



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:03 PM UTC

PDB ID : 1ZSN / pdb_00001zsn
Title : Synthesis, Biological Activity, and X-Ray Crystal Structural Analysis of Diaryl Ether Inhibitors of Malarial Enoyl ACP Reductase. Part 1:4'-Substituted Triclosan Derivatives
Authors : Freundlich, J.S.; Anderson, J.W.; Sarantakis, D.; Shieh, H.M.; Yu, M.; Lucumi, E.; Kuo, M.; Schiehser, G.A.; Jacobus, D.P.; Jacobs Jr., W.R.; Fidock, D.A.; Sacchettini, J.C.
Deposited on : 2005-05-24
Resolution : 2.99 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)

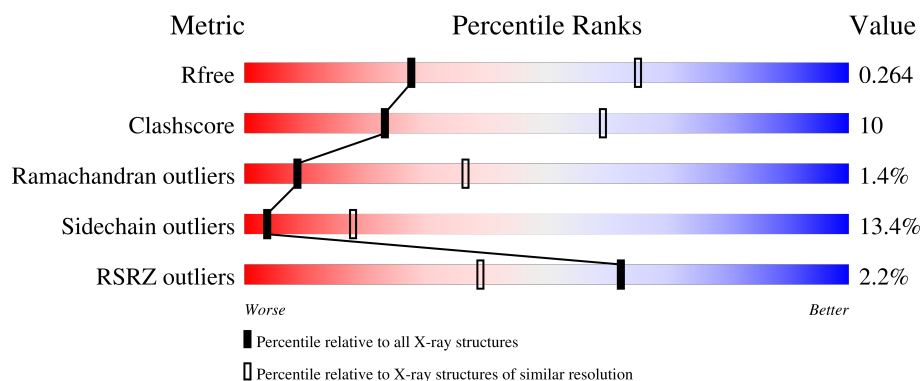
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	2% 61% 22% • 13%
1	B	336	• 56% 28% • 13%

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4764 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called enoyl-acyl carrier reductase.

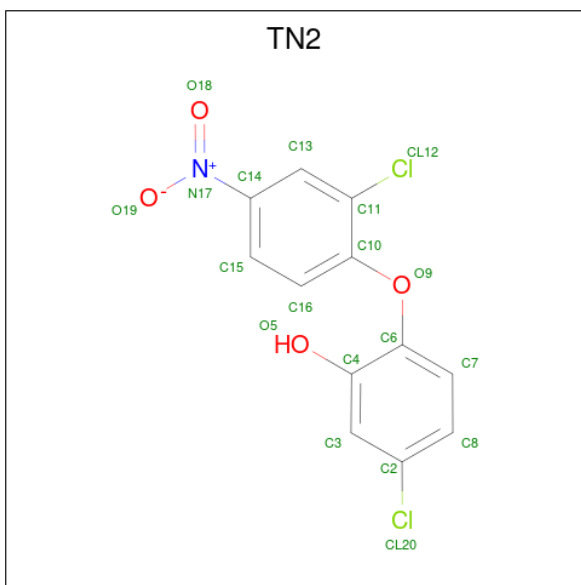
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	2	0
			2321	1479	390	441	11			
1	B	292	Total	C	N	O	S	0	0	0
			2317	1477	390	439	11			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



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

- Molecule 3 is 5-CHLORO-2-(2-CHLORO-4-NITROPHENOXY)PHENOL (CCD ID: TN2) (formula: $C_{12}H_7Cl_2NO_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			19	12	2	1	4		
3	B	1	Total	C	Cl	N	O	0	0
			19	12	2	1	4		

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	131.03Å 131.03Å 82.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.68 – 2.99 29.68 – 2.99	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.68-2.99) 99.7 (29.68-2.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.03 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.188 , 0.263 0.188 , 0.264	Depositor DCC
R_{free} test set	758 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	39.2	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4764	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% 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, TN2

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	0.73	1/2372 (0.0%)	0.96	3/3200 (0.1%)
1	B	0.73	1/2360 (0.0%)	0.96	4/3184 (0.1%)
All	All	0.73	2/4732 (0.0%)	0.96	7/6384 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	273	VAL	CA-CB	6.20	1.61	1.54
1	A	274	VAL	CA-CB	5.79	1.59	1.54

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	PRO	N-CA-C	6.68	118.86	110.70
1	B	132	PRO	CA-C-N	-6.46	112.97	119.56
1	B	132	PRO	C-N-CA	-6.46	112.97	119.56
1	B	294	VAL	N-CA-C	5.61	116.25	110.36
1	A	257	LYS	CA-C-N	-5.56	114.05	119.78
1	A	257	LYS	C-N-CA	-5.56	114.05	119.78
1	A	274	VAL	N-CA-C	5.37	113.47	108.15

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2321	0	2325	48	0
1	B	2317	0	2323	52	0
2	A	44	0	26	3	0
2	B	44	0	26	1	0
3	A	19	0	6	2	0
3	B	19	0	7	0	0
All	All	4764	0	4713	98	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 10.

