG3	1:D:22:PRO:HD2	1.93	0.50
1:C:35:ALA:HA	1:C:329:PRO:HG3	1.93	0.50
1:C:266:ASP:OD2	1:C:430:ARG:NH2	2.37	0.50
1:E:3:THR:HG22	1:E:321:LEU:HD12	1.93	0.50
1:H:345:VAL:HA	1:H:348:GLU:HG2	1.94	0.50
1:A:301:LEU:HD22	1:A:401:SER:HB3	1.93	0.50
1:C:362:PRO:HG2	1:C:367:LEU:HB2	1.94	0.50
1:E:253:LEU:HB2	1:E:255:LEU:CD1	2.42	0.50
1:B:71:MET:HE2	1:C:453:VAL:HG11	1.93	0.50
1:F:124:ALA:HB2	1:F:172:ALA:HB1	1.94	0.49
1:A:75:ARG:NH2	1:A:79:GLU:OE2	2.41	0.49
1:D:8:VAL:HG21	1:D:12:LEU:HD21	1.95	0.49
1:G:106:ALA:O	1:G:110:ILE:HG12	2.12	0.49
1:G:317:ILE:HB	1:G:360:TYR:CE2	2.46	0.49
1:G:458:GLY:HA3	1:G:467:ARG:HD3	1.95	0.49
1:F:344:LYS:HA	1:F:347:LYS:HE2	1.94	0.49
1:A:221:GLN:HE21	1:A:243:MET:HG2	1.75	0.49
1:A:257:GLY:HA2	1:A:417:PHE:CD1	2.48	0.49
1:B:107:ARG:NH1	1:B:323:GLU:OE1	2.44	0.49
1:C:301:LEU:HD22	1:C:401:SER:HB2	1.95	0.49
1:B:101:LYS:HG3	1:B:283:THR:HG23	1.95	0.48
1:E:127:MET:HE3	1:E:144:ARG:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:ASN:ND2	1:A:56:GLN:OE1	2.45	0.48
1:G:101:LYS:HE2	1:G:283:THR:HG23	1.94	0.48
1:A:75:ARG:NH1	1:D:118:GLU:OE2	2.46	0.48
1:C:56:GLN:NE2	1:C:224:ASP:OD2	2.47	0.48
1:A:416:THR:HB	1:A:462:LYS:HD2	1.96	0.48
1:B:123:LEU:HD23	1:B:474:ILE:HD11	1.95	0.48
1:B:153:ILE:HG23	1:B:180:LYS:HE3	1.96	0.48
1:E:482:THR:HG23	1:F:455:LEU:HD13	1.94	0.48
1:H:296:VAL:HB	1:H:301:LEU:HD12	1.95	0.48
1:D:253:LEU:HB3	1:D:255:LEU:HD13	1.94	0.48
1:A:435:VAL:HG22	1:A:443:CYS:HB3	1.94	0.48
1:C:65:TRP:NE1	1:C:73:ARG:HD2	2.29	0.48
1:D:327:MET:HE1	1:D:395:PRO:HG3	1.96	0.48
1:E:287:VAL:HG12	1:E:289:CYS:H	1.79	0.48
1:H:35:ALA:HA	1:H:329:PRO:HG3	1.94	0.48
1:B:289:CYS:HB2	1:B:420:ALA:HB2	1.96	0.48
1:C:438:LEU:HD12	1:C:438:LEU:HA	1.76	0.48
1:E:319:ASP:HB3	1:E:322:LEU:HG	1.95	0.48
1:C:12:LEU:O	1:C:190:LEU:HD11	2.15	0.47
1:G:245:ALA:O	1:H:238:MET:HG3	2.14	0.47
1:G:493:ALA:O	1:H:326:ARG:NE	2.47	0.47
1:H:336:LEU:HD11	1:H:373:MET:HB3	1.96	0.47
1:B:352:LYS:HE3	1:B:354:LEU:HD23	1.96	0.47
1:C:84:ILE:HG12	1:C:195:ILE:HD13	1.96	0.47
1:C:241:MET:HG3	1:C:253:LEU:HD11	1.96	0.47
1:C:257:GLY:HA2	1:C:417:PHE:CD1	2.49	0.47
1:C:456:PRO:HB2	1:C:467:ARG:HD2	1.95	0.47
1:E:35:ALA:HA	1:E:329:PRO:HG3	1.97	0.47
1:A:35:ALA:HA	1:A:329:PRO:HG3	1.97	0.47
1:A:248:ILE:HD13	1:B:255:LEU:HD23	1.97	0.47
1:B:458:GLY:HA3	1:B:467:ARG:HD3	1.97	0.47
1:D:317:ILE:HB	1:D:360:TYR:CE2	2.50	0.47
1:C:458:GLY:HA3	1:C:467:ARG:HD3	1.97	0.47
1:D:460:TYR:HB3	1:D:461:LYS:HG3	1.97	0.47
1:E:455:LEU:HD22	1:F:142:THR:HG23	1.97	0.47
1:D:35:ALA:HA	1:D:329:PRO:HG3	1.97	0.47
1:E:3:THR:HG21	1:E:319:ASP:OD1	2.15	0.47
1:F:273:VAL:HG21	1:F:307:GLU:HB3	1.96	0.47
1:D:31:ALA:HB3	1:D:41:ALA:HB3	1.97	0.46
1:G:111:ASP:HA	1:G:114:TRP:NE1	2.29	0.46
1:F:284:GLN:HG3	1:F:327:MET:HG3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:375:PRO:HA	1:F:395:PRO:HB2	1.97	0.46
1:G:303:LYS:HE2	1:G:307:GLU:HG2	1.96	0.46
1:D:409:LEU:HD21	1:D:434:VAL:HG13	1.97	0.46
1:E:129:GLY:HA3	1:E:142:THR:O	2.15	0.46
1:G:123:LEU:HD23	1:G:474:ILE:HD11	1.96	0.46
1:C:486:GLU:HB2	1:D:447:ASN:HB2	1.97	0.46
1:E:142:THR:HG23	1:F:455:LEU:HD22	1.97	0.46
1:A:85:ARG:NH1	1:A:118:GLU:OE2	2.49	0.46
1:A:142:THR:HG23	1:B:455:LEU:HD22	1.98	0.46
1:A:428:ILE:HB	1:C:428:ILE:HA	1.95	0.46
1:F:257:GLY:HA2	1:F:417:PHE:CD1	2.51	0.46
1:B:327:MET:HE1	1:B:375:PRO:HB3	1.98	0.46
1:C:278:MET:HE3	1:C:282:LEU:HD11	1.97	0.46
1:F:319:ASP:HB3	1:F:322:LEU:HG	1.97	0.46
1:G:234:VAL:HG22	1:G:255:LEU:HB3	1.97	0.46
1:C:454:GLU:HB3	1:D:132:ILE:HD13	1.97	0.46
1:D:19:ARG:HH21	1:D:190:LEU:HD22	1.79	0.46
1:D:458:GLY:HA3	1:D:467:ARG:HD3	1.97	0.46
1:F:111:ASP:HA	1:F:114:TRP:NE1	2.31	0.46
1:A:130:GLU:OE2	1:B:471:ARG:HD2	2.16	0.46
1:A:130:GLU:N	1:A:142:THR:OG1	2.36	0.46
1:C:36:THR:OG1	1:C:38:ARG:HG2	2.16	0.46
1:D:180:LYS:NZ	2:D:501:NAD:H1B	2.31	0.45
1:A:127:MET:HE3	1:A:144:ARG:HG2	1.98	0.45
1:B:438:LEU:HD12	1:B:438:LEU:HA	1.80	0.45
1:D:384:ASP:HA	1:D:389:LYS:HE3	1.97	0.45
1:H:52:ASN:O	1:H:56:GLN:HG2	2.16	0.45
1:B:487:MET:HE1	1:C:429:GLN:HA	1.99	0.45
1:G:65:TRP:HZ3	1:G:76:ILE:HD12	1.81	0.45
1:B:257:GLY:HA2	1:B:417:PHE:CD1	2.51	0.45
1:E:494:PHE:HB3	1:F:315:ILE:HG12	1.98	0.45
1:F:123:LEU:HD21	1:F:471:ARG:HA	1.99	0.45
1:A:265:SER:HA	1:A:300:ILE:HD13	1.99	0.45
1:A:402:PHE:CD1	1:A:408:VAL:HB	2.51	0.45
1:C:111:ASP:HA	1:C:114:TRP:CD1	2.52	0.45
1:A:248:ILE:HD12	1:B:462:LYS:HG2	1.98	0.45
1:B:85:ARG:NH1	1:B:118:GLU:OE2	2.50	0.45
1:F:428:ILE:HB	1:G:428:ILE:HA	1.99	0.45
1:H:258:LYS:HD2	1:H:293:ARG:HG3	1.98	0.45
1:A:352:LYS:HB3	1:A:379:THR:HG22	1.99	0.45
1:B:111:ASP:HA	1:B:114:TRP:NE1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:190:LEU:O	1:B:194:GLU:HG3	2.16	0.45
1:C:227:LYS:HE2	1:C:476:TYR:O	2.17	0.45
1:C:258:LYS:HE3	1:C:293:ARG:HG3	1.98	0.45
1:E:127:MET:SD	1:E:173:CYS:HA	2.57	0.45
1:A:487:MET:HE1	1:D:429:GLN:HA	1.99	0.45
1:A:493:ALA:H	1:B:278:MET:CE	2.30	0.45
1:B:241:MET:HG3	1:B:253:LEU:HD11	1.99	0.45
1:D:12:LEU:HD12	1:D:43:PHE:HB3	1.99	0.45
1:D:96:CYS:SG	1:D:103:ILE:HA	2.57	0.45
1:D:258:LYS:HE2	1:D:388:VAL:O	2.17	0.45
1:H:309:VAL:O	1:H:313:GLN:HG3	2.16	0.45
1:E:111:ASP:HA	1:E:114:TRP:NE1	2.32	0.44
1:E:143:ARG:HG2	1:H:131:HIS:CE1	2.52	0.44
1:F:428:ILE:HA	1:G:428:ILE:HB	1.99	0.44
1:E:124:ALA:HB2	1:E:172:ALA:HB1	1.99	0.44
1:F:332:ASN:HA	1:F:371:TYR:CE2	2.53	0.44
1:D:101:LYS:HE2	1:D:283:THR:HG23	2.00	0.44
1:D:213:ALA:O	1:D:217:GLN:HG3	2.17	0.44
1:F:7:VAL:HG13	1:F:38:ARG:HH12	1.81	0.44
1:A:429:GLN:HA	1:D:487:MET:HE1	2.00	0.44
1:B:88:GLU:HG3	1:B:89:ASP:N	2.32	0.44
1:F:460:TYR:HB3	1:F:461:LYS:HG3	2.00	0.44
1:A:230:PHE:HB3	1:A:253:LEU:HD23	2.00	0.44
1:G:75:ARG:NH1	1:G:79:GLU:OE2	2.40	0.44
1:C:217:GLN:HG2	1:C:243:MET:SD	2.58	0.44
1:H:101:LYS:HE2	1:H:101:LYS:HB2	1.72	0.44
1:B:284:GLN:HG3	1:B:327:MET:HG3	1.99	0.44
