



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:51 PM UTC

PDB ID : 2OP1 / pdb_00002op1
Title : Crystal structure of plasmodium falciparum enoyl ACP reductase with tri-closan reductase
Authors : Tsai, H.
Deposited on : 2007-01-26
Resolution : 2.60 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

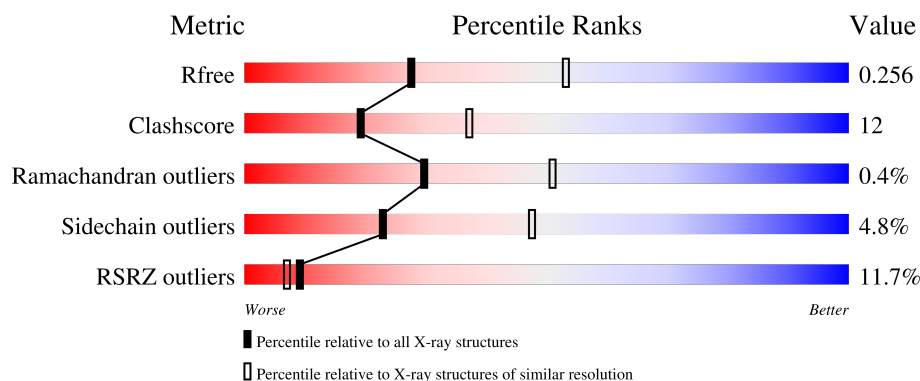
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	338	10% 65% 15% • 18%
1	B	338	9% 67% 15% • 17%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	8PC	A	500	-	-	X	-
3	8PC	B	500	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4656 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	277	Total	C	N	O	S	0	0	0
			2192	1400	366	415	11			
1	B	280	Total	C	N	O	S	0	0	0
			2207	1408	372	416	11			

There are 16 discrepancies between the modelled and reference sequences:

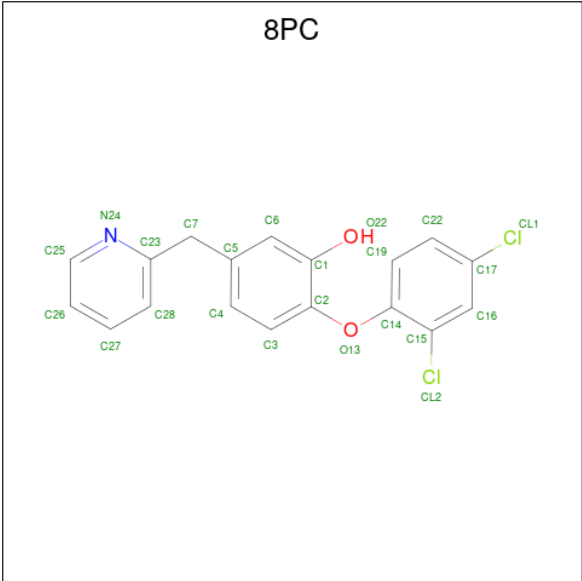
Chain	Residue	Modelled	Actual	Comment	Reference
A	88	MET	-	cloning artifact	UNP Q9BH77
A	89	VAL	-	cloning artifact	UNP Q9BH77
A	90	HIS	-	expression tag	UNP Q9BH77
A	91	HIS	-	expression tag	UNP Q9BH77
A	92	HIS	-	expression tag	UNP Q9BH77
A	93	HIS	-	expression tag	UNP Q9BH77
A	94	HIS	-	expression tag	UNP Q9BH77
A	95	HIS	-	expression tag	UNP Q9BH77
B	88	MET	-	cloning artifact	UNP Q9BH77
B	89	VAL	-	cloning artifact	UNP Q9BH77
B	90	HIS	-	expression tag	UNP Q9BH77
B	91	HIS	-	expression tag	UNP Q9BH77
B	92	HIS	-	expression tag	UNP Q9BH77
B	93	HIS	-	expression tag	UNP Q9BH77
B	94	HIS	-	expression tag	UNP Q9BH77
B	95	HIS	-	expression tag	UNP Q9BH77

- 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 2-(2,4-DICHLOROPHENOXY)-5-(PYRIDIN-2-YLMETHYL)PHENOL (CCD ID: 8PC) (formula: C₁₈H₁₃Cl₂NO₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			23	18	2	1	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	Cl	N	O	0	0
			23	18	2	1	2		

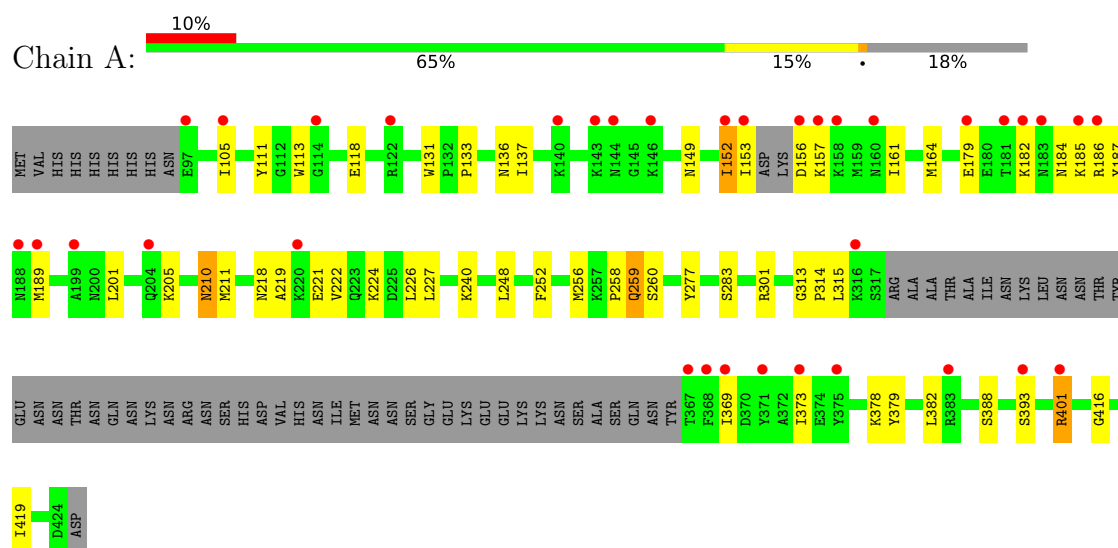
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	58	Total	O	0	0
			58	58		
4	B	65	Total	O	0	0
			65	65		