All (98) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:153:ILE:HB	1:B:157:LYS:HB3	1.51	0.90
1:B:217:ALA:HA	1:B:241:SER:HB3	1.56	0.86
1:B:145:GLY:HA2	1:B:148:ASP:OD2	1.79	0.82
1:B:139:MET:SD	1:B:164:MET:CE	2.76	0.73
1:A:306:ARG:HG2	1:B:382:LEU:HD21	1.72	0.72
1:B:139:MET:SD	1:B:164:MET:HE3	2.30	0.72
1:A:167:PHE:HD1	1:A:198:VAL:HG21	1.57	0.70
1:A:256:MET:HE2	1:A:260:SER:HB3	1.74	0.69
1:A:161:ILE:HG21	1:A:164:MET:HE3	1.77	0.66
1:A:366:TYR:O	1:A:370:ASP:HB2	1.99	0.62
1:B:189:MET:HE1	1:B:190:LEU:HD23	1.83	0.60
1:A:161:ILE:HD13	1:A:164:MET:HE3	1.84	0.60
1:A:387:LEU:O	1:A:390:ASP:HB2	2.02	0.60
1:B:145:GLY:CA	1:B:148:ASP:OD2	2.50	0.60
1:A:297:TYR:HA	1:B:381:PRO:HB3	1.84	0.59
1:A:168:ASP:OD2	1:A:187:TYR:OH	2.16	0.59
1:A:167:PHE:CD1	1:A:198:VAL:HG21	2.40	0.56
1:B:217:ALA:HB1	1:B:281:MET:HE1	1.88	0.55
1:B:184:ASN:ND2	1:B:186:ARG:H	2.03	0.55
1:A:99:ILE:HB	1:A:209:ILE:HG22	1.88	0.55
1:A:175:ASN:ND2	1:A:175:ASN:H	2.04	0.54
1:B:184:ASN:HD22	1:B:186:ARG:H	1.56	0.54
1:B:366:TYR:CD2	1:B:370:ASP:HB2	2.43	0.54
1:A:277:TYR:CE2	1:A:281:MET:HB3	2.43	0.53
1:B:162:LEU:HD22	1:B:206:TYR:CE1	2.44	0.53
1:A:367:THR:C	1:A:369:ILE:H	2.17	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:MET:HE2	1:A:260:SER:CB	2.39	0.53
1:A:301:ARG:HH21	1:B:379:TYR:HA	1.73	0.52
1:A:140:LYS:HG3	1:A:144:ASN:ND2	2.23	0.52
1:B:373:ILE:O	1:B:377:GLU:HG3	2.10	0.52
1:A:169:ALA:HB1	1:A:244:SER:HB2	1.92	0.52
1:B:259:GLN:HG3	1:B:304:ASN:ND2	2.24	0.52
1:B:131:TRP:CG	1:B:133:PRO:HD2	2.45	0.52
1:B:176:ASP:O	1:B:177:ILE:C	2.53	0.51
1:A:314:PRO:HA	2:A:450:NAD:O7N	2.11	0.51
1:A:218:ASN:HA	3:A:500:TN2:O19	2.10	0.51
1:A:264:SER:HB2	1:A:288:LEU:HD21	1.91	0.51
1:B:401:ARG:NH2	1:B:404:ARG:HE	2.08	0.51
1:A:153:ILE:O	1:A:154:ASP:HB3	2.12	0.50
1:B:252:PHE:CE1	1:B:255:ILE:HD11	2.47	0.50
1:A:108:THR:HG22	1:A:113:TRP:CE2	2.48	0.49
1:A:256:MET:CE	1:A:260:SER:HB3	2.42	0.49
1:A:223:GLN:NE2	1:A:323:ILE:O	2.46	0.49
1:B:119:LEU:O	1:B:124:VAL:HG13	2.12	0.49
1:A:153:ILE:HD11	1:A:159:MET:HG3	1.94	0.49
1:A:259:GLN:HG2	1:A:304:ASN:ND2	2.27	0.49
1:B:274:VAL:HG22	1:B:274:VAL:O	2.12	0.49
1:A:366:TYR:CD2	1:A:366:TYR:N	2.81	0.48
1:A:132:PRO:HB2	1:A:133:PRO:HD3	1.95	0.48
1:A:145:GLY:HA2	1:A:148:ASP:OD2	2.13	0.48
1:B:209:ILE:O	1:B:256:MET:HA	2.13	0.47
1:B:243:TYR:CE2	1:B:247:SER:HB2	2.49	0.47
1:A:366:TYR:N	1:A:366:TYR:HD2	2.12	0.47
1:B:221:GLU:O	1:B:279:GLY:HA3	2.15	0.47
1:A:140:LYS:HG3	1:A:144:ASN:HD21	1.81	0.46
2:A:450:NAD:O1N	2:A:450:NAD:H2N	2.15	0.46
1:B:252:PHE:CD1	1:B:255:ILE:HD11	2.50	0.46
1:A:269:ALA:HA	1:A:274:VAL:HG13	1.98	0.46
1:B:163:ASP:HB2	1:B:206:TYR:OH	2.16	0.45
1:B:266:THR:HA	1:B:285:LYS:HD2	1.98	0.45
1:B:274:VAL:O	1:B:274:VAL:CG2	2.65	0.45
1:B:290:SER:HA	1:B:293:ARG:NH1	2.31	0.45
1:B:210:ASN:HA	1:B:260:SER:OG	2.16	0.45
1:B:121:LYS:C	1:B:123:ASN:H	2.26	0.44
1:B:394:VAL:HG11	1:B:413:VAL:HG21	1.99	0.44
1:B:378:LYS:HA	1:B:383:ARG:NH1	2.33	0.44
1:A:249:CYS:O	1:A:253:VAL:HB	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:TYR:O	1:B:244:SER:C	2.61	0.43
1:B:401:ARG:HA	1:B:401:ARG:HD2	1.81	0.43
1:A:266:THR:O	2:A:450:NAD:H6N	2.18	0.43
1:A:161:ILE:HD13	1:A:164:MET:CE	2.48	0.43
1:B:262:ILE:O	1:B:307:ILE:HA	2.17	0.43
1:A:301:ARG:NH2	1:B:379:TYR:HA	2.32	0.43
2:B:451:NAD:H2N	2:B:451:NAD:O1N	2.18	0.43
1:A:296:ALA:HA	1:A:307:ILE:CG2	2.48	0.43
1:A:378:LYS:HG2	1:A:379:TYR:CE2	2.54	0.43
1:B:248:LEU:O	1:B:252:PHE:HB2	2.18	0.43
1:A:159:MET:HE2	1:A:161:ILE:CG1	2.49	0.42
1:B:416:GLY:O	1:B:419:ILE:HG12	2.18	0.42
1:B:111:TYR:CE1	1:B:391:ILE:HD13	2.54	0.42
1:B:272:LYS:HD3	1:B:272:LYS:HA	1.89	0.42
1:A:175:ASN:H	1:A:175:ASN:HD22	1.65	0.42
1:A:181:THR:HA	1:A:184:ASN:HB2	2.02	0.42
1:B:382:LEU:HD12	1:B:382:LEU:HA	1.82	0.42
1:A:369:ILE:HD13	3:A:500:TN2:H8	2.01	0.42
1:B:108:THR:HG22	1:B:113:TRP:CD2	2.55	0.42
1:B:120:SER:O	1:B:121:LYS:C	2.63	0.41
1:B:258:PRO:O	1:B:259:GLN:HB2	2.20	0.41
1:A:244:SER:O	1:A:248:LEU:HB2	2.20	0.41
1:A:179:GLU:CD	1:A:179:GLU:H	2.29	0.41
1:B:189:MET:C	1:B:189:MET:SD	3.03	0.41
1:B:243:TYR:C	1:B:245:LEU:N	2.76	0.41
1:B:214:HIS:O	1:B:264:SER:HA	2.20	0.41
1:A:128:PHE:CZ	1:A:159:MET:HE1	2.55	0.41
1:B:165:LEU:HA	1:B:166:PRO:HD2	1.91	0.41
1:B:194:THR:O	1:B:198:VAL:HG22	2.20	0.41
1:A:324:ASN:CB	1:A:367:THR:HG22	2.51	0.41
1:A:159:MET:HE2	1:A:161:ILE:HG12	2.03	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	290/336 (86%)	262 (90%)	24 (8%)	4 (1%)	9	36
1	B	288/336 (86%)	261 (91%)	23 (8%)	4 (1%)	9	36
All	All	578/672 (86%)	523 (90%)	47 (8%)	8 (1%)	9	36