1:B:43:PHE:CE1	1:B:186:PRO:HG3	2.53	0.44
1:B:52:ASN:O	1:B:56:GLN:HB2	2.17	0.43
1:D:190:LEU:O	1:D:194:GLU:HG3	2.18	0.43
1:F:7:VAL:HG13	1:F:38:ARG:NH1	2.33	0.43
1:F:253:LEU:HB3	1:F:255:LEU:CD1	2.47	0.43
1:H:418:GLY:O	1:H:460:TYR:HB2	2.18	0.43
1:F:418:GLY:O	1:F:460:TYR:HB2	2.18	0.43
1:F:438:LEU:HD12	1:F:438:LEU:HA	1.87	0.43
1:A:248:ILE:HD11	1:B:234:VAL:HG13	1.98	0.43
1:G:317:ILE:HA	1:G:327:MET:O	2.18	0.43
1:C:8:VAL:HG13	1:C:41:ALA:HB2	1.99	0.43
1:B:49:LYS:O	1:B:53:LEU:HG	2.19	0.43
1:D:230:PHE:HB3	1:D:253:LEU:HD23	2.01	0.43
1:D:381:CYS:HB2	1:D:400:LEU:HG	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:405:GLU:OE1	1:D:430:ARG:HG3	2.19	0.43
1:E:317:ILE:HA	1:E:327:MET:O	2.18	0.43
1:E:458:GLY:HA3	1:E:467:ARG:HD3	2.01	0.43
1:F:487:MET:HE1	1:H:429:GLN:HA	2.00	0.43
1:G:484:CYS:SG	1:H:452:PRO:HD3	2.58	0.43
1:A:253:LEU:HB3	1:A:255:LEU:HD13	2.00	0.43
1:C:265:SER:HA	1:C:300:ILE:HD13	1.99	0.43
1:E:12:LEU:HD12	1:E:43:PHE:HB3	2.01	0.43
1:G:123:LEU:HA	1:G:123:LEU:HD12	1.78	0.43
1:H:99:ASN:OD1	1:H:101:LYS:HB2	2.18	0.43
1:H:257:GLY:HA2	1:H:417:PHE:CG	2.54	0.43
1:C:127:MET:HE2	1:C:144:ARG:HG2	2.00	0.43
1:E:22:PRO:HG2	1:E:44:THR:HB	2.00	0.43
1:H:241:MET:SD	1:H:253:LEU:HD21	2.59	0.43
1:H:253:LEU:HD13	1:H:464:GLY:HA2	2.01	0.43
1:E:51:VAL:HG13	1:E:219:LEU:HD23	2.01	0.43
1:H:287:VAL:HB	1:H:290:ASN:CG	2.43	0.43
1:B:82:ARG:NH1	1:B:86:GLU:OE2	2.52	0.43
1:C:61:ALA:HB2	1:C:203:PRO:O	2.19	0.43
1:E:295:PHE:HB3	1:E:402:PHE:CD2	2.54	0.43
1:B:123:LEU:HA	1:B:123:LEU:HD12	1.70	0.42
1:C:241:MET:HE2	1:C:241:MET:HB3	1.94	0.42
1:E:99:ASN:ND2	1:E:156:TRP:O	2.49	0.42
1:F:230:PHE:HB3	1:F:253:LEU:HD23	2.01	0.42
1:G:98:ASN:OD1	1:G:185:THR:HA	2.19	0.42
1:B:83:ILE:HB	1:B:195:ILE:HG23	2.01	0.42
1:C:142:THR:HG23	1:D:455:LEU:HD22	2.00	0.42
1:C:230:PHE:HB3	1:C:253:LEU:HD23	2.01	0.42
1:A:13:ASN:HB2	1:A:20:VAL:O	2.19	0.42
1:B:35:ALA:HA	1:B:329:PRO:HG3	2.02	0.42
1:B:428:ILE:HB	1:D:428:ILE:HA	2.02	0.42
1:C:156:TRP:NE1	2:C:501:NAD:O1N	2.51	0.42
1:F:261:LEU:O	1:F:295:PHE:N	2.48	0.42
1:C:154:GLY:O	2:C:501:NAD:O3B	2.34	0.42
1:F:343:VAL:O	1:F:347:LYS:HG2	2.19	0.42
1:F:381:CYS:HB2	1:F:400:LEU:HG	2.02	0.42
1:C:190:LEU:O	1:C:194:GLU:HG3	2.18	0.42
1:G:358:ASP:OD1	1:G:358:ASP:N	2.46	0.42
1:A:111:ASP:HA	1:A:114:TRP:CD1	2.54	0.42
1:C:355:CYS:O	1:C:376:CYS:HA	2.20	0.42
1:D:34:PRO:HB2	1:D:329:PRO:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:289:CYS:HB2	1:F:420:ALA:HB2	2.02	0.42
1:F:429:GLN:HA	1:H:487:MET:HE1	2.01	0.42
1:C:123:LEU:HD12	1:C:123:LEU:HA	1.90	0.42
1:F:409:LEU:HD21	1:F:434:VAL:HG13	2.01	0.42
1:H:356:GLY:HA2	1:H:374:ARG:HB2	2.02	0.42
1:A:418:GLY:O	1:A:460:TYR:HB2	2.20	0.42
1:D:287:VAL:HB	1:D:290:ASN:ND2	2.35	0.42
1:E:36:THR:HG23	1:E:366:LYS:O	2.20	0.42
1:H:438:LEU:HD12	1:H:438:LEU:HA	1.87	0.42
1:A:112:ILE:HG21	1:A:161:GLN:NE2	2.35	0.42
1:D:111:ASP:HA	1:D:114:TRP:NE1	2.35	0.42
1:E:101:LYS:HE2	1:E:283:THR:HG23	2.02	0.42
1:H:106:ALA:O	1:H:110:ILE:HG12	2.19	0.41
1:C:65:TRP:CE2	1:C:73:ARG:HD2	2.55	0.41
1:F:33:GLU:OE1	1:F:36:THR:OG1	2.38	0.41
1:F:79:GLU:OE1	1:F:82:ARG:NE	2.47	0.41
1:H:153:ILE:HG23	1:H:180:LYS:HE3	2.02	0.41
1:B:150:CYS:O	1:B:177:MET:HA	2.20	0.41
1:E:253:LEU:HB2	1:E:255:LEU:HD11	2.02	0.41
1:C:180:LYS:NZ	2:C:501:NAD:O2B	2.38	0.41
1:C:289:CYS:HB2	1:C:420:ALA:HB2	2.01	0.41
1:E:14:TYR:CD2	1:E:193:ALA:HB1	2.56	0.41
1:E:230:PHE:O	1:E:253:LEU:HA	2.21	0.41
1:H:15:ARG:HD3	1:H:53:LEU:C	2.45	0.41
1:B:265:SER:HA	1:B:300:ILE:HD13	2.03	0.41
1:D:98:ASN:OD1	1:D:185:THR:HA	2.20	0.41
1:D:257:GLY:HA2	1:D:417:PHE:CD1	2.56	0.41
1:E:62:PHE:CZ	1:E:148:GLY:HA2	2.55	0.41
1:B:158:TYR:HB3	1:B:161:GLN:HB3	2.01	0.41
1:H:127:MET:HE2	1:H:127:MET:HB3	1.91	0.41
1:E:234:VAL:HG22	1:E:255:LEU:HB3	2.02	0.41
1:E:238:MET:HE3	1:E:238:MET:HB2	1.95	0.41
1:C:35:ALA:CA	1:C:329:PRO:HG3	2.50	0.41
1:E:364:ASP:HB3	1:E:367:LEU:HG	2.02	0.41
1:A:95:GLU:O	1:A:99:ASN:HB3	2.21	0.41
1:A:409:LEU:HD23	1:A:409:LEU:HA	1.91	0.41
1:B:118:GLU:OE2	1:C:75:ARG:NE	2.51	0.41
1:B:416:THR:HB	1:B:462:LYS:HD2	2.02	0.41
1:B:435:VAL:HG22	1:B:443:CYS:HB3	2.03	0.41
1:E:217:GLN:HG2	1:E:243:MET:SD	2.60	0.41
1:F:303:LYS:HA	1:F:303:LYS:HD2	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:ILE:O	1:B:107:ARG:HG3	2.21	0.41
1:E:95:GLU:O	1:E:99:ASN:HB3	2.20	0.41
1:H:35:ALA:CA	1:H:329:PRO:HG3	2.51	0.41
1:D:299:GLU:OE1	1:D:299:GLU:N	2.45	0.40
1:E:147:LEU:N	1:E:175:ASN:OD1	2.46	0.40
1:E:293:ARG:HD3	1:E:388:VAL:O	2.20	0.40
1:E:429:GLN:HA	1:G:487:MET:HE1	2.02	0.40
1:F:65:TRP:CZ3	1:F:76:ILE:HD12	2.48	0.40
1:F:133:GLN:HE21	1:F:133:GLN:HB2	1.58	0.40
1:G:158:TYR:HB3	1:G:161:GLN:HB3	2.02	0.40
1:H:147:LEU:HD12	1:H:479:GLN:HE21	1.86	0.40
1:A:68:LYS:HB3	1:A:72:GLU:HB2	2.04	0.40
1:A:493:ALA:H	1:B:278:MET:HE1	1.86	0.40
1:E:466:GLY:O	1:E:467:ARG:NH1	2.48	0.40
1:A:43:PHE:CE2	1:A:210:GLN:HB3	2.56	0.40
1:E:428:ILE:HB	1:H:428:ILE:HA	2.02	0.40
1:E:381:CYS:HB2	1:E:400:LEU:HG	2.04	0.40
1:F:456:PRO:HB2	1:F:467:ARG:HD2	2.03	0.40
1:G:147:LEU:HD23	1:G:227:LYS:HB2	2.04	0.40
1:H:284:GLN:HG3	1:H:327:MET:HG3	2.02	0.40
1:A:303:LYS:NZ	1:A:307:GLU:OE1	2.47	0.40
1:B:358:ASP:OD1	1:B:358:ASP:N	2.55	0.40
1:E:226:ALA:O	1:E:250:PRO:HD2	2.21	0.40
1:E:243:MET:HE3	1:E:243:MET:HB2	1.99	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	490/493 (99%)	477 (97%)	13 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	490/493 (99%)	477 (97%)	13 (3%)	0	100	100
1	C	490/493 (99%)	477 (97%)	12 (2%)	1 (0%)	43	63
1	D	491/493 (100%)	478 (97%)	13 (3%)	0	100	100
1	E	491/493 (100%)	476 (97%)	15 (3%)	0	100	100
1	F	490/493 (99%)	477 (97%)	13 (3%)	0	100	100
1	G	491/493 (100%)	478 (97%)	13 (3%)	0	100	100
1	H	490/493 (99%)	477 (97%)	13 (3%)	0	100	100
All	All	3923/3944 (100%)	3817 (97%)	105 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	4	GLY