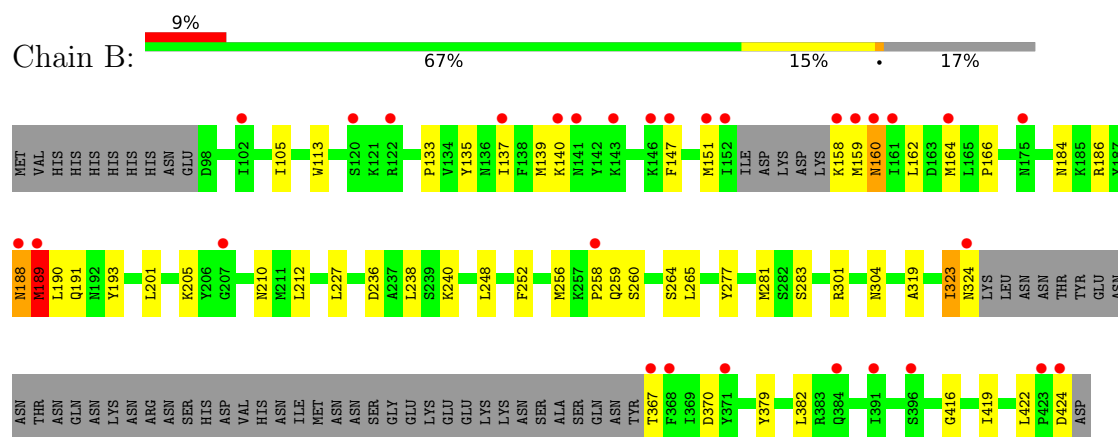
3 Residue-property plots [i](#)

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

• Molecule 1: Enoyl-acyl carrier reductase



• Molecule 1: Enoyl-acyl carrier reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	131.50Å 131.50Å 82.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 30.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	94.9 (30.00-2.60) 98.9 (30.00-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.61Å)	Xtriage
Refinement program	PHENIX, REFMAC	Depositor
R, R_{free}	0.207 , 0.270 0.259 , 0.256	Depositor DCC
R_{free} test set	1148 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	44.2	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4656	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 3.37% 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, 8PC

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	0.40	0/2232	0.73	0/3009
1	B	0.39	0/2247	0.78	4/3031 (0.1%)
All	All	0.40	0/4479	0.76	4/6040 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	258	PRO	N-CA-C	-6.51	100.81	111.68
1	B	188	ASN	CA-C-N	6.24	132.92	121.70
1	B	188	ASN	C-N-CA	6.24	132.92	121.70
1	B	188	ASN	N-CA-C	5.13	121.73	110.80

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	2192	0	2201	63	0
1	B	2207	0	2219	44	0
2	A	44	0	26	4	0
2	B	44	0	26	0	0
3	A	23	0	13	13	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	23	0	12	8	0
4	A	58	0	0	0	0
4	B	65	0	0	1	0
All	All	4656	0	4497	106	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 12.