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	367	THR
1	A	105	ILE
1	B	154	ASP
1	A	155	LYS
1	A	368	PHE
1	B	156	ASP
1	B	177	ILE
1	B	323	ILE

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	255/295 (86%)	220 (86%)	35 (14%)	3	17
1	B	253/295 (86%)	220 (87%)	33 (13%)	4	19
All	All	508/590 (86%)	440 (87%)	68 (13%)	4	18

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	ILE
1	A	105	ILE
1	A	109	ASN
1	A	137	ILE
1	A	155	LYS

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Mol	Chain	Res	Type
1	A	156	ASP
1	A	162	LEU
1	A	175	ASN
1	A	179	GLU
1	A	186	ARG
1	A	191	GLN
1	A	201	LEU
1	A	218	ASN
1	A	223	GLN
1	A	226	LEU
1	A	227	LEU
1	A	232	LYS
1	A	236	ASP
1	A	238	LEU
1	A	248	LEU
1	A	254	ASN
1	A	264	SER
1	A	273	VAL
1	A	274	VAL
1	A	290	SER
1	A	311	SER
1	A	321	THR
1	A	366	TYR
1	A	374	GLU
1	A	382	LEU
1	A	384	GLN
1	A	385	LYS
1	A	417	LEU
1	A	426	ILE
1	A	429	ASN
1	B	105	ILE
1	B	120	SER
1	B	124	VAL
1	B	134	VAL
1	B	137	ILE
1	B	146	LYS
1	B	155	LYS
1	B	160	ASN
1	B	162	LEU
1	B	177	ILE
1	B	181	THR
1	B	182	LYS

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Mol	Chain	Res	Type
1	B	198	VAL
1	B	201	LEU
1	B	208	LYS
1	B	218	ASN
1	B	223	GLN
1	B	226	LEU
1	B	227	LEU
1	B	232	LYS
1	B	238	LEU
1	B	248	LEU
1	B	253	VAL
1	B	273	VAL
1	B	274	VAL
1	B	283	SER
1	B	311	SER
1	B	366	TYR
1	B	367	THR
1	B	382	LEU
1	B	384	GLN
1	B	417	LEU
1	B	426	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	144	ASN
1	A	175	ASN
1	A	184	ASN
1	A	188	ASN
1	A	191	GLN
1	A	200	ASN
1	A	218	ASN
1	A	302	ASN
1	A	304	ASN
1	A	415	ASN
1	B	123	ASN
1	B	184	ASN
1	B	188	ASN
1	B	200	ASN
1	B	218	ASN
1	B	223	GLN
1	B	304	ASN

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Mol	Chain	Res	Type
1	B	384	GLN
1	B	415	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 ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	TN2	B	501	-	20,20,20	1.08	2 (10%)	26,28,28	1.14	3 (11%)
3	TN2	A	500	-	20,20,20	1.06	1 (5%)	26,28,28	1.25	4 (15%)
2	NAD	A	450	-	46,48,48	1.57	6 (13%)	64,73,73	1.82	12 (18%)
2	NAD	B	451	-	46,48,48	1.52	4 (8%)	64,73,73	1.80	15 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TN2	B	501	-	-	0/6/8/8	0/2/2/2
3	TN2	A	500	-	-	0/6/8/8	0/2/2/2
2	NAD	A	450	-	-	7/30/62/62	0/5/5/5
2	NAD	B	451	-	-	11/30/62/62	0/5/5/5

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	451	NAD	C5A-C4A	5.70	1.49	1.39
2	A	450	NAD	C5A-C4A	5.45	1.48	1.39
2	B	451	NAD	O7N-C7N	5.23	1.33	1.24
2	A	450	NAD	O7N-C7N	4.53	1.32	1.24
2	B	451	NAD	C7N-N7N	-3.83	1.25	1.33
2	A	450	NAD	C7N-N7N	-3.52	1.26	1.33
2	A	450	NAD	PA-O3	3.19	1.62	1.59
2	A	450	NAD	C8A-N7A	2.91	1.37	1.31
2	A	450	NAD	PN-O3	2.81	1.62	1.59
2	B	451	NAD	C8A-N7A	2.77	1.37	1.31
3	A	500	TN2	C11-CL12	2.63	1.79	1.73
3	B	501	TN2	C2-CL20	2.31	1.79	1.74
3	B	501	TN2	C11-CL12	2.01	1.78	1.73