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	378/402 (94%)	356 (94%)	22 (6%)	18	38
1	B	374/402 (93%)	354 (95%)	20 (5%)	20	42
1	C	371/402 (92%)	358 (96%)	13 (4%)	32	58
1	D	373/402 (93%)	356 (95%)	17 (5%)	24	48
1	E	358/402 (89%)	342 (96%)	16 (4%)	24	49
1	F	367/402 (91%)	349 (95%)	18 (5%)	22	45
1	G	368/402 (92%)	352 (96%)	16 (4%)	26	51
1	H	358/402 (89%)	338 (94%)	20 (6%)	19	39
All	All	2947/3216 (92%)	2805 (95%)	142 (5%)	23	46

All (142) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	GLU
1	A	26	SER
1	A	32	PHE
1	A	48	GLU
1	A	52	ASN
1	A	56	GLN
1	A	67	GLN
1	A	76	ILE
1	A	89	ASP
1	A	97	ILE
1	A	112	ILE
1	A	147	LEU
1	A	190	LEU
1	A	228	VAL
1	A	255	LEU
1	A	306	GLU
1	A	308	VAL
1	A	358	ASP
1	A	415	THR
1	A	438	LEU
1	A	451	SER
1	A	471	ARG
1	B	3	THR
1	B	10	GLN
1	B	42	THR
1	B	56	GLN
1	B	67	GLN
1	B	88	GLU
1	B	89	ASP
1	B	101	LYS
1	B	112	ILE
1	B	123	LEU
1	B	147	LEU
1	B	255	LEU
1	B	270	ASN
1	B	324	ASP
1	B	352	LYS
1	B	368	LYS
1	B	415	THR
1	B	438	LEU
1	B	453	VAL
1	B	492	SER
1	C	3	THR

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Mol	Chain	Res	Type
1	C	8	VAL
1	C	21	GLU
1	C	56	GLN
1	C	110	ILE
1	C	127	MET
1	C	133	GLN
1	C	147	LEU
1	C	151	VAL
1	C	316	LYS
1	C	393	PHE
1	C	415	THR
1	C	438	LEU
1	D	5	THR
1	D	7	VAL
1	D	21	GLU
1	D	42	THR
1	D	52	ASN
1	D	56	GLN
1	D	75	ARG
1	D	89	ASP
1	D	133	GLN
1	D	197	SER
1	D	240	ILE
1	D	254	GLU
1	D	255	LEU
1	D	415	THR
1	D	438	LEU
1	D	453	VAL
1	D	492	SER
1	E	3	THR
1	E	5	THR
1	E	112	ILE
1	E	132	ILE
1	E	197	SER
1	E	251	VAL
1	E	253	LEU
1	E	255	LEU
1	E	259	SER
1	E	310	LYS
1	E	338	ARG
1	E	349	GLN
1	E	366	LYS

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Mol	Chain	Res	Type
1	E	415	THR
1	E	438	LEU
1	E	451	SER
1	F	7	VAL
1	F	10	GLN
1	F	42	THR
1	F	52	ASN
1	F	75	ARG
1	F	117	LEU
1	F	133	GLN
1	F	138	SER
1	F	147	LEU
1	F	227	LYS
1	F	242	GLU
1	F	255	LEU
1	F	324	ASP
1	F	393	PHE
1	F	415	THR
1	F	438	LEU
1	F	453	VAL
1	F	475	GLU
1	G	40	ILE
1	G	42	THR
1	G	75	ARG
1	G	93	THR
1	G	112	ILE
1	G	123	LEU
1	G	133	GLN
1	G	147	LEU
1	G	254	GLU
1	G	255	LEU
1	G	265	SER
1	G	299	GLU
1	G	303	LYS
1	G	327	MET
1	G	415	THR
1	G	438	LEU
1	H	3	THR
1	H	8	VAL
1	H	75	ARG
1	H	101	LYS
1	H	123	LEU

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Mol	Chain	Res	Type
1	H	147	LEU
1	H	171	LEU
1	H	221	GLN
1	H	253	LEU
1	H	254	GLU
1	H	255	LEU
1	H	258	LYS
1	H	292	THR
1	H	399	ILE
1	H	415	THR
1	H	438	LEU
1	H	471	ARG
1	H	474	ILE
1	H	475	GLU
1	H	491	GLU

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

Mol	Chain	Res	Type
1	A	52	ASN
1	A	67	GLN
1	A	115	GLN
1	A	133	GLN
1	A	221	GLN
1	A	380	ASN
1	B	56	GLN
1	B	67	GLN
1	B	131	HIS
1	B	446	ASN
1	C	56	GLN
1	C	131	HIS
1	C	133	GLN
1	C	286	GLN
1	D	313	GLN
1	D	380	ASN
1	E	56	GLN
1	F	133	GLN
1	F	221	GLN
1	F	380	ASN
1	G	133	GLN
1	G	221	GLN
1	H	161	GLN

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	H	501	-	28,29,48	2.27	7 (25%)	43,45,73	1.99	10 (23%)
2	NAD	F	501	-	28,29,48	1.91	7 (25%)	43,45,73	1.76	12 (27%)
2	NAD	B	501	-	28,29,48	1.81	5 (17%)	43,45,73	2.06	12 (27%)
2	NAD	C	501	-	28,29,48	1.87	6 (21%)	43,45,73	2.05	12 (27%)
2	NAD	E	1001	-	28,29,48	2.24	5 (17%)	43,45,73	2.08	10 (23%)
2	NAD	A	501	-	46,48,48	1.52	8 (17%)	64,73,73	1.82	15 (23%)
2	NAD	G	501	-	28,29,48	1.87	6 (21%)	43,45,73	1.94	13 (30%)
2	NAD	D	501	-	28,29,48	2.23	7 (25%)	43,45,73	2.01	11 (25%)

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	H	501	-	-	10/16/32/62	0/3/3/5
2	NAD	F	501	-	-	3/16/32/62	0/3/3/5
2	NAD	B	501	-	-	7/16/32/62	0/3/3/5
2	NAD	C	501	-	-	3/16/32/62	0/3/3/5
2	NAD	E	1001	-	-	8/16/32/62	0/3/3/5
2	NAD	A	501	-	-	8/30/62/62	0/5/5/5
2	NAD	G	501	-	-	2/16/32/62	0/3/3/5
2	NAD	D	501	-	-	6/16/32/62	0/3/3/5

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	NAD	PN-O1N	9.21	1.79	1.50
2	H	501	NAD	PN-O1N	9.14	1.78	1.50
2	E	1001	NAD	PN-O1N	9.06	1.78	1.50
2	G	501	NAD	PN-O5D	6.53	1.79	1.54
2	C	501	NAD	PN-O5D	6.53	1.79	1.54
2	F	501	NAD	PN-O5D	6.48	1.78	1.54
2	B	501	NAD	PN-O5D	6.32	1.78	1.54
2	A	501	NAD	PN-O5D	4.45	1.76	1.59
2	H	501	NAD	PA-O5B	4.15	1.75	1.59
2	F	501	NAD	PA-O5B	3.86	1.74	1.59
2	E	1001	NAD	PA-O5B	3.86	1.74	1.59
2	A	501	NAD	PA-O5B	3.84	1.74	1.59
2	G	501	NAD	PA-O5B	3.72	1.74	1.59
2	C	501	NAD	PA-O5B	3.70	1.73	1.59
2	B	501	NAD	PA-O5B	3.68	1.73	1.59
2	D	501	NAD	PA-O5B	3.55	1.73	1.59
2	E	1001	NAD	PA-O3	3.18	1.62	1.59
2	A	501	NAD	C2N-N1N	3.08	1.38	1.35
2	F	501	NAD	PA-O3	2.94	1.62	1.59
2	C	501	NAD	PA-O3	2.81	1.62	1.59
2	A	501	NAD	C7N-N7N	2.55	1.37	1.33
2	H	501	NAD	PA-O3	2.49	1.62	1.59
2	H	501	NAD	C5A-C4A	2.30	1.43	1.39
2	D	501	NAD	C8A-N9A	2.26	1.41	1.37
2	G	501	NAD	C5A-C4A	2.25	1.43	1.39
2	F	501	NAD	C5A-C4A	2.24	1.43	1.39
2	B	501	NAD	C4A-N3A	2.22	1.38	1.34
2	B	501	NAD	C5A-C4A	2.22	1.43	1.39
2	A	501	NAD	C8A-N9A	2.22	1.41	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NAD	C5A-C4A	2.21	1.43	1.39
2	D	501	NAD	C4A-N3A	2.19	1.38	1.34
2	F	501	NAD	C8A-N9A	2.19	1.41	1.37
2	G	501	NAD	C4A-N3A	2.18	1.38	1.34
2	D	501	NAD	C5A-C4A	2.17	1.43	1.39
2	C	501	NAD	C5A-C4A	2.16	1.42	1.39
2	H	501	NAD	C4A-N3A	2.15	1.38	1.34
2	A	501	NAD	O5D-C5D	-2.12	1.36	1.44
2	F	501	NAD	C4A-N3A	2.11	1.38	1.34
2	G	501	NAD	C8A-N9A	2.11	1.41	1.37
2	H	501	NAD	C8A-N9A	2.09	1.41	1.37
2	C	501	NAD	C4A-N3A	2.06	1.38	1.34
2	D	501	NAD	C2A-N1A	2.06	1.37	1.33
2	G	501	NAD	C2A-N1A	2.04	1.37	1.33
2	B	501	NAD	C8A-N9A	2.04	1.41	1.37
2	E	1001	NAD	C5A-C4A	2.03	1.42	1.39
2	C	501	NAD	C8A-N9A	2.01	1.41	1.37
2	A	501	NAD	C4A-N3A	2.01	1.38	1.34
2	E	1001	NAD	C8A-N9A	2.01	1.41	1.37
2	D	501	NAD	PA-O3	2.01	1.61	1.59
2	H	501	NAD	C2A-N1A	2.01	1.37	1.33
2	F	501	NAD	C2A-N1A	2.00	1.37	1.33