All (106) 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:401:ARG:HG2	1:A:401:ARG:HH11	1.14	1.09
1:A:369:ILE:HA	3:A:500:8PC:H27	1.42	1.01
3:A:500:8PC:H28	3:A:500:8PC:H4	1.47	0.97
1:A:259:GLN:HE21	1:A:401:ARG:NH2	1.63	0.95
1:B:188:ASN:HB3	1:B:189:MET:HG2	1.49	0.93
1:A:401:ARG:HG2	1:A:401:ARG:NH1	1.78	0.93
1:B:188:ASN:HB3	1:B:189:MET:HB2	1.49	0.92
1:B:188:ASN:CB	1:B:189:MET:HB2	2.00	0.91
1:B:188:ASN:HB3	1:B:189:MET:CB	2.01	0.91
1:A:259:GLN:NE2	1:A:401:ARG:HH22	1.68	0.91
1:B:188:ASN:HB3	1:B:189:MET:CG	2.05	0.86
1:A:111:TYR:HE2	2:A:450:NAD:C2N	1.88	0.86
1:A:259:GLN:HE21	1:A:401:ARG:HH22	0.86	0.85
1:A:401:ARG:HH11	1:A:401:ARG:CG	1.92	0.81
1:A:161:ILE:HG21	1:A:164:MET:HE3	1.66	0.76
1:B:184:ASN:ND2	1:B:186:ARG:H	1.84	0.74
1:A:369:ILE:CA	3:A:500:8PC:H27	2.17	0.74
1:B:319:ALA:CB	3:B:500:8PC:CL2	2.73	0.73
1:B:319:ALA:HB1	3:B:500:8PC:CL2	2.27	0.71
1:A:252:PHE:O	1:A:256:MET:HG3	1.90	0.71
1:B:323:ILE:HD12	3:B:500:8PC:H27	1.71	0.71
1:A:218:ASN:HB3	1:A:240:LYS:HD3	1.74	0.68
1:A:256:MET:HE2	1:A:260:SER:HB3	1.76	0.68
1:B:188:ASN:CA	1:B:189:MET:HB2	2.24	0.67
1:A:153:ILE:HB	1:A:157:LYS:HB3	1.75	0.67
1:A:201:LEU:HD22	1:A:205:LYS:HE3	1.76	0.67
1:B:367:THR:HA	1:B:370:ASP:OD2	1.96	0.65
1:A:259:GLN:NE2	1:A:401:ARG:NH2	2.37	0.65
3:A:500:8PC:H4	3:A:500:8PC:C28	2.25	0.65
1:A:136:ASN:HB2	1:A:186:ARG:NH1	2.13	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:500:8PC:H28	3:A:500:8PC:C4	2.26	0.64
1:A:222:VAL:HG21	3:A:500:8PC:H22	1.79	0.63
1:A:161:ILE:HD13	1:A:164:MET:HE3	1.80	0.62
1:A:258:PRO:C	1:A:259:GLN:HG2	2.24	0.62
1:B:184:ASN:HD22	1:B:186:ARG:H	1.47	0.62
1:B:281:MET:HG3	3:B:500:8PC:H22	1.81	0.62
1:A:369:ILE:HA	3:A:500:8PC:C27	2.25	0.61
1:A:277:TYR:HE1	3:A:500:8PC:C6	2.13	0.61
1:A:258:PRO:O	1:A:259:GLN:HG2	2.02	0.60
1:A:219:ALA:N	3:A:500:8PC:CL1	2.70	0.59
1:A:379:TYR:HA	1:B:301:ARG:NH2	2.17	0.59
1:A:111:TYR:CE2	2:A:450:NAD:C2N	2.79	0.59
1:B:201:LEU:HD11	1:B:205:LYS:HE2	1.84	0.59
1:B:252:PHE:O	1:B:256:MET:HG3	2.02	0.58
1:B:259:GLN:HG2	1:B:304:ASN:ND2	2.20	0.57
1:B:139:MET:SD	1:B:164:MET:HE3	2.45	0.57
1:A:259:GLN:HG3	1:A:401:ARG:NH2	2.20	0.56
1:A:369:ILE:HD13	3:A:500:8PC:H28	1.88	0.56
1:A:378:LYS:HD2	1:A:379:TYR:CE2	2.41	0.55
1:B:277:TYR:OH	3:B:500:8PC:O22	2.20	0.55
3:B:500:8PC:C4	3:B:500:8PC:H28	2.36	0.55
1:A:301:ARG:NH2	1:B:379:TYR:HA	2.21	0.55
1:A:378:LYS:HD2	1:A:379:TYR:CZ	2.41	0.55
1:A:314:PRO:HA	2:A:450:NAD:O7N	2.06	0.54
1:B:264:SER:C	1:B:265:LEU:HD12	2.32	0.54
1:B:281:MET:HG3	3:B:500:8PC:C22	2.39	0.53
1:A:161:ILE:HD13	1:A:164:MET:CE	2.38	0.53
1:B:160:ASN:C	1:B:160:ASN:HD22	2.17	0.52
1:B:105:ILE:HD11	1:B:113:TRP:HE3	1.75	0.52
1:A:111:TYR:HE2	2:A:450:NAD:C3N	2.23	0.51
1:A:277:TYR:CE1	3:A:500:8PC:C6	2.93	0.51
1:A:179:GLU:CD	1:A:182:LYS:HD3	2.37	0.50
1:A:149:ASN:O	1:A:152:ILE:HG12	2.12	0.50
1:A:131:TRP:CE2	1:A:133:PRO:HG2	2.47	0.49
1:B:151:MET:HE3	1:B:158:LYS:HE3	1.94	0.48
1:A:301:ARG:HH21	1:B:379:TYR:C	2.21	0.48
1:A:105:ILE:HD11	1:A:113:TRP:HE3	1.78	0.48
3:A:500:8PC:C28	3:A:500:8PC:C4	2.82	0.48
1:A:256:MET:HE2	1:A:260:SER:CB	2.44	0.48
1:A:111:TYR:OH	1:A:313:GLY:O	2.32	0.47
1:A:131:TRP:CG	1:A:133:PRO:HD2	2.48	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:ASN:HA	1:A:260:SER:OG	2.14	0.47
1:B:210:ASN:HA	1:B:260:SER:OG	2.15	0.47
1:A:184:ASN:HD22	1:A:187:TYR:HD2	1.62	0.47
1:B:166:PRO:HD2	4:B:606:HOH:O	2.14	0.47
1:A:379:TYR:HA	1:B:301:ARG:HH22	1.80	0.46
1:B:137:ILE:CD1	1:B:140:LYS:HE2	2.45	0.46
1:B:133:PRO:O	1:B:186:ARG:HD3	2.16	0.46
1:B:137:ILE:HD12	1:B:140:LYS:HE2	1.99	0.45
1:A:416:GLY:O	1:A:419:ILE:HG12	2.17	0.45
1:A:184:ASN:ND2	1:A:187:TYR:HD2	2.14	0.45
1:A:118:GLU:HG3	1:A:393:SER:N	2.32	0.45
1:A:131:TRP:CZ2	1:A:133:PRO:HG2	2.52	0.45
1:A:189:MET:HA	1:A:189:MET:HE2	1.99	0.45
1:A:379:TYR:C	1:B:301:ARG:HH21	2.26	0.43
1:A:136:ASN:HB2	1:A:186:ARG:HH12	1.83	0.43
1:B:166:PRO:HB2	1:B:193:TYR:HB3	1.99	0.43
1:B:147:PHE:O	1:B:151:MET:HG3	2.18	0.43
1:A:137:ILE:HD12	1:A:186:ARG:HH12	1.83	0.43
1:A:210:ASN:HD22	1:A:211:MET:HG3	1.84	0.43
1:A:314:PRO:HB2	1:A:373:ILE:HG12	2.01	0.43
1:B:135:TYR:O	1:B:139:MET:HG2	2.19	0.43
1:A:184:ASN:HD22	1:A:187:TYR:H	1.67	0.42
1:B:159:MET:HE2	1:B:159:MET:HB3	1.88	0.42
1:B:416:GLY:O	1:B:419:ILE:HG12	2.20	0.42
1:A:277:TYR:CE1	3:A:500:8PC:H6	2.55	0.42
1:B:212:LEU:HD21	1:B:248:LEU:HG	2.02	0.42
1:B:256:MET:HE2	1:B:260:SER:HB3	2.02	0.42
1:A:137:ILE:HD12	1:A:186:ARG:NH1	2.35	0.41
1:A:301:ARG:HH21	1:B:379:TYR:HA	1.84	0.41
1:A:315:LEU:HD11	1:A:388:SER:HB3	2.02	0.41
1:B:236:ASP:O	1:B:240:LYS:HG2	2.21	0.41
1:B:319:ALA:HB1	3:B:500:8PC:C15	2.51	0.41
1:A:221:GLU:HB3	1:A:224:LYS:HD3	2.04	0.40
1:B:301:ARG:HD3	1:B:301:ARG:HA	1.80	0.40
1:A:315:LEU:HD11	1:A:388:SER:CB	2.51	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	271/338 (80%)	261 (96%)	9 (3%)	1 (0%)	30	51
1	B	274/338 (81%)	261 (95%)	12 (4%)	1 (0%)	30	51
All	All	545/676 (81%)	522 (96%)	21 (4%)	2 (0%)	30	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	189	MET
1	A	185	LYS

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	241/297 (81%)	231 (96%)	10 (4%)	27	54
1	B	241/297 (81%)	228 (95%)	13 (5%)	20	42
All	All	482/594 (81%)	459 (95%)	23 (5%)	23	47