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	451	NAD	C5A-C4A-N3A	-5.92	118.56	126.72
2	A	450	NAD	C5A-C4A-N3A	-5.36	119.33	126.72
2	A	450	NAD	N3A-C4A-N9A	4.72	135.19	127.17
2	A	450	NAD	C3N-C7N-N7N	4.71	123.54	117.74
2	B	451	NAD	N3A-C4A-N9A	4.40	134.65	127.17
2	A	450	NAD	N3A-C2A-N1A	-4.37	121.96	128.58
2	B	451	NAD	C4A-C5A-N7A	-4.12	105.87	110.58
2	B	451	NAD	N3A-C2A-N1A	-3.83	122.79	128.58
2	A	450	NAD	C4A-N9A-C8A	3.79	109.72	105.74
2	B	451	NAD	O7N-C7N-N7N	-3.74	117.22	122.62
2	A	450	NAD	O7N-C7N-N7N	-3.51	117.54	122.62
2	A	450	NAD	C4A-C5A-N7A	-3.37	106.73	110.58
2	B	451	NAD	C2A-N3A-C4A	3.25	119.76	111.83
2	A	450	NAD	C2A-N3A-C4A	3.23	119.71	111.83
3	A	500	TN2	C13-C14-N17	2.88	121.22	118.74
2	A	450	NAD	C5A-N7A-C8A	2.86	107.94	103.45
3	A	500	TN2	C13-C11-CL12	2.83	123.08	118.45
2	B	451	NAD	C5A-N7A-C8A	2.72	107.73	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	450	NAD	N9A-C8A-N7A	-2.68	110.13	113.94
2	B	451	NAD	C6N-N1N-C1D	-2.61	114.61	119.73
3	A	500	TN2	C10-C11-CL12	-2.59	116.48	119.44
3	B	501	TN2	C6-O9-C10	2.54	124.15	118.09
2	B	451	NAD	O3D-C3D-C4D	-2.42	104.13	111.08
2	B	451	NAD	C3N-C7N-N7N	2.39	120.69	117.74
2	A	450	NAD	C2A-N1A-C6A	2.39	122.65	118.73
3	A	500	TN2	O9-C6-C4	2.33	120.53	116.59
2	B	451	NAD	C4A-N9A-C8A	2.30	108.15	105.74
3	B	501	TN2	O18-N17-C14	2.26	121.93	118.82
2	A	450	NAD	C4B-O4B-C1B	-2.17	104.67	109.47
2	B	451	NAD	C6A-C5A-N7A	2.12	136.17	132.09
2	B	451	NAD	C5B-C4B-C3B	-2.06	107.81	115.21
3	B	501	TN2	C13-C14-N17	2.04	120.50	118.74
2	B	451	NAD	O7N-C7N-C3N	2.04	122.09	119.60
2	B	451	NAD	O3-PN-O1N	-2.03	104.59	110.70

There are no chirality outliers.

All (18) torsion outliers are listed below:

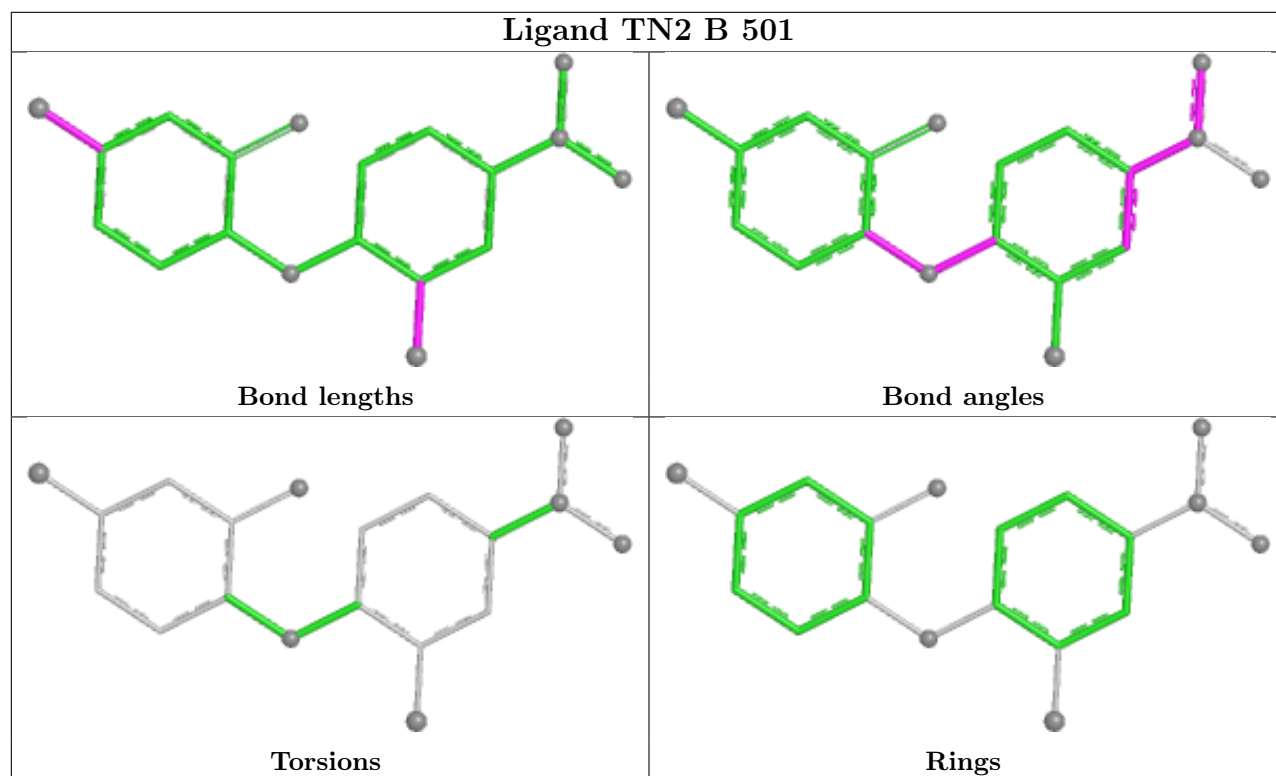
Mol	Chain	Res	Type	Atoms
2	A	450	NAD	C5D-O5D-PN-O3
2	B	451	NAD	C5B-O5B-PA-O1A
2	B	451	NAD	C5B-O5B-PA-O3
2	B	451	NAD	C5D-O5D-PN-O3
2	B	451	NAD	C5D-O5D-PN-O1N
2	B	451	NAD	C5D-O5D-PN-O2N
2	B	451	NAD	O4B-C4B-C5B-O5B
2	B	451	NAD	C3B-C4B-C5B-O5B
2	A	450	NAD	C3B-C4B-C5B-O5B
2	A	450	NAD	O4B-C4B-C5B-O5B
2	B	451	NAD	PN-O3-PA-O5B
2	A	450	NAD	C5D-O5D-PN-O1N
2	B	451	NAD	C5B-O5B-PA-O2A
2	B	451	NAD	C4B-C5B-O5B-PA
2	A	450	NAD	O4D-C1D-N1N-C2N
2	A	450	NAD	O4D-C1D-N1N-C6N
2	B	451	NAD	O4D-C1D-N1N-C6N
2	A	450	NAD	C4D-C5D-O5D-PN