All (95) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	501	NAD	O5D-PN-O2N	6.08	130.61	107.80
2	C	501	NAD	O2N-PN-O3	5.94	124.55	104.64
2	A	501	NAD	C4D-O4D-C1D	-5.91	104.52	109.92
2	E	1001	NAD	O5D-PN-O2N	5.84	129.71	107.80
2	D	501	NAD	O5D-PN-O2N	5.83	129.66	107.80
2	E	1001	NAD	O5D-PN-O3	5.41	122.77	104.64
2	G	501	NAD	O2N-PN-O1N	5.06	130.54	110.83
2	D	501	NAD	O5D-PN-O3	5.04	121.54	104.64
2	B	501	NAD	O2N-PN-O1N	4.96	130.15	110.83
2	B	501	NAD	O2N-PN-O3	4.95	121.22	104.64
2	G	501	NAD	O2N-PN-O3	4.93	121.16	104.64
2	F	501	NAD	O2N-PN-O1N	4.84	129.69	110.83
2	H	501	NAD	O5D-PN-O3	4.71	120.42	104.64
2	C	501	NAD	O2N-PN-O1N	4.61	128.79	110.83
2	A	501	NAD	O3-PA-O1A	-4.50	97.16	110.70
2	B	501	NAD	O3-PA-O1A	-4.46	97.28	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	NAD	O2A-PA-O3	4.32	118.94	107.27
2	D	501	NAD	O2A-PA-O1A	4.05	131.27	112.44
2	B	501	NAD	O2A-PA-O1A	4.04	131.25	112.44
2	G	501	NAD	O2A-PA-O1A	4.00	131.05	112.44
2	A	501	NAD	O2A-PA-O1A	3.98	130.95	112.44
2	A	501	NAD	O2N-PN-O1N	3.96	130.89	112.44
2	H	501	NAD	O2A-PA-O1A	3.96	130.86	112.44
2	A	501	NAD	O2A-PA-O3	3.87	117.74	107.27
2	C	501	NAD	O2A-PA-O1A	3.84	130.29	112.44
2	F	501	NAD	O2A-PA-O1A	3.83	130.24	112.44
2	E	1001	NAD	O2A-PA-O1A	3.81	130.16	112.44
2	C	501	NAD	O3-PA-O1A	-3.80	99.27	110.70
2	E	1001	NAD	O2N-PN-O1N	-3.74	96.25	110.83
2	C	501	NAD	O5D-PN-O1N	-3.72	96.34	110.83
2	H	501	NAD	O2N-PN-O1N	-3.71	96.38	110.83
2	G	501	NAD	O5D-PN-O1N	-3.67	96.52	110.83
2	C	501	NAD	O2A-PA-O3	3.67	117.19	107.27
2	D	501	NAD	O2N-PN-O1N	-3.65	96.62	110.83
2	H	501	NAD	O2A-PA-O3	-3.63	97.45	107.27
2	E	1001	NAD	O3-PA-O1A	-3.63	99.79	110.70
2	B	501	NAD	O5D-PN-O1N	-3.58	96.90	110.83
2	G	501	NAD	O2A-PA-O3	-3.54	97.71	107.27
2	E	1001	NAD	O2A-PA-O3	3.48	116.68	107.27
2	E	1001	NAD	O5D-PN-O1N	-3.44	97.43	110.83
2	F	501	NAD	O5D-PN-O1N	-3.37	97.69	110.83
2	A	501	NAD	O3-PN-O1N	3.34	120.77	110.70
2	D	501	NAD	O2A-PA-O3	-3.34	98.23	107.27
2	H	501	NAD	O5D-PN-O1N	-3.29	98.03	110.83
2	A	501	NAD	PN-O5D-C5D	-3.21	102.94	121.35
2	D	501	NAD	O5D-PN-O1N	-3.18	98.46	110.83
2	F	501	NAD	O2A-PA-O3	-3.08	98.94	107.27
2	F	501	NAD	O5D-PN-O2N	-3.03	96.45	107.80
2	B	501	NAD	O5B-PA-O1A	-3.00	97.05	108.94
2	C	501	NAD	O5B-PA-O1A	-2.80	97.84	108.94
2	E	1001	NAD	O5B-PA-O1A	-2.76	97.99	108.94
2	E	1001	NAD	PA-O5B-C5B	-2.75	105.59	121.35
2	A	501	NAD	O5D-PN-O1N	-2.62	98.54	108.94
2	G	501	NAD	O5D-PN-O2N	-2.61	98.00	107.80
2	C	501	NAD	O5D-PN-O2N	-2.57	98.17	107.80
2	A	501	NAD	O5B-PA-O1A	-2.57	98.76	108.94
2	G	501	NAD	PA-O5B-C5B	-2.56	106.66	121.35
2	A	501	NAD	O2N-PN-O3	-2.56	100.36	107.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	NAD	PA-O5B-C5B	-2.55	106.71	121.35
2	H	501	NAD	PA-O5B-C5B	-2.55	106.75	121.35
2	B	501	NAD	PA-O5B-C5B	-2.54	106.78	121.35
2	C	501	NAD	PA-O5B-C5B	-2.53	106.83	121.35
2	F	501	NAD	PA-O5B-C5B	-2.52	106.89	121.35
2	B	501	NAD	C5B-C4B-C3B	-2.51	106.16	115.21
2	C	501	NAD	O3-PN-O1N	-2.49	97.95	111.04
2	D	501	NAD	C5B-C4B-C3B	-2.48	106.28	115.21
2	D	501	NAD	O3-PA-O1A	2.48	118.16	110.70
2	B	501	NAD	O5D-PN-O2N	-2.46	98.59	107.80
2	A	501	NAD	O2N-PN-O5D	-2.39	96.75	107.57
2	C	501	NAD	C5B-C4B-C3B	-2.37	106.69	115.21
2	A	501	NAD	PA-O5B-C5B	-2.35	107.86	121.35
2	G	501	NAD	O3B-C3B-C4B	-2.35	104.33	111.08
2	D	501	NAD	O2A-PA-O5B	-2.32	97.05	107.57
2	F	501	NAD	O3-PN-O1N	2.32	123.25	111.04
2	H	501	NAD	O2A-PA-O5B	-2.26	97.34	107.57
2	B	501	NAD	O3-PN-O1N	-2.24	99.23	111.04
2	G	501	NAD	O2A-PA-O5B	-2.23	97.44	107.57
2	H	501	NAD	O3B-C3B-C4B	-2.22	104.72	111.08
2	A	501	NAD	C2D-C3D-C4D	-2.21	98.34	102.61
2	C	501	NAD	O3B-C3B-C4B	-2.20	104.76	111.08
2	G	501	NAD	O3-PA-O1A	2.20	117.31	110.70
2	E	1001	NAD	O3B-C3B-C4B	-2.18	104.83	111.08
2	F	501	NAD	O2A-PA-O5B	-2.17	97.71	107.57
2	F	501	NAD	O3B-C3B-C4B	-2.17	104.84	111.08
2	B	501	NAD	O3B-C3B-C4B	-2.13	104.97	111.08
2	A	501	NAD	C5B-C4B-C3B	-2.11	107.61	115.21
2	F	501	NAD	C5B-C4B-C3B	-2.11	107.62	115.21
2	A	501	NAD	O3B-C3B-C4B	-2.11	105.03	111.08
2	G	501	NAD	O3-PN-O1N	-2.10	99.96	111.04
2	F	501	NAD	O3-PA-O1A	2.09	116.98	110.70
2	F	501	NAD	O5B-PA-O1A	-2.05	100.79	108.94
2	G	501	NAD	O5B-PA-O1A	-2.04	100.84	108.94
2	D	501	NAD	O5B-PA-O1A	-2.03	100.89	108.94
2	G	501	NAD	O4B-C4B-C3B	2.02	109.16	105.15
2	H	501	NAD	O3-PA-O1A	2.01	116.75	110.70

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	NAD	C5B-O5B-PA-O1A
2	A	501	NAD	C5D-O5D-PN-O1N
2	A	501	NAD	O4D-C1D-N1N-C6N
2	B	501	NAD	C5B-O5B-PA-O1A
2	B	501	NAD	C5B-O5B-PA-O2A
2	B	501	NAD	O4B-C4B-C5B-O5B
2	B	501	NAD	C3B-C4B-C5B-O5B
2	C	501	NAD	PA-O3-PN-O2N
2	D	501	NAD	C5B-O5B-PA-O3
2	D	501	NAD	O4B-C4B-C5B-O5B
2	E	1001	NAD	C5B-O5B-PA-O1A
2	E	1001	NAD	C5B-O5B-PA-O2A
2	E	1001	NAD	C5B-O5B-PA-O3
2	E	1001	NAD	O4B-C4B-C5B-O5B
2	G	501	NAD	PN-O3-PA-O5B
2	H	501	NAD	C5B-O5B-PA-O1A
2	H	501	NAD	C5B-O5B-PA-O3
2	C	501	NAD	O4B-C4B-C5B-O5B
2	E	1001	NAD	C3B-C4B-C5B-O5B
2	D	501	NAD	C3B-C4B-C5B-O5B
2	C	501	NAD	C3B-C4B-C5B-O5B
2	H	501	NAD	C3B-C4B-C5B-O5B
2	H	501	NAD	O4B-C4B-C5B-O5B
2	H	501	NAD	PN-O3-PA-O5B
2	B	501	NAD	PA-O3-PN-O1N
2	F	501	NAD	PA-O3-PN-O5D
2	A	501	NAD	C2B-C1B-N9A-C8A
2	E	1001	NAD	C2B-C1B-N9A-C8A
2	H	501	NAD	C2B-C1B-N9A-C8A
2	A	501	NAD	C5B-O5B-PA-O2A
2	A	501	NAD	C5D-O5D-PN-O2N
2	B	501	NAD	C5B-O5B-PA-O3
2	D	501	NAD	C5B-O5B-PA-O1A
2	D	501	NAD	C5B-O5B-PA-O2A
2	H	501	NAD	C5B-O5B-PA-O2A
2	G	501	NAD	C2B-C1B-N9A-C8A
2	A	501	NAD	O4D-C1D-N1N-C2N
2	H	501	NAD	PN-O3-PA-O1A
2	E	1001	NAD	O4B-C1B-N9A-C8A
2	F	501	NAD	PA-O3-PN-O2N
2	B	501	NAD	C2B-C1B-N9A-C8A
2	F	501	NAD	O4B-C4B-C5B-O5B
2	E	1001	NAD	C2B-C1B-N9A-C4A