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	ILE
1	A	156	ASP
1	A	210	ASN
1	A	226	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	227	LEU
1	A	248	LEU
1	A	259	GLN
1	A	283	SER
1	A	382	LEU
1	A	401	ARG
1	B	160	ASN
1	B	162	LEU
1	B	189	MET
1	B	190	LEU
1	B	191	GLN
1	B	227	LEU
1	B	238	LEU
1	B	283	SER
1	B	323	ILE
1	B	324	ASN
1	B	382	LEU
1	B	422	LEU
1	B	424	ASP

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	136	ASN
1	A	184	ASN
1	A	188	ASN
1	A	200	ASN
1	A	203	HIS
1	A	210	ASN
1	A	228	ASN
1	A	254	ASN
1	A	259	GLN
1	A	302	ASN
1	B	160	ASN
1	B	184	ASN
1	B	200	ASN
1	B	203	HIS
1	B	228	ASN
1	B	254	ASN
1	B	302	ASN
1	B	324	ASN
1	B	409	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 ⓘ

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	8PC	A	500	-	25,25,25	0.93	2 (8%)	34,34,34	1.28	2 (5%)
2	NAD	A	450	-	46,48,48	1.58	10 (21%)	64,73,73	1.71	10 (15%)
2	NAD	B	450	-	46,48,48	1.61	11 (23%)	64,73,73	1.60	10 (15%)
3	8PC	B	500	-	25,25,25	0.90	2 (8%)	34,34,34	1.03	1 (2%)

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	8PC	A	500	-	-	1/8/8/8	0/3/3/3
2	NAD	A	450	-	-	7/30/62/62	0/5/5/5
2	NAD	B	450	-	-	9/30/62/62	0/5/5/5
3	8PC	B	500	-	-	4/8/8/8	0/3/3/3

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	450	NAD	O7N-C7N	4.86	1.33	1.24
2	B	450	NAD	O7N-C7N	4.78	1.33	1.24
2	A	450	NAD	C7N-N7N	-3.52	1.26	1.33
2	B	450	NAD	C7N-N7N	-3.44	1.26	1.33
2	B	450	NAD	C2A-N3A	-3.39	1.27	1.33
2	A	450	NAD	C8A-N7A	3.35	1.38	1.31
2	A	450	NAD	C2A-N3A	-3.34	1.28	1.33
2	A	450	NAD	C5A-C4A	3.28	1.44	1.39
2	A	450	NAD	C2A-N1A	-3.21	1.28	1.33
2	B	450	NAD	C8A-N7A	3.08	1.37	1.31
3	A	500	8PC	C15-CL2	3.08	1.80	1.73
2	B	450	NAD	C5A-C4A	3.01	1.44	1.39
2	B	450	NAD	C2A-N1A	-2.95	1.28	1.33
3	B	500	8PC	C15-CL2	2.84	1.80	1.73
2	B	450	NAD	PA-O3	2.70	1.62	1.59
2	B	450	NAD	PN-O3	2.66	1.62	1.59
2	B	450	NAD	O4D-C1D	2.64	1.44	1.40
2	A	450	NAD	C5A-C6A	2.58	1.48	1.41
3	A	500	8PC	C17-CL1	2.46	1.80	1.74
2	B	450	NAD	C4A-N9A	-2.43	1.32	1.37
2	B	450	NAD	C5A-C6A	2.38	1.47	1.41
3	B	500	8PC	C17-CL1	2.37	1.80	1.74
2	A	450	NAD	O4D-C1D	2.30	1.43	1.40
2	A	450	NAD	C4A-N9A	-2.21	1.33	1.37
2	A	450	NAD	C5A-N7A	-2.09	1.35	1.39

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	450	NAD	C5A-C4A-N3A	-5.50	119.14	126.72
2	A	450	NAD	C5A-C4A-N9A	5.05	111.31	105.81
2	B	450	NAD	C5A-C4A-N3A	-4.88	120.00	126.72
2	A	450	NAD	C4A-C5A-N7A	-4.87	105.02	110.58
2	B	450	NAD	C4A-C5A-N7A	-4.26	105.71	110.58
2	B	450	NAD	C5A-C4A-N9A	4.24	110.44	105.81
3	A	500	8PC	O13-C2-C1	4.00	123.36	116.59
2	A	450	NAD	C6A-C5A-N7A	3.65	139.12	132.09
2	B	450	NAD	C3N-C7N-N7N	3.52	122.07	117.74
2	B	450	NAD	C6A-C5A-N7A	3.41	138.66	132.09
2	A	450	NAD	C2A-N3A-C4A	3.20	119.65	111.83
2	A	450	NAD	O4B-C1B-N9A	3.10	114.04	108.09
2	B	450	NAD	C2A-N1A-C6A	3.05	123.74	118.73

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	450	NAD	C2A-N3A-C4A	3.03	119.23	111.83
3	A	500	8PC	C25-N24-C23	2.87	121.44	117.41
2	A	450	NAD	C2A-N1A-C6A	2.87	123.44	118.73
2	A	450	NAD	C3N-C7N-N7N	2.66	121.02	117.74
2	B	450	NAD	O7N-C7N-N7N	-2.64	118.80	122.62
2	A	450	NAD	O7N-C7N-N7N	-2.63	118.81	122.62
2	B	450	NAD	N3A-C2A-N1A	-2.42	124.92	128.58
3	B	500	8PC	C25-N24-C23	2.38	120.75	117.41
2	B	450	NAD	N6A-C6A-N1A	2.17	123.20	118.38
2	A	450	NAD	C5A-N7A-C8A	2.11	106.77	103.45

There are no chirality outliers.