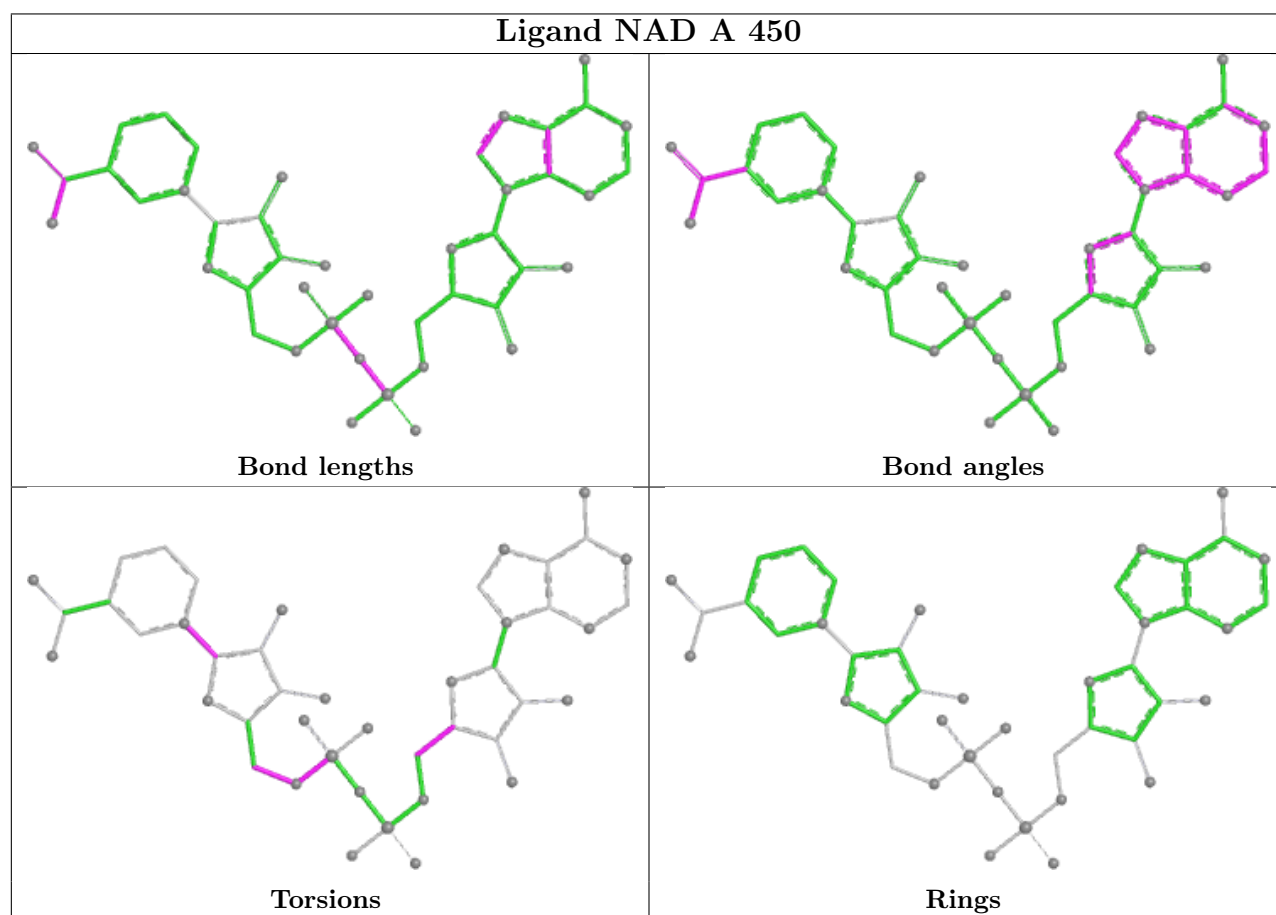
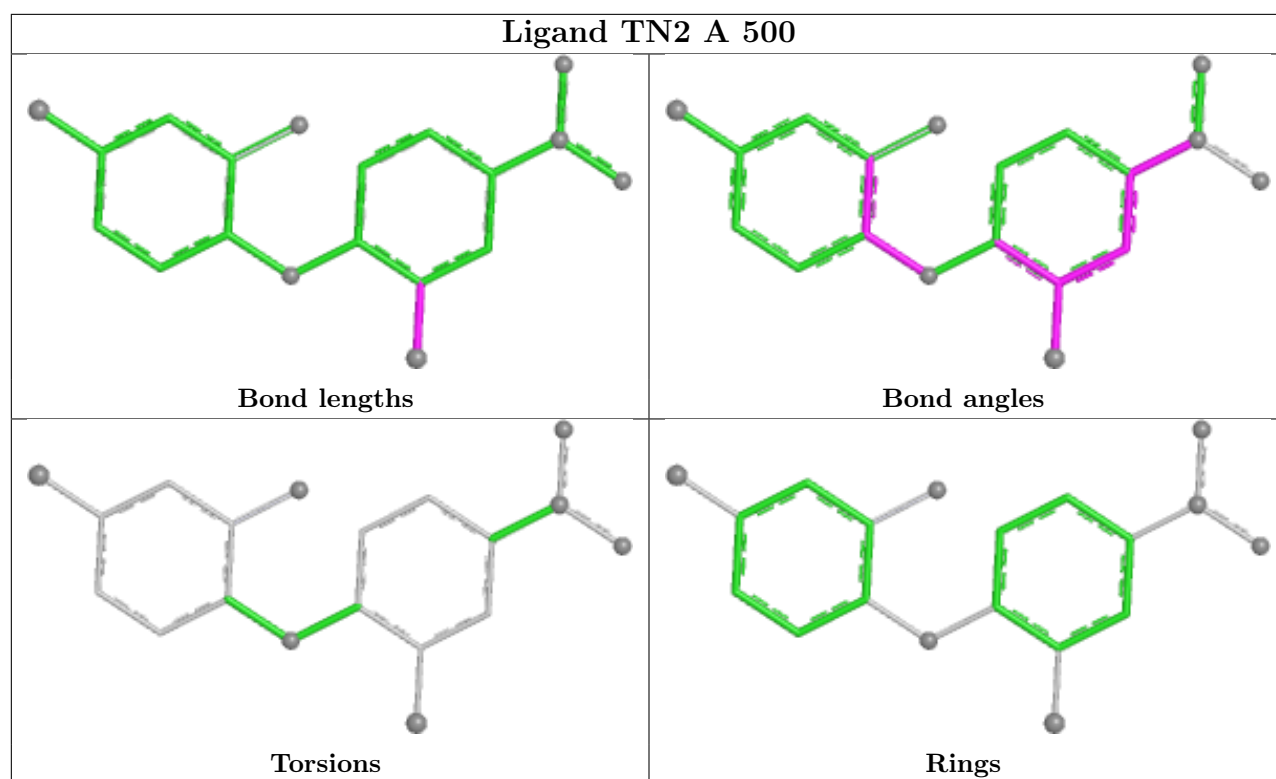
There are no ring outliers.