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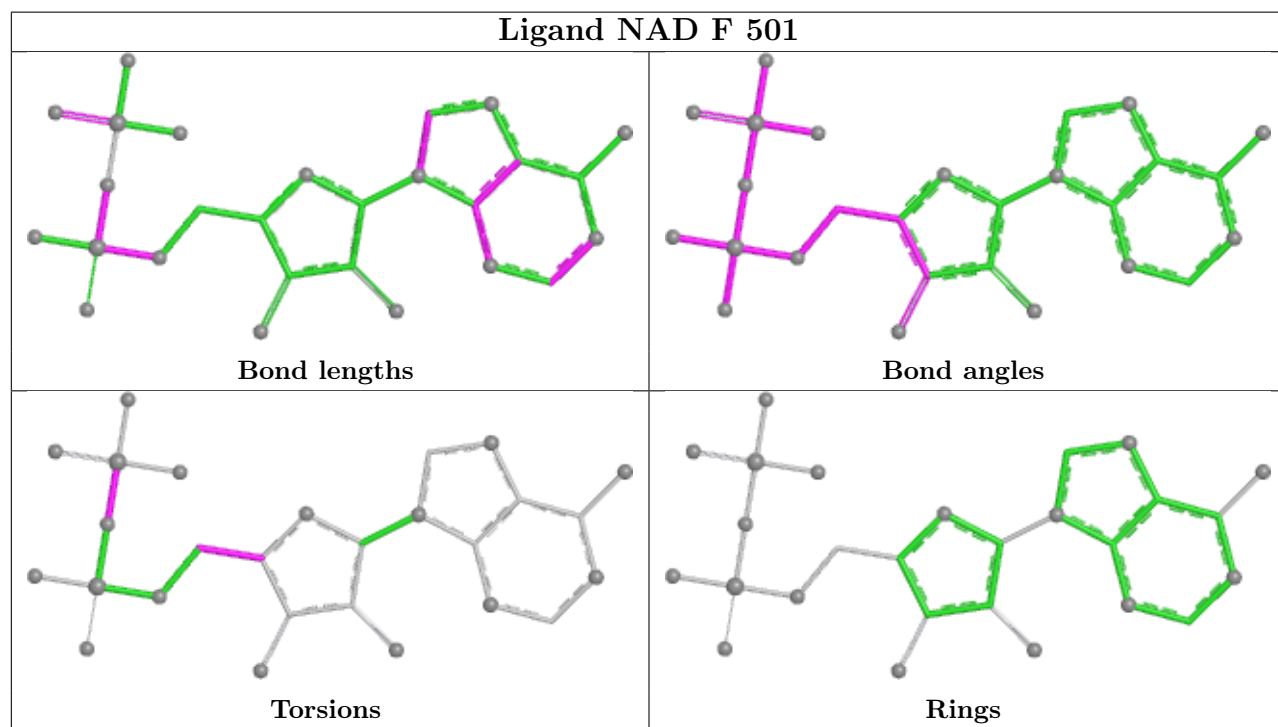
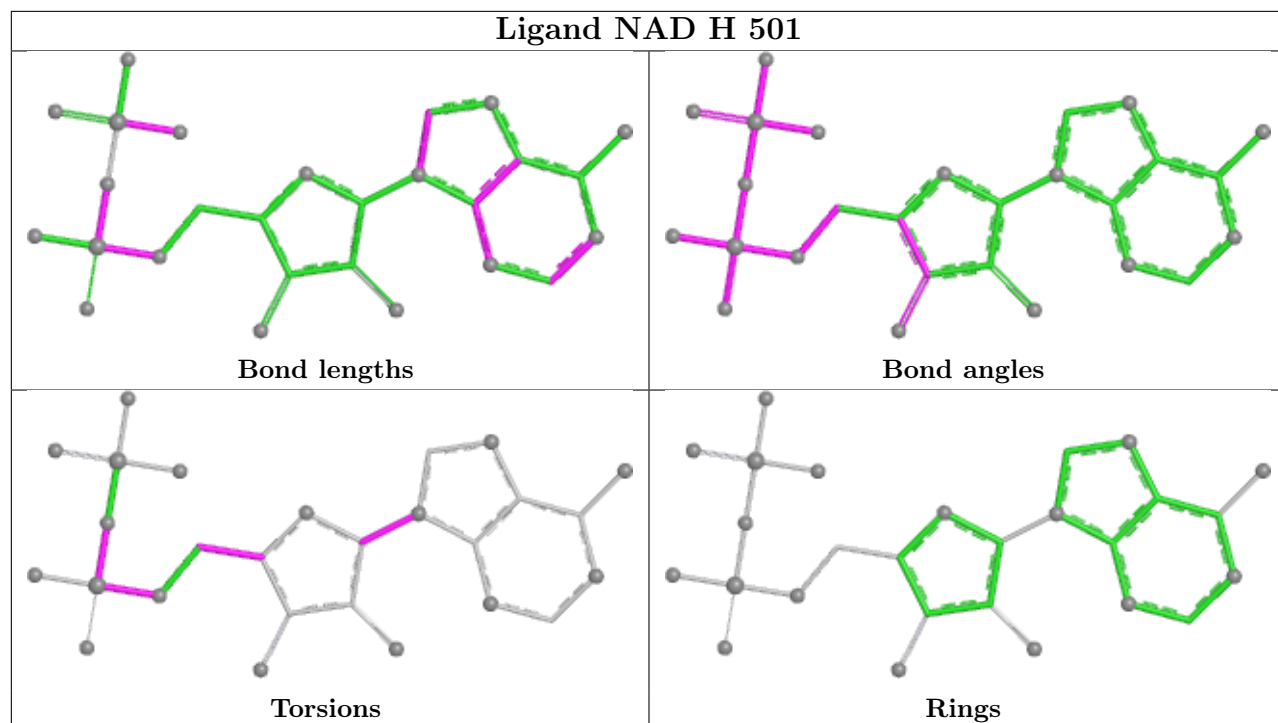
Mol	Chain	Res	Type	Atoms
2	H	501	NAD	O4B-C1B-N9A-C8A
2	H	501	NAD	C2B-C1B-N9A-C4A
2	A	501	NAD	O4B-C1B-N9A-C8A
2	D	501	NAD	C2B-C1B-N9A-C8A

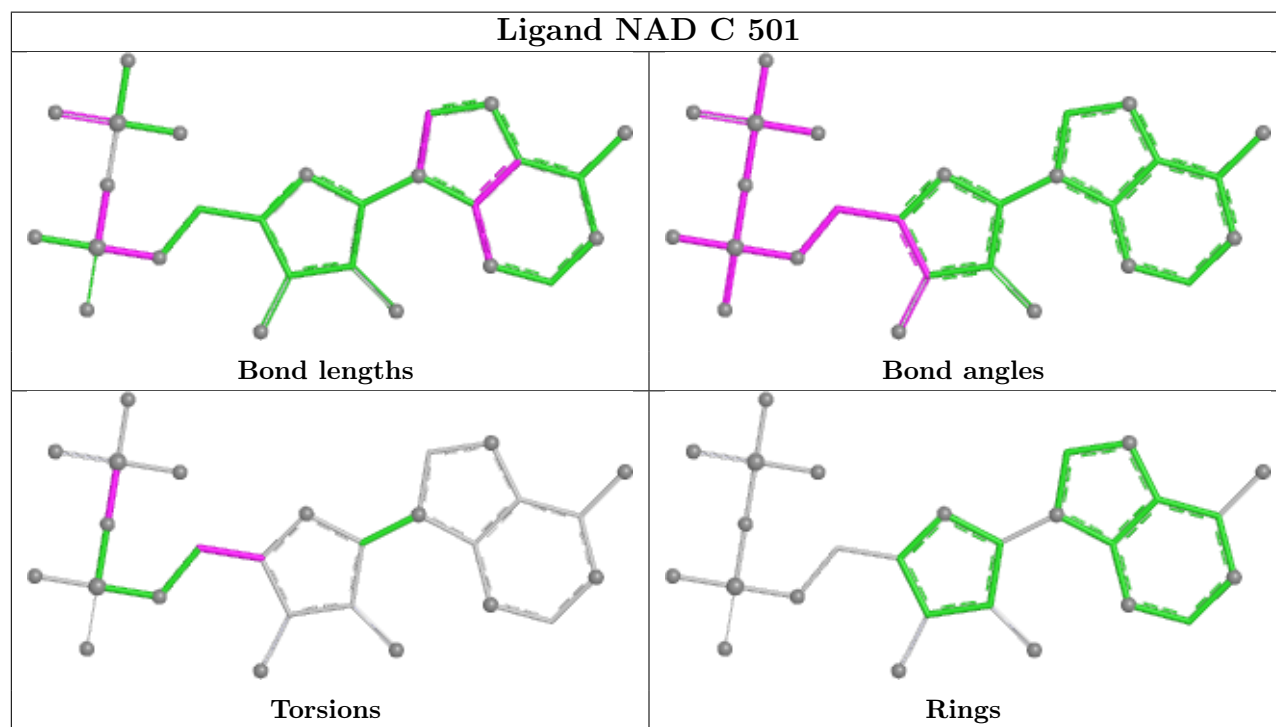
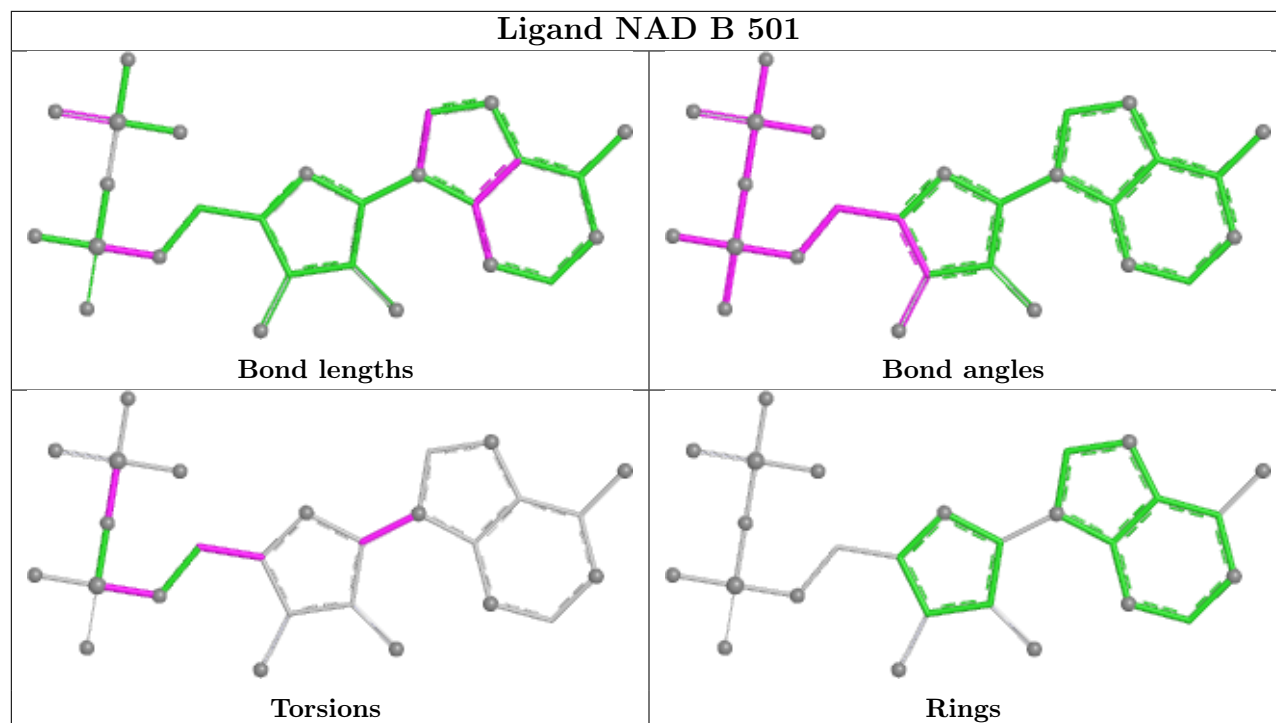
There are no ring outliers.