All (21) torsion outliers are listed below:

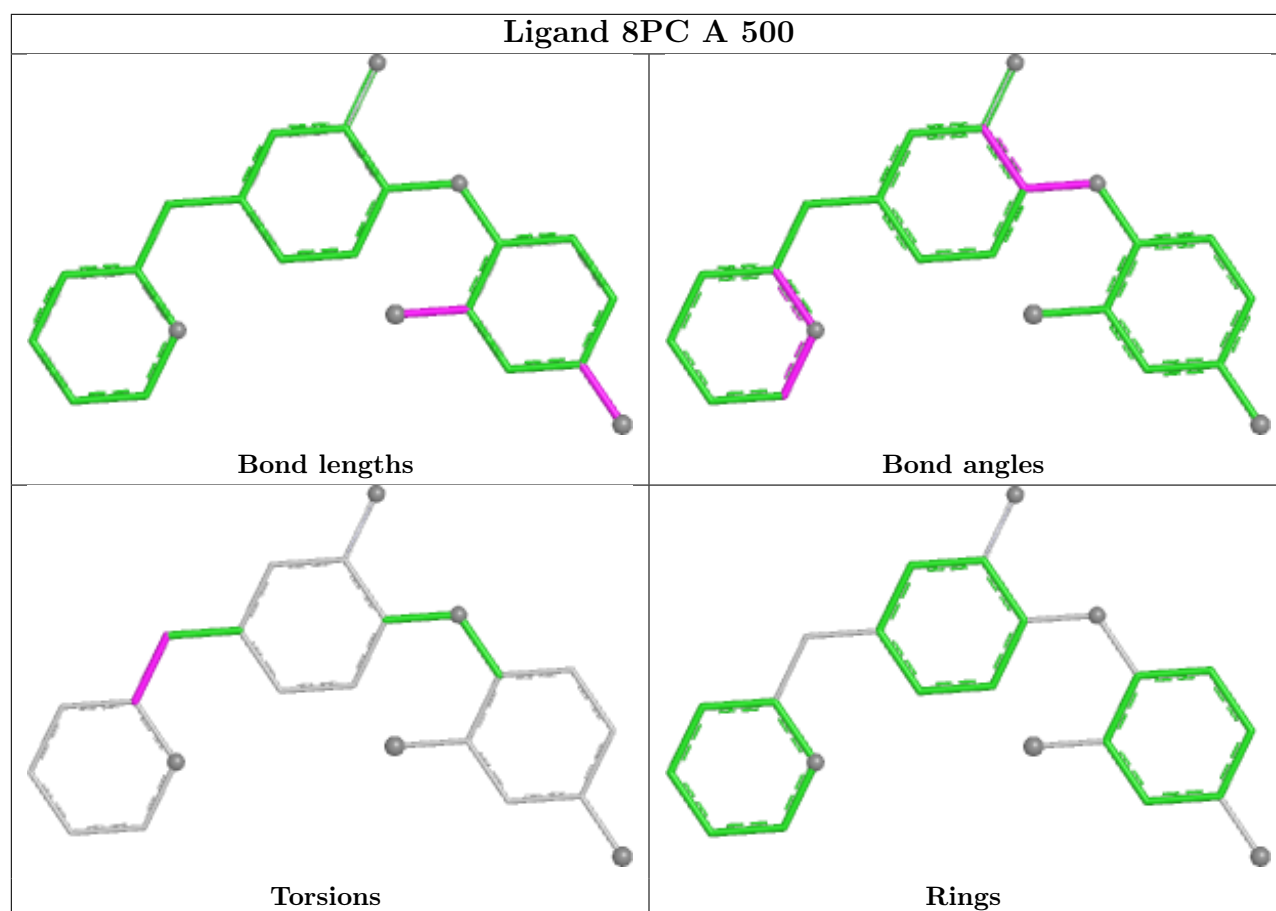
Mol	Chain	Res	Type	Atoms
2	A	450	NAD	C5D-O5D-PN-O3
2	A	450	NAD	C5D-O5D-PN-O1N
2	A	450	NAD	C5D-O5D-PN-O2N
2	B	450	NAD	C5D-O5D-PN-O3
2	B	450	NAD	C5D-O5D-PN-O1N
2	B	450	NAD	C5D-O5D-PN-O2N
2	B	450	NAD	O4D-C1D-N1N-C2N
2	A	450	NAD	O4B-C4B-C5B-O5B
2	A	450	NAD	C3B-C4B-C5B-O5B
2	B	450	NAD	O4B-C4B-C5B-O5B
2	B	450	NAD	C3B-C4B-C5B-O5B
2	A	450	NAD	PN-O3-PA-O5B
2	B	450	NAD	PN-O3-PA-O5B
2	A	450	NAD	C4B-C5B-O5B-PA
3	B	500	8PC	N24-C23-C7-C5
3	B	500	8PC	C28-C23-C7-C5
2	B	450	NAD	O4D-C1D-N1N-C6N
3	B	500	8PC	C15-C14-O13-C2
2	B	450	NAD	C4B-C5B-O5B-PA
3	B	500	8PC	C1-C2-O13-C14
3	A	500	8PC	N24-C23-C7-C5

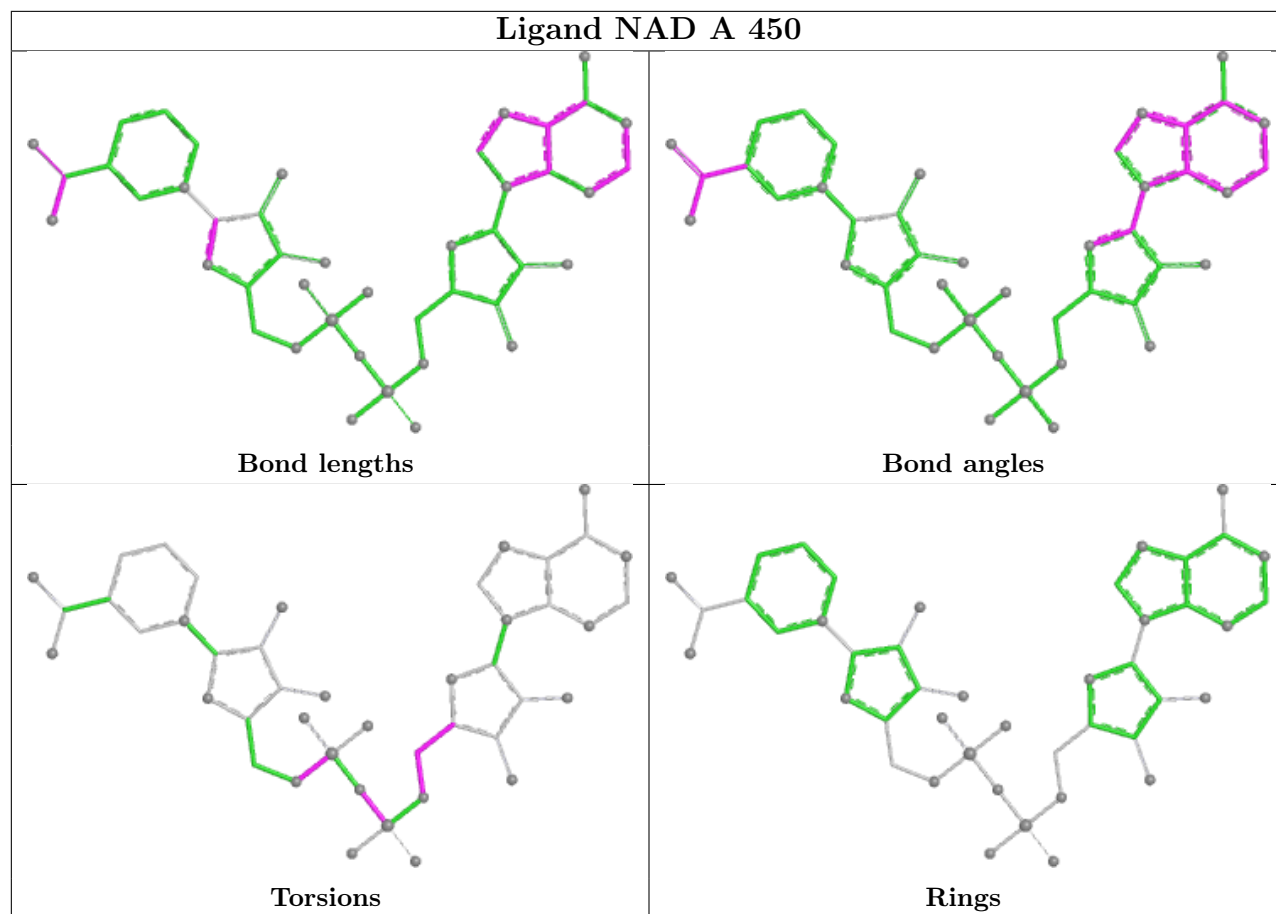
There are no ring outliers.