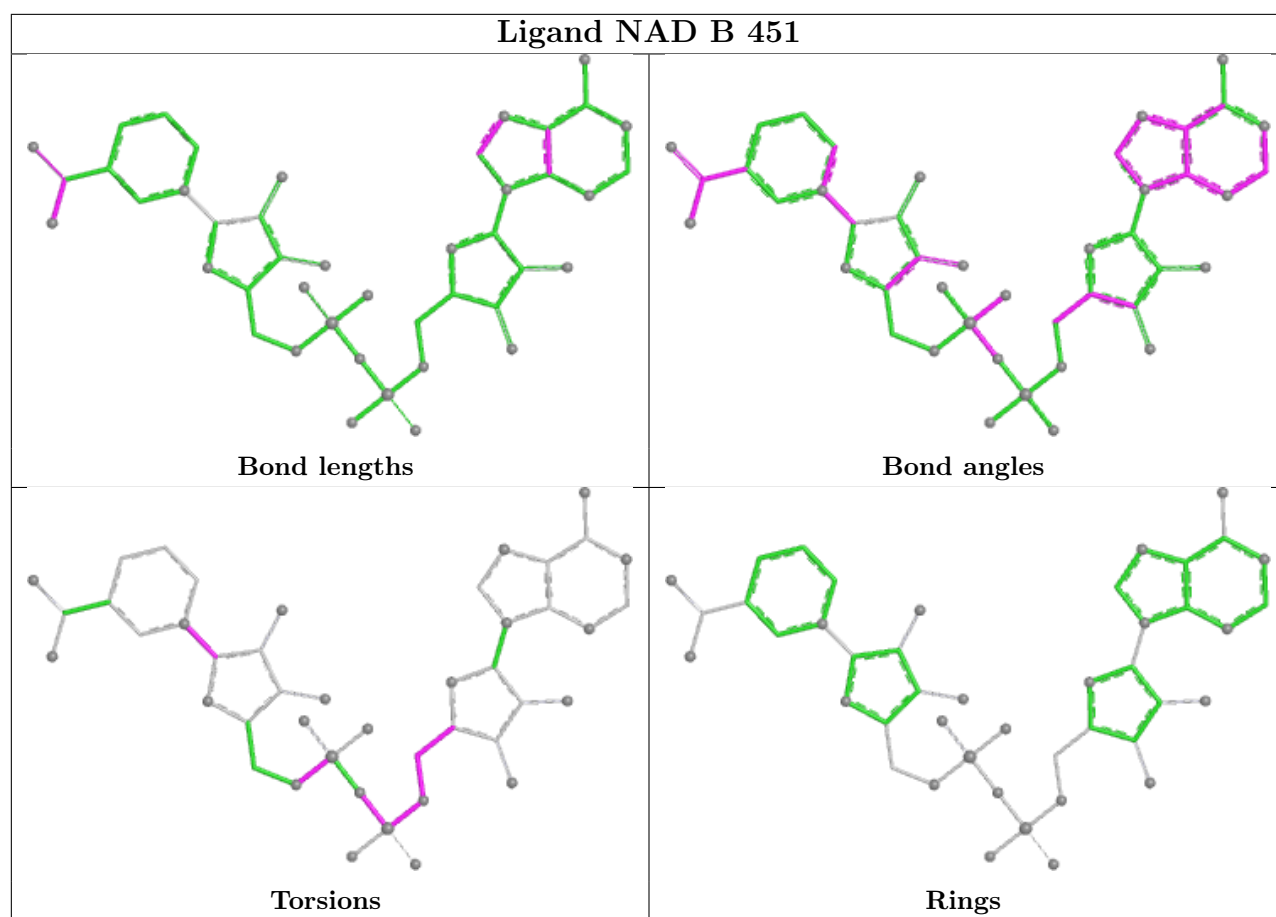
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	500	TN2	2	0
2	A	450	NAD	3	0
2	B	451	NAD	1	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	292/336 (86%)	-0.12	8 (2%)	56 33	10, 25, 57, 80	2 (0%)
1	B	292/336 (86%)	-0.18	5 (1%)	69 45	10, 25, 57, 91	0
All	All	584/672 (86%)	-0.15	13 (2%)	62 39	10, 25, 57, 91	2 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	368	PHE	5.3
1	A	366	TYR	5.0
1	A	368	PHE	4.5
1	A	426	ILE	3.9
1	A	156	ASP	3.5
1	B	366	TYR	3.1
1	B	155	LYS	2.8
1	B	427	TYR	2.8
1	A	178	ASP	2.8
1	B	160	ASN	2.4
1	A	182	LYS	2.3
1	A	186	ARG	2.2
1	A	183	ASN	2.2