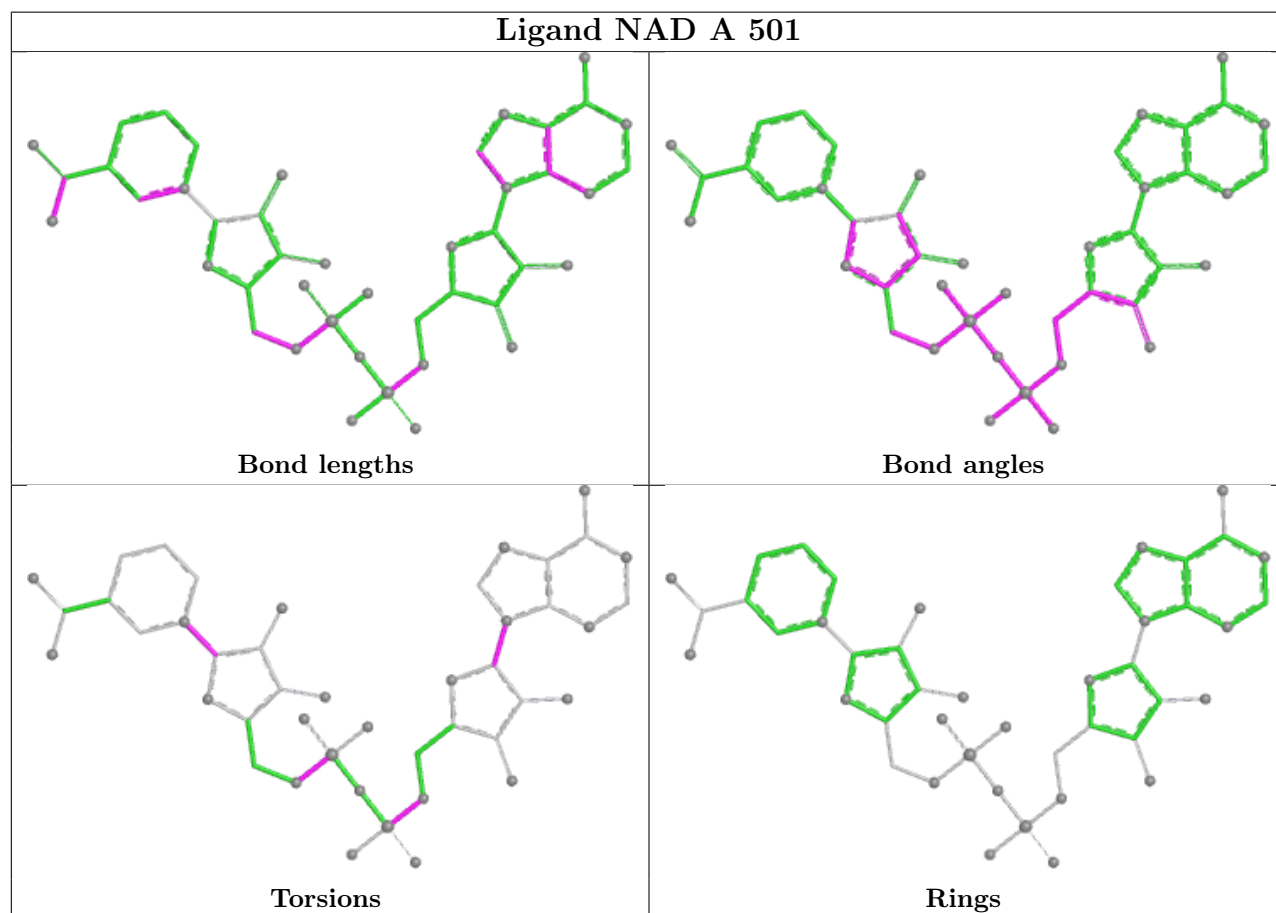
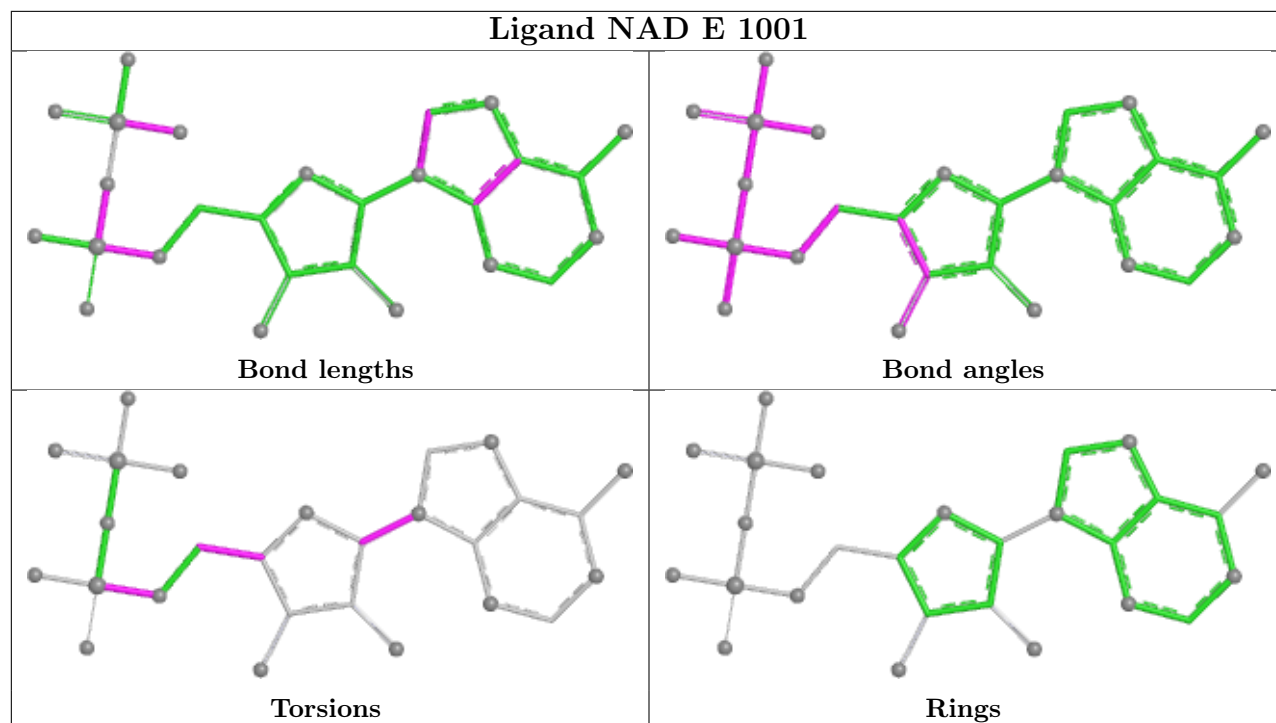
3 monomers are involved in 6 short contacts:

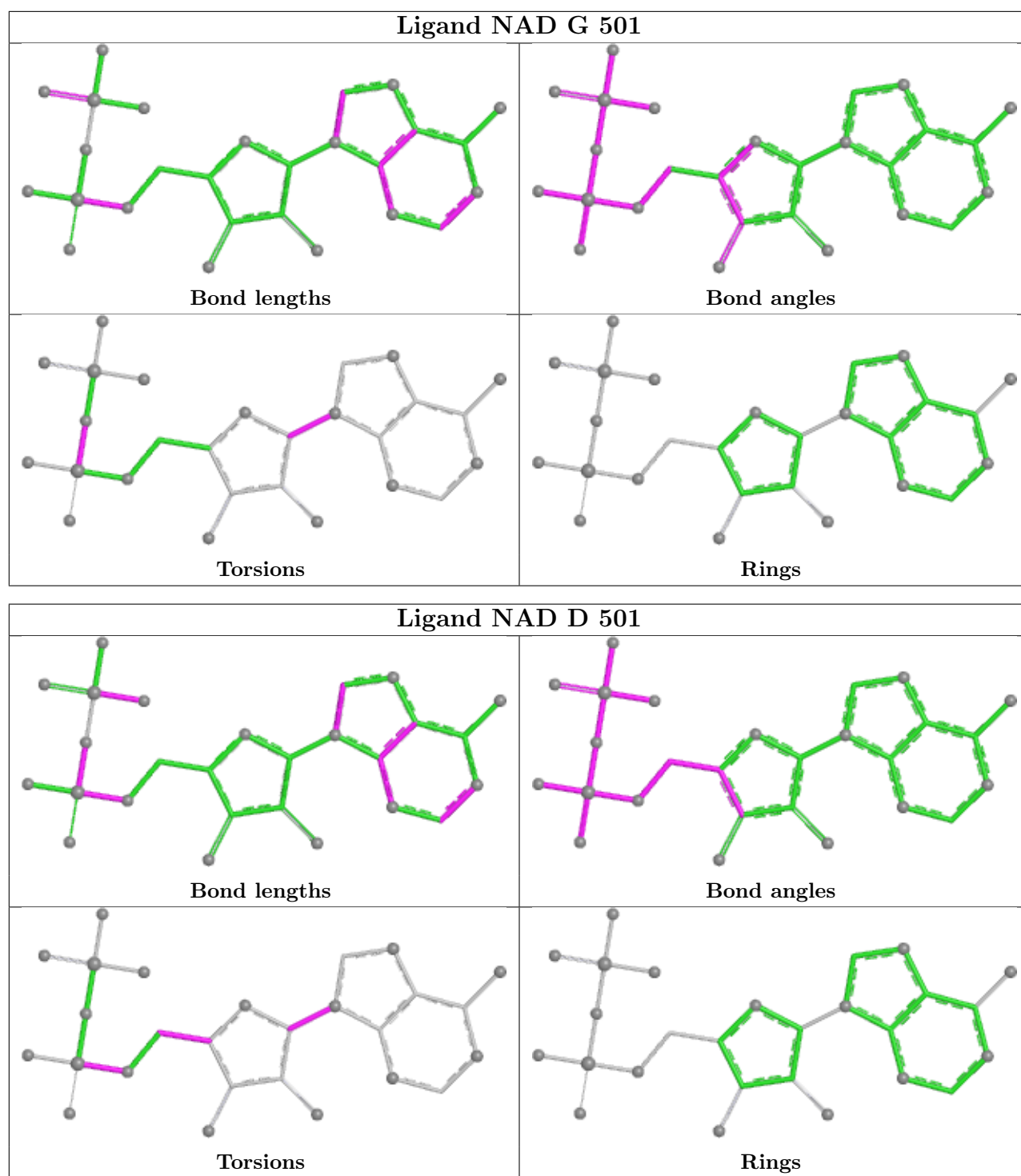
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	NAD	3	0
2	E	1001	NAD	1	0
2	D	501	NAD	2	0