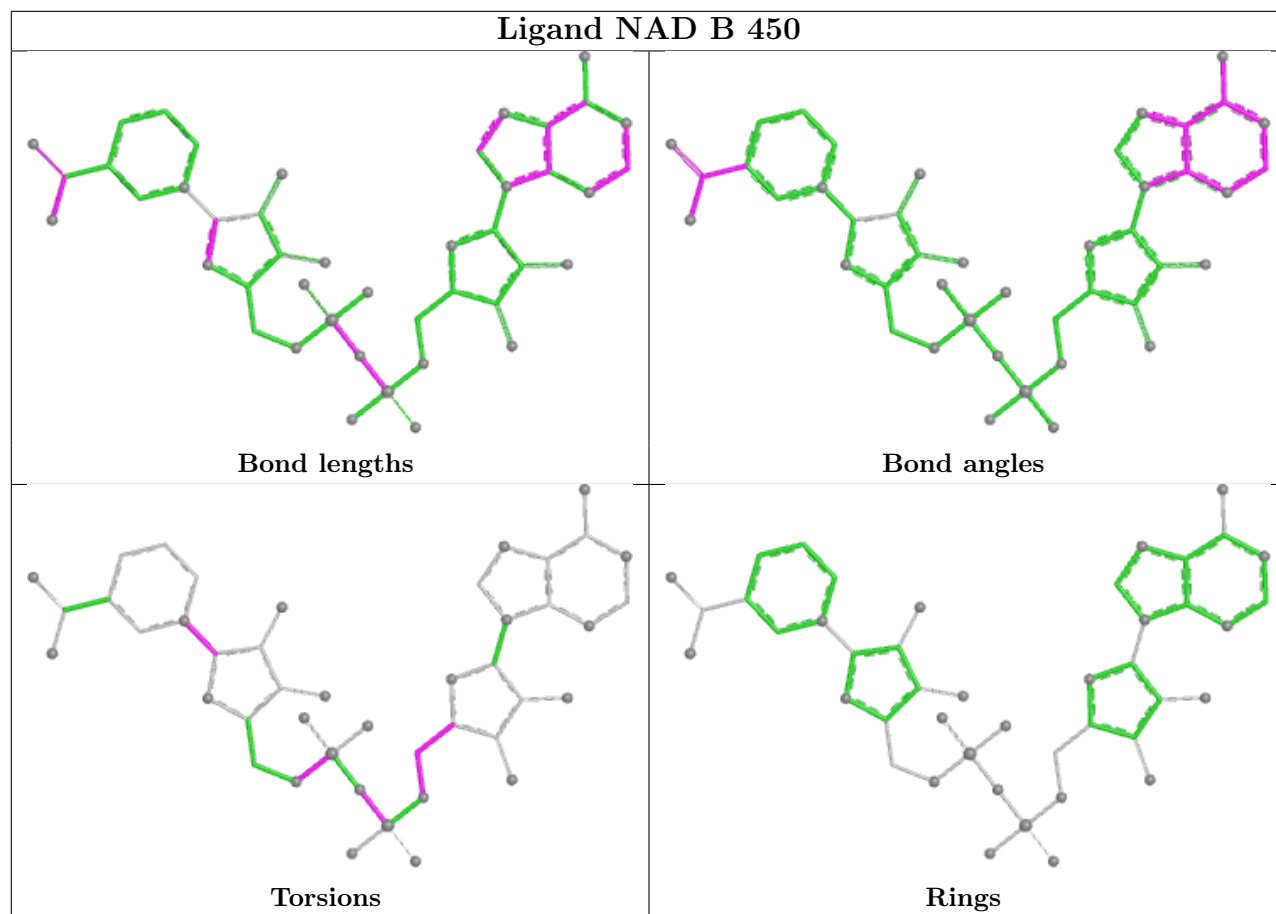
3 monomers are involved in 25 short contacts:

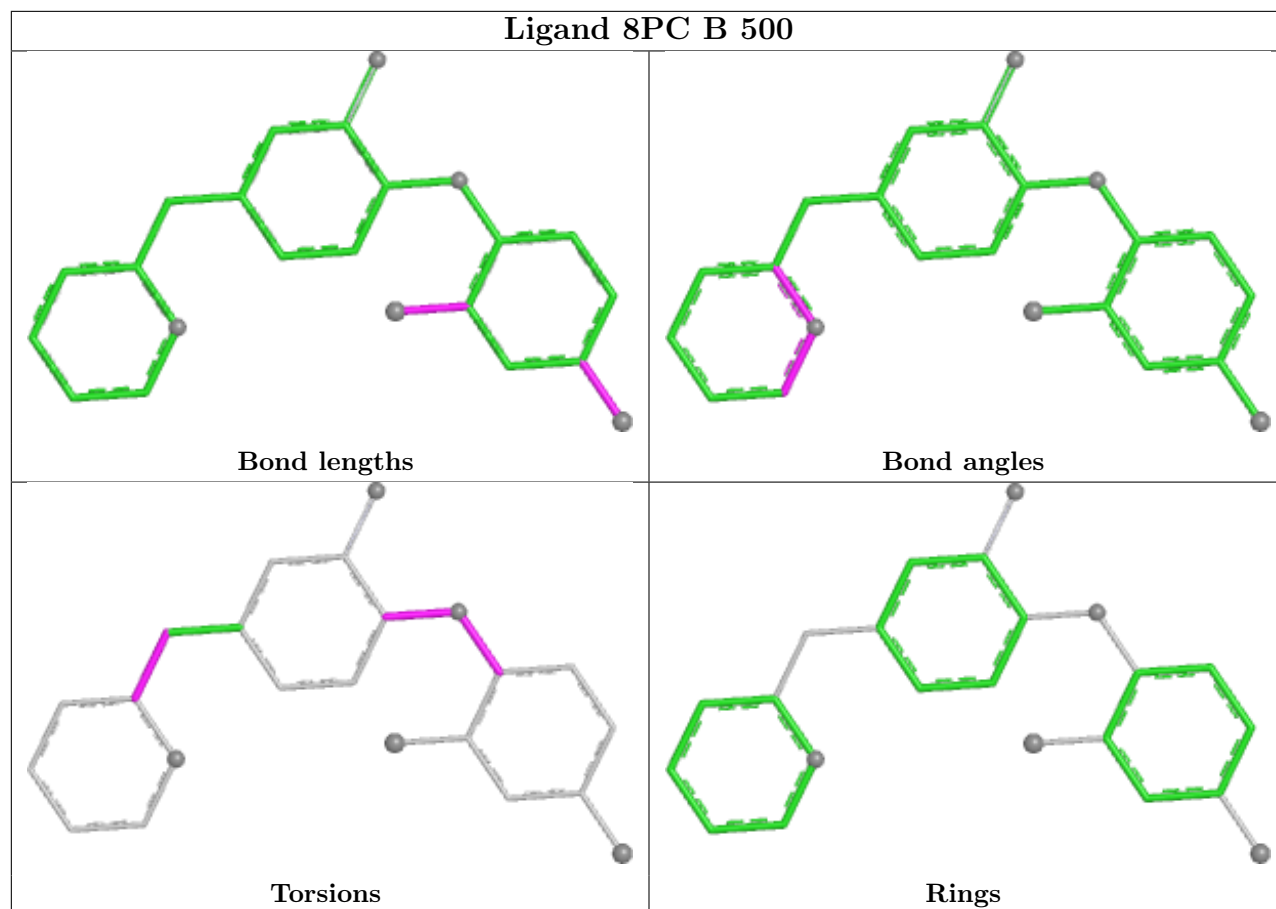
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	500	8PC	13	0
2	A	450	NAD	4	0
3	B	500	8PC	8	0

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	277/338 (81%)	1.06	35 (12%) 8 6	19, 34, 69, 91	0
1	B	280/338 (82%)	0.96	30 (10%) 11 9	19, 35, 72, 94	0
All	All	557/676 (82%)	1.01	65 (11%) 9 7	19, 34, 72, 94	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	156	ASP	4.9
1	B	152	ILE	4.8
1	B	368	PHE	4.5
1	B	143	LYS	4.4
1	B	160	ASN	4.2
1	B	367	THR	4.2
1	A	181	THR	4.2
1	A	153	ILE	4.1
1	A	368	PHE	4.0
1	B	137	ILE	3.6
1	B	189	MET	3.6
1	A	373	ILE	3.4
1	B	158	LYS	3.4
1	B	324	ASN	3.4
1	A	189	MET	3.3
1	B	175	ASN	3.3
1	A	186	ARG	3.2
1	B	207	GLY	3.2
1	A	158	LYS	3.2
1	A	185	LYS	3.0
1	A	122	ARG	3.0
1	A	220	LYS	3.0
1	A	369	ILE	2.9
1	B	188	ASN	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	159	MET	2.8
1	A	160	ASN	2.8
1	A	367	THR	2.7
1	B	122	ARG	2.6
1	B	141	ASN	2.6
1	B	161	ILE	2.5
1	A	383	ARG	2.5
1	A	371	TYR	2.5
1	A	188	ASN	2.5
1	B	164	MET	2.5
1	B	258	PRO	2.5
1	A	105	ILE	2.4
1	A	157	LYS	2.4
1	A	199	ALA	2.4
1	B	147	PHE	2.4
1	B	424	ASP	2.4
1	A	375	TYR	2.4
1	A	182	LYS	2.4
1	A	152	ILE	2.3
1	A	204	GLN	2.2
1	A	140	LYS	2.2
1	B	102	ILE	2.2
1	A	97	GLU	2.2
1	A	179	GLU	2.2
1	B	371	TYR	2.2
1	B	396	SER	2.2
1	A	183	ASN	2.2
1	A	316	LYS	2.2
1	A	143	LYS	2.1
1	A	144	ASN	2.1
1	B	384	GLN	2.1
1	A	393	SER	2.1
1	A	146	LYS	2.1
1	B	391	ILE	2.1
1	A	114	GLY	2.1
1	B	140	LYS	2.1
1	B	120	SER	2.0
1	B	146	LYS	2.0
1	B	423	PRO	2.0
1	A	401	ARG	2.0
1	B	151	MET	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](#)