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](#)

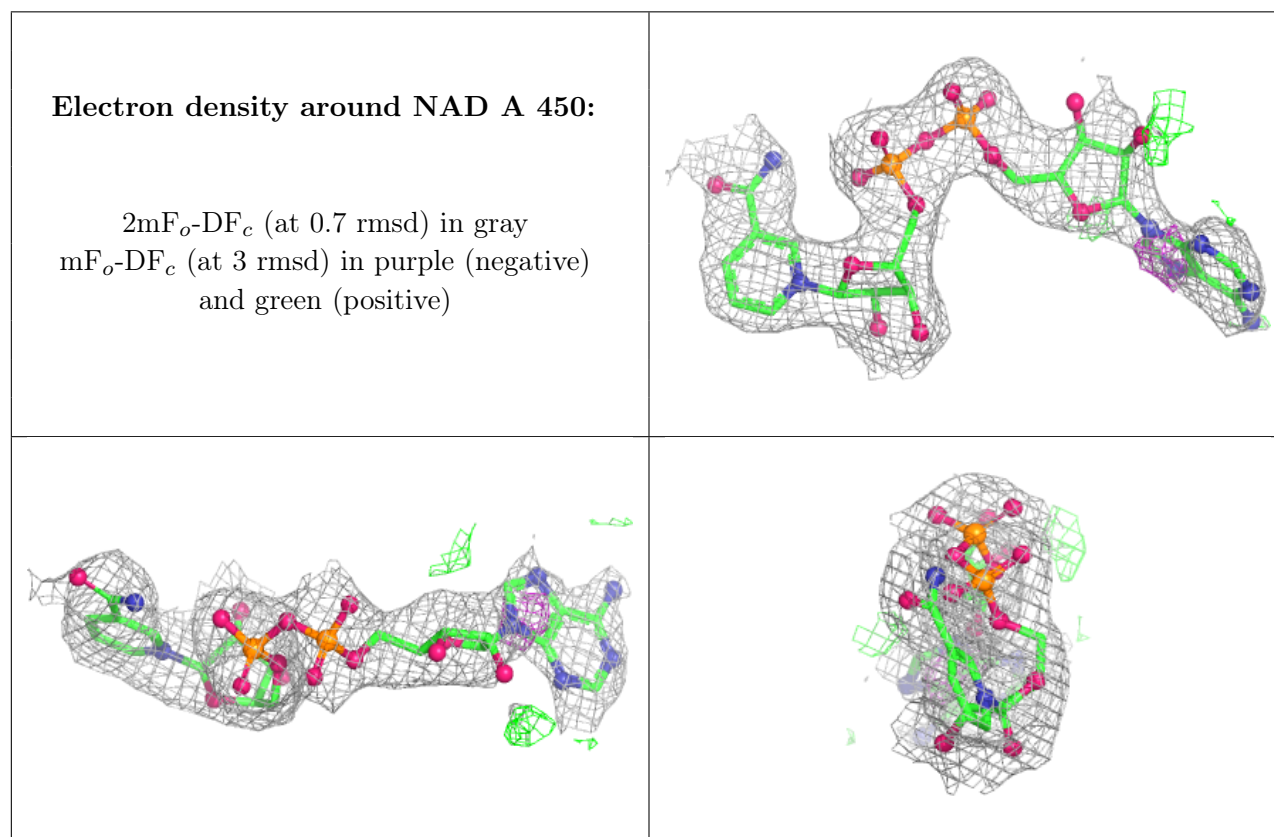
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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.

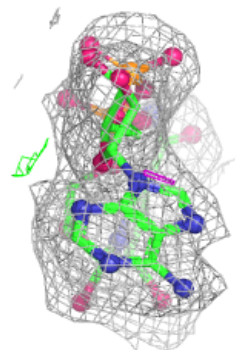
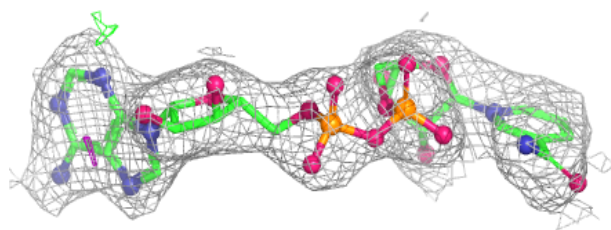
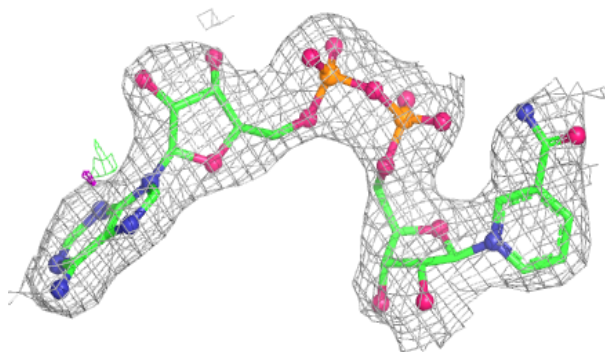
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAD	A	450	44/44	0.96	0.09	2,24,43,48	0
2	NAD	B	451	44/44	0.96	0.09	8,26,39,46	0
3	TN2	B	501	19/19	0.96	0.08	15,23,34,36	0
3	TN2	A	500	19/19	0.97	0.06	12,24,32,33	0

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.