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	492/493 (99%)	0.23	9 (1%) 67 64	28, 37, 47, 61	0
1	B	492/493 (99%)	0.43	11 (2%) 62 58	29, 42, 54, 83	0
1	C	492/493 (99%)	0.35	15 (3%) 52 48	27, 39, 52, 65	0
1	D	493/493 (100%)	0.36	10 (2%) 65 61	28, 37, 49, 60	0
1	E	493/493 (100%)	0.23	10 (2%) 65 61	27, 35, 46, 67	0
1	F	492/493 (99%)	0.35	11 (2%) 62 58	27, 38, 50, 66	0
1	G	493/493 (100%)	0.37	9 (1%) 67 64	28, 37, 46, 60	0
1	H	492/493 (99%)	0.33	12 (2%) 59 55	26, 37, 53, 82	0
All	All	3939/3944 (99%)	0.33	87 (2%) 62 58	26, 38, 51, 83	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	422	GLY	4.8
1	G	328	GLY	4.5
1	D	172	ALA	4.5
1	G	288	CYS	3.9
1	G	188	SER	3.6
1	F	361	VAL	3.5
1	E	201	VAL	3.5
1	H	97	ILE	3.4
1	F	288	CYS	3.4
1	A	253	LEU	3.3
1	H	247	GLY	3.3
1	A	295	PHE	3.2
1	G	289	CYS	3.2
1	C	288	CYS	3.2
1	H	367	LEU	3.1
1	G	276	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	418	GLY	3.1
1	D	394	GLY	3.1
1	E	116	CYS	3.0
1	H	288	CYS	3.0
1	C	199	ALA	3.0
1	D	253	LEU	2.9
1	A	276	ALA	2.9
1	D	197	SER	2.9
1	C	291	GLY	2.9
1	C	441	GLY	2.9
1	B	457	PHE	2.8
1	D	168	ALA	2.8
1	F	47	GLY	2.8
1	G	282	LEU	2.8
1	B	12	LEU	2.7
1	D	25	ALA	2.7
1	B	200	GLY	2.6
1	C	221	GLN	2.6
1	H	269	MET	2.6
1	C	52	ASN	2.5
1	B	150	CYS	2.5
1	C	3	THR	2.5
1	H	113	SER	2.5
1	E	288	CYS	2.5
1	C	25	ALA	2.5
1	A	195	ILE	2.4
1	E	351	ALA	2.4
1	A	442	THR	2.4
1	F	190	LEU	2.4
1	C	92	ALA	2.4
1	F	113	SER	2.4
1	C	39	VAL	2.4
1	E	162	ILE	2.3
1	G	464	GLY	2.3
1	C	6	PHE	2.3
1	B	168	ALA	2.3
1	G	58	ALA	2.3
1	E	2	SER	2.3
1	D	400	LEU	2.3
1	B	288	CYS	2.3
1	B	36	THR	2.3
1	B	425	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	422	GLY	2.3
1	F	253	LEU	2.3
1	A	32	PHE	2.3
1	A	420	ALA	2.2
1	E	357	GLY	2.2
1	H	413	ASN	2.2
1	D	379	THR	2.2
1	F	394	GLY	2.2
1	H	357	GLY	2.2
1	E	471	ARG	2.2
1	F	273	VAL	2.2
1	H	439	GLN	2.2
1	C	420	ALA	2.1
1	F	168	ALA	2.1
1	B	28	THR	2.1
1	B	231	THR	2.1
1	B	394	GLY	2.1
1	E	93	THR	2.1
1	F	418	GLY	2.1
1	H	451	SER	2.1
1	D	80	ALA	2.1
1	H	440	ALA	2.1
1	C	154	GLY	2.1
1	D	195	ILE	2.1
1	C	101	LYS	2.1
1	F	20	VAL	2.0
1	H	32	PHE	2.0
1	E	470	GLY	2.0
1	A	89	ASP	2.0

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

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

6.3 Carbohydrates ⓘ

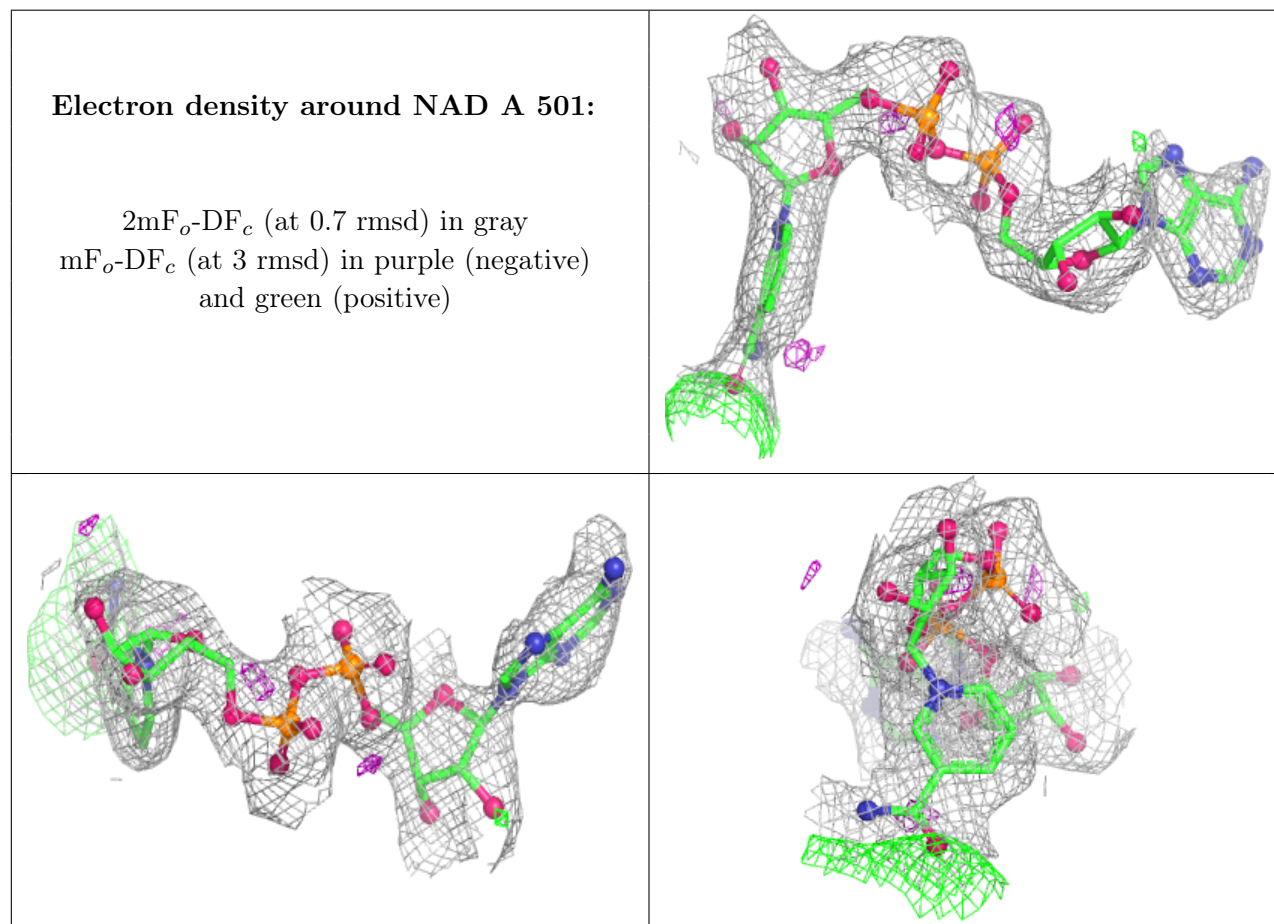
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

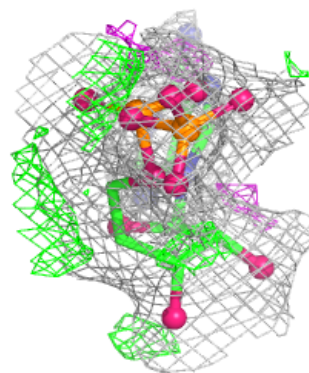
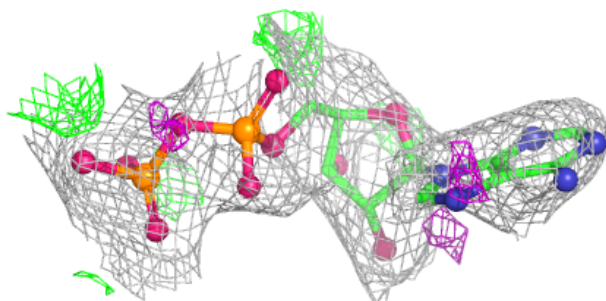
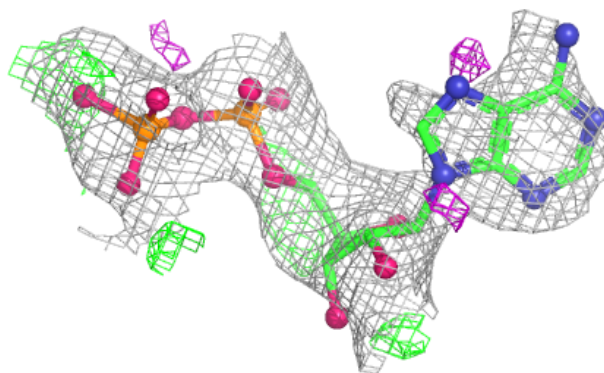
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAD	A	501	44/44	0.82	0.12	19,37,51,56	0
2	NAD	E	1001	27/44	0.88	0.11	23,43,52,54	0
2	NAD	D	501	27/44	0.89	0.11	29,39,52,53	0
2	NAD	C	501	27/44	0.90	0.12	34,46,50,53	0
2	NAD	F	501	27/44	0.90	0.10	27,34,48,53	0
2	NAD	H	501	27/44	0.91	0.11	26,40,52,54	0
2	NAD	G	501	27/44	0.93	0.09	9,34,49,63	0
2	NAD	B	501	27/44	0.93	0.09	23,38,48,53	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.