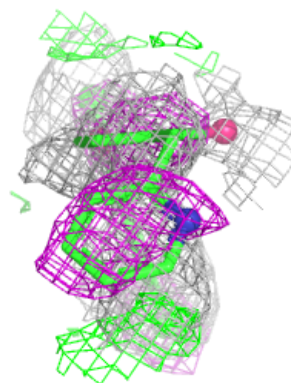
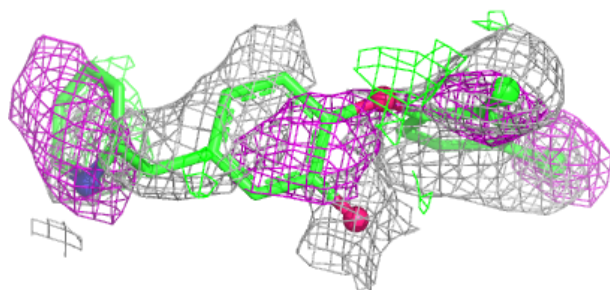
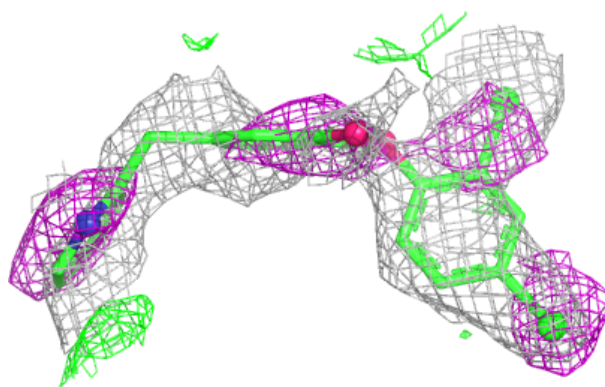
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	8PC	A	500	23/23	0.65	0.18	28,44,55,59	0
2	NAD	A	450	44/44	0.76	0.29	25,37,45,48	44
3	8PC	B	500	23/23	0.78	0.14	13,27,41,54	0
2	NAD	B	450	44/44	0.87	0.13	29,35,45,48	0

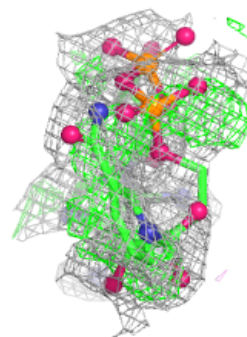
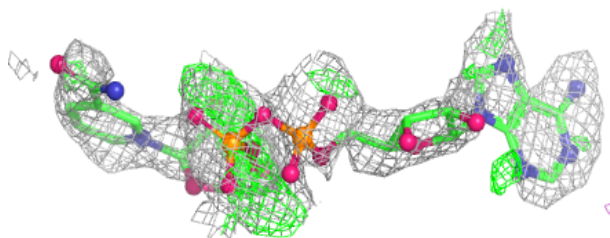
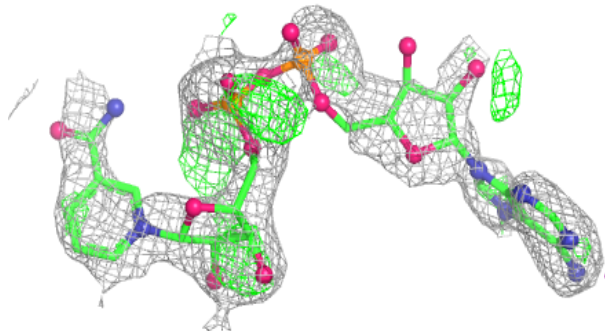
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 8PC A 500:

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

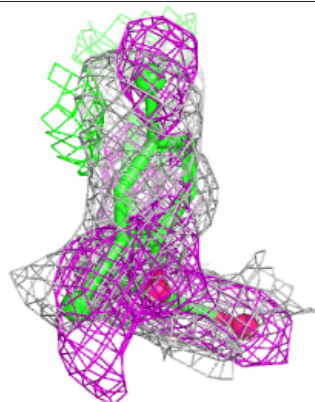
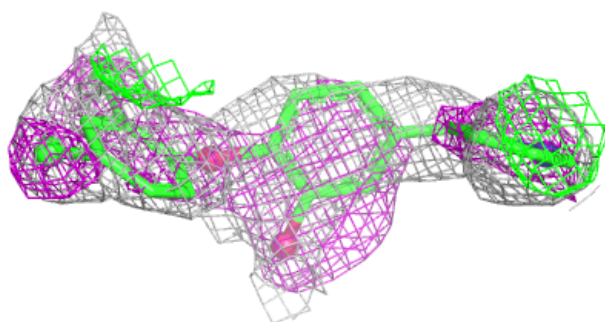
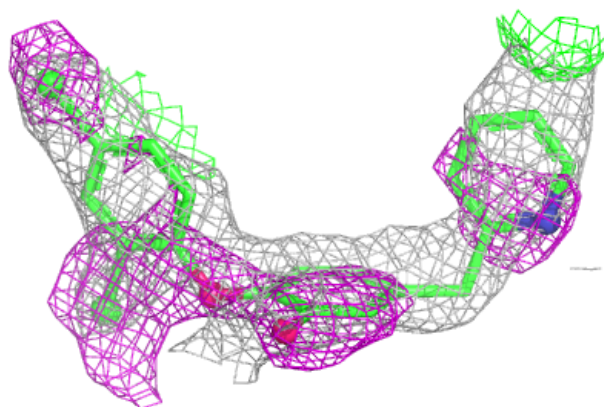
**Electron density around NAD A 450:**

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

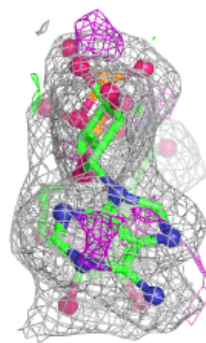
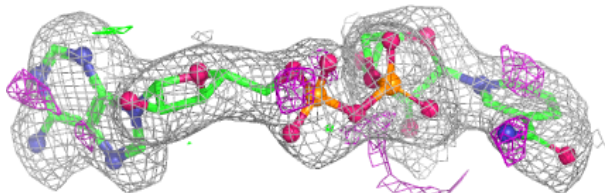
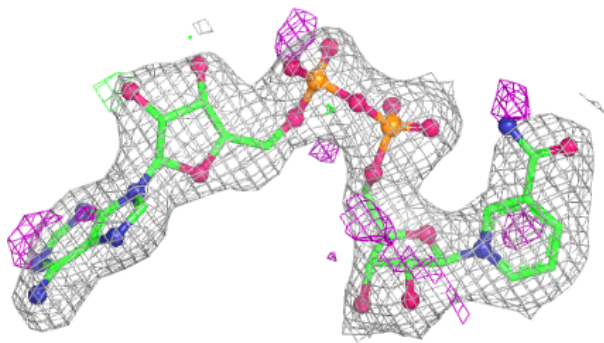


Electron density around 8PC B 500:

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

**Electron density around NAD B 450:**

$2mF_o-DF_c$ (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.