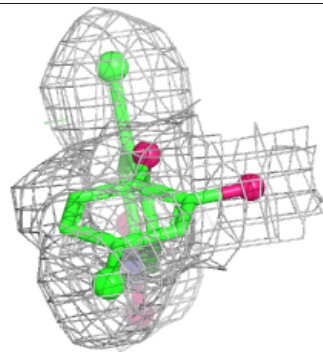
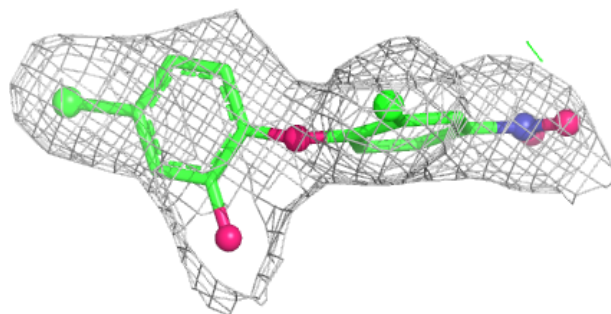
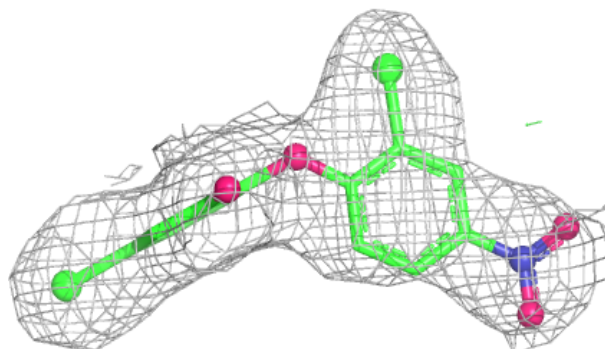


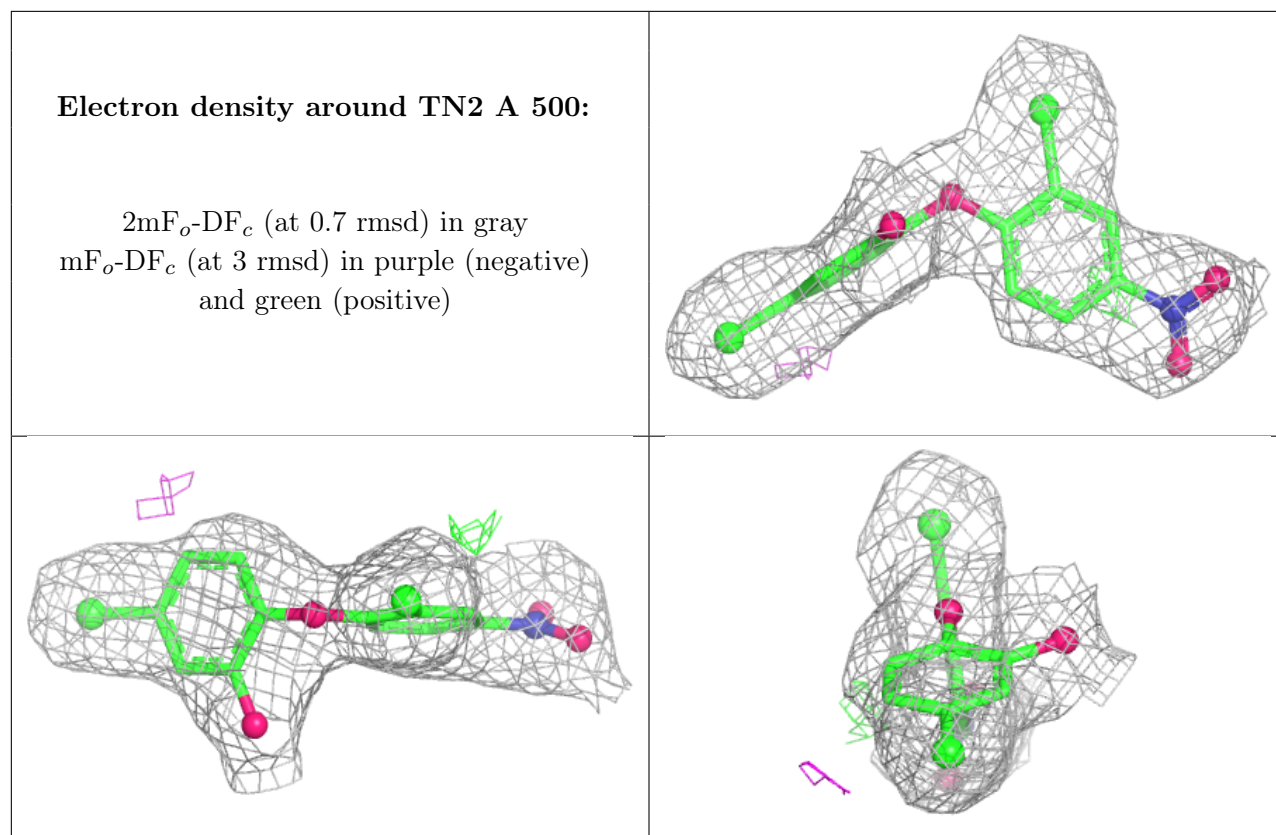
Electron density around NAD B 451:

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

**Electron density around TN2 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.