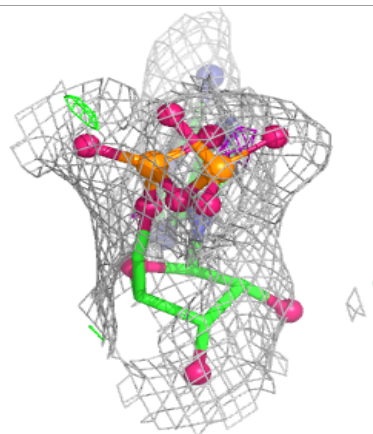
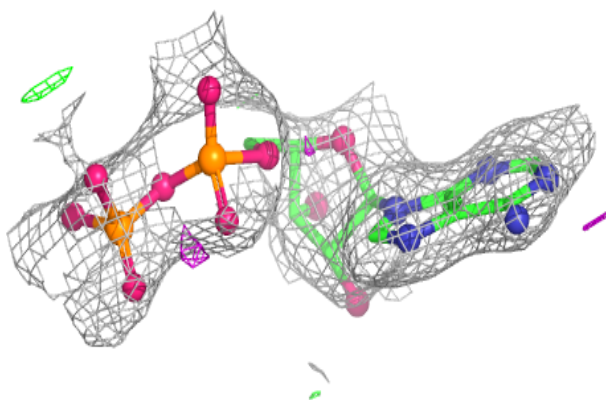
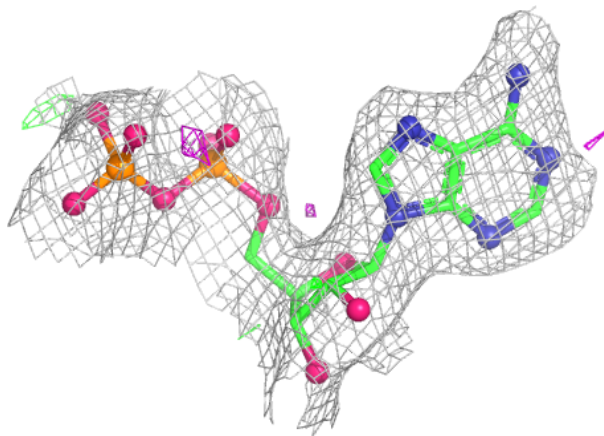


Electron density around NAD E 1001:

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

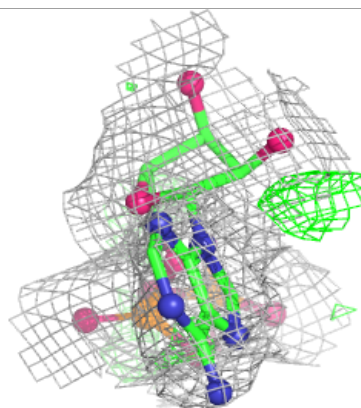
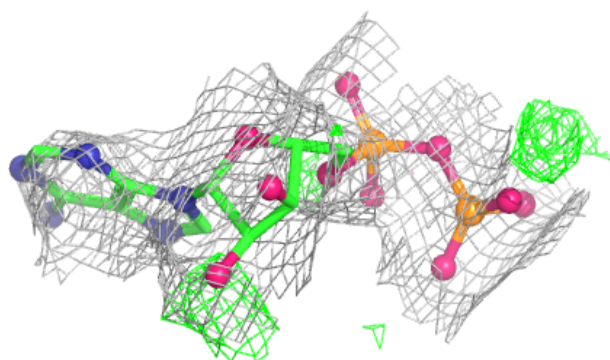
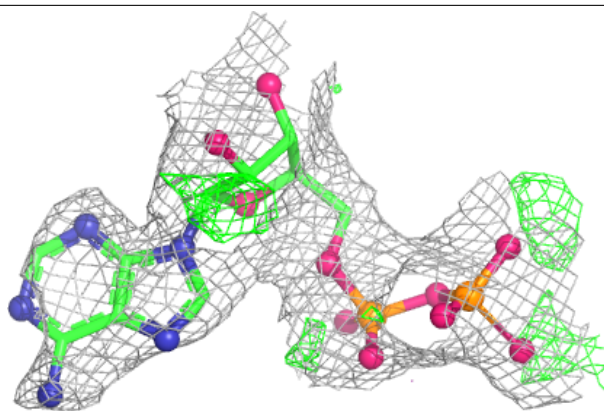
**Electron density around NAD D 501:**

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

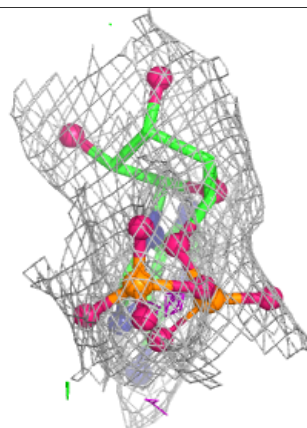
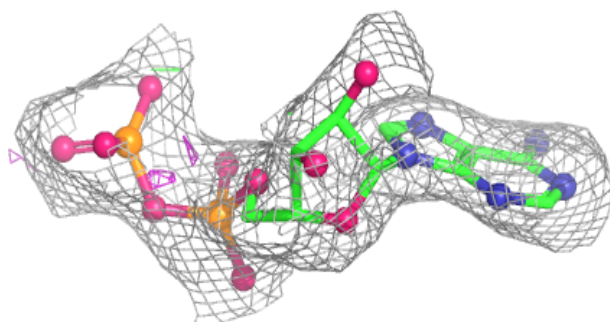
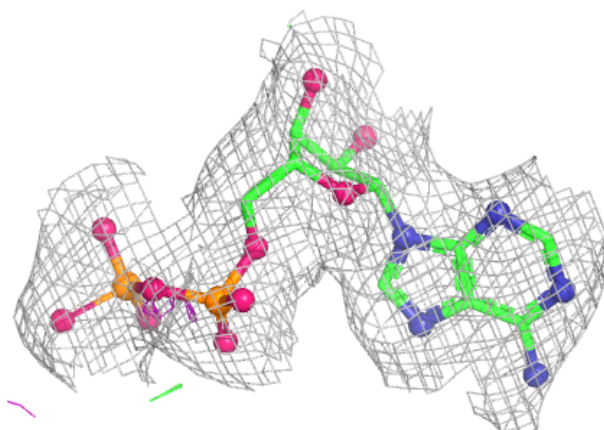


Electron density around NAD C 501:

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

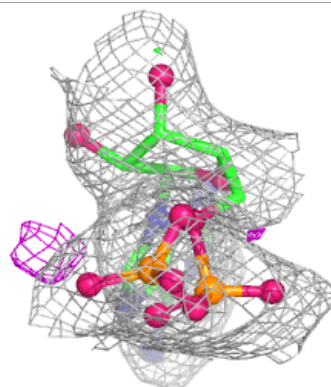
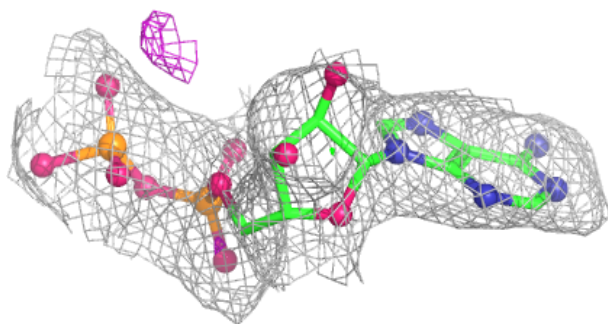
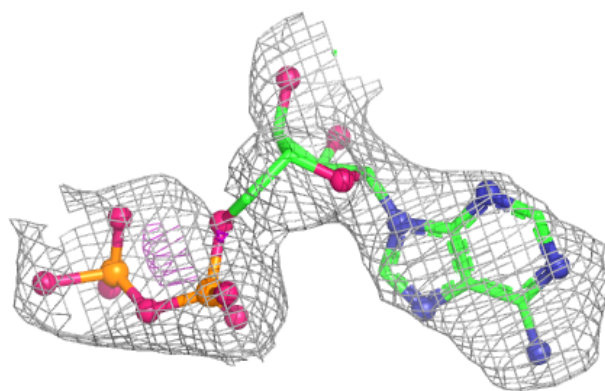
**Electron density around NAD F 501:**

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

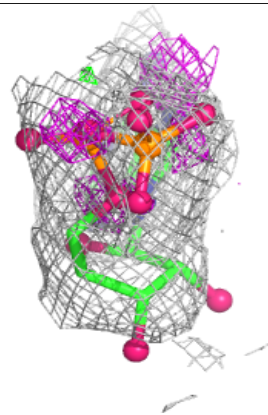
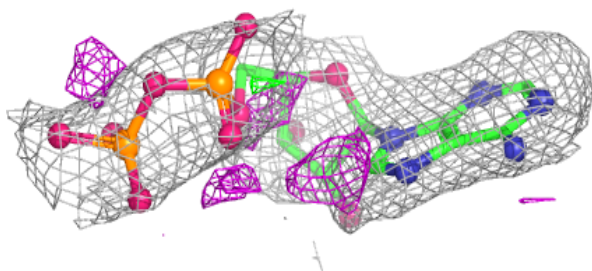
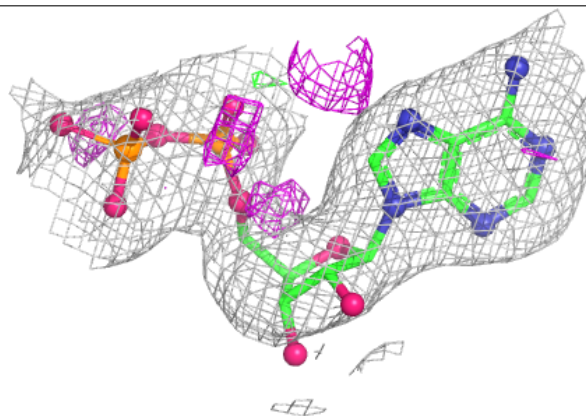


Electron density around NAD H 501:

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

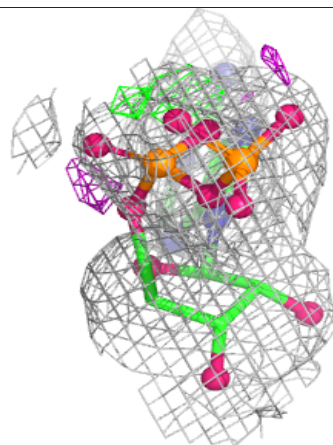
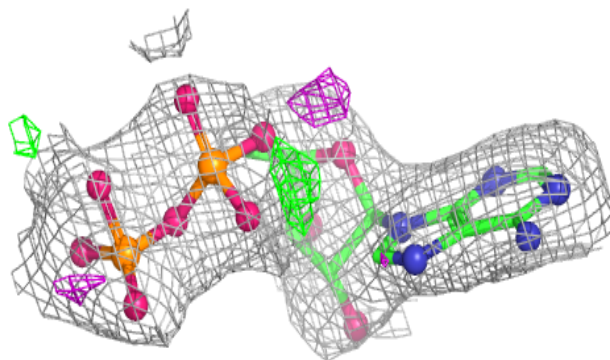
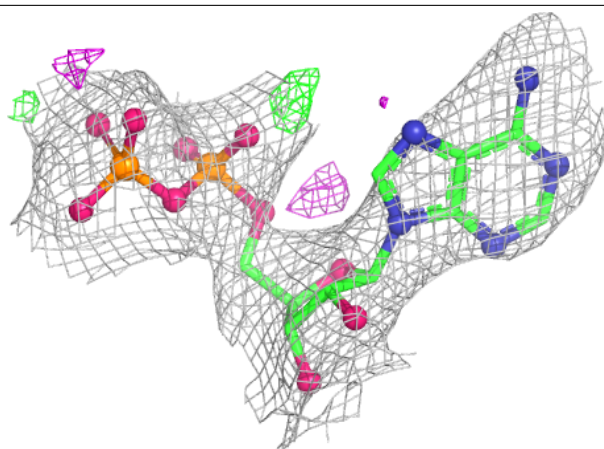
**Electron density around NAD G 501:**

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



Electron density around NAD B 501:

$2mF_o-DF_c$ (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.