



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 14, 2025 – 10:36 AM JST

PDB ID : 9JZ8 / pdb_00009jz8
Title : PfDXR - Mn²⁺ - NADPH - MAMK150 quaternary complex
Authors : Takada, S.; Sakamoto, Y.; Tanaka, N.
Deposited on : 2024-10-14
Resolution : 1.53 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

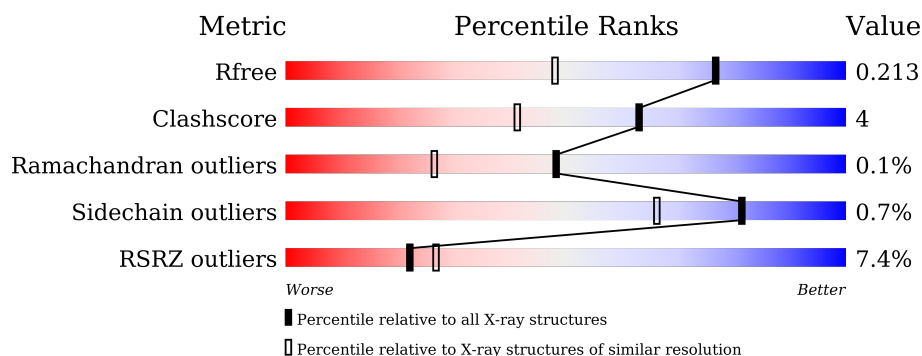
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.53 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}	164625	3511 (1.56-1.52)
Clashscore	180529	3784 (1.56-1.52)
Ramachandran outliers	177936	3720 (1.56-1.52)
Sidechain outliers	177891	3717 (1.56-1.52)
RSRZ outliers	164620	3510 (1.56-1.52)

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	488	
1	B	488	

2 Entry composition [i](#)

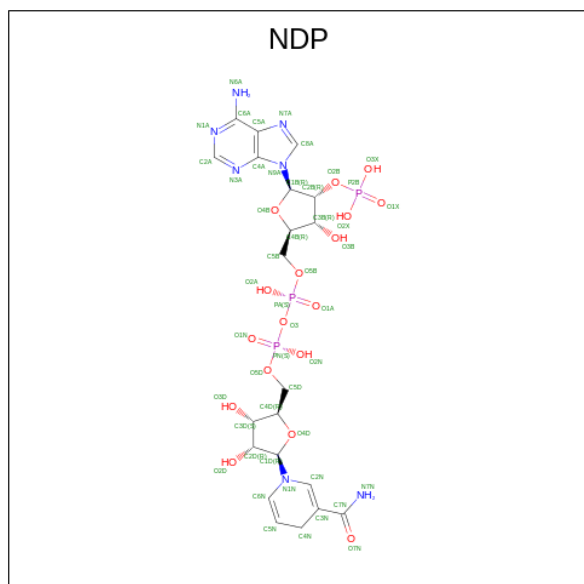
There are 6 unique types of molecules in this entry. The entry contains 7255 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total	C	N	O	S	0	1	0
			3293	2113	540	620	20			
1	B	411	Total	C	N	O	S	0	1	0
			3293	2113	540	620	20			

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).

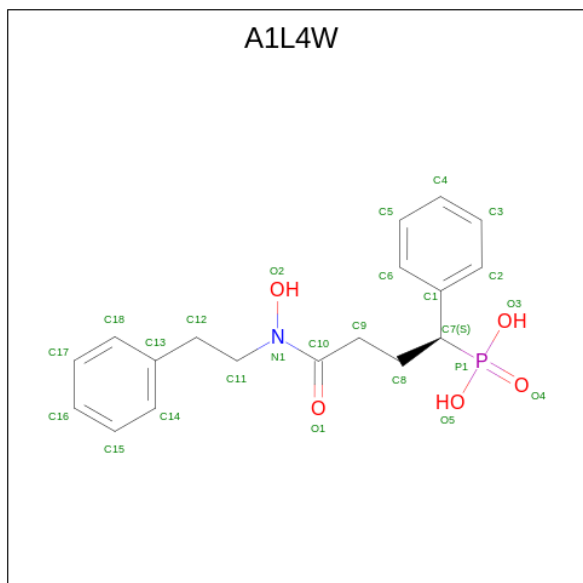


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mn 1 1	0	0
3	B	1	Total Mn 1 1	0	0

- Molecule 4 is [(1 {S})-4-oxidanylidene-4-[oxidanyl(2-phenylethyl)amino]-1-phenyl-butyl]phosphonic acid (CCD ID: A1L4W) (formula: C₁₈H₂₂NO₅P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O P 25 18 1 5 1	0	0
4	B	1	Total C N O P 25 18 1 5 1	0	0

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	3	Total Ca 3 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	231	Total O 231 231	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	287	Total 287	O 287	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.61Å 77.68Å 111.06Å 90.00° 92.75° 90.00°	Depositor
Resolution (Å)	55.47 – 1.53 55.47 – 1.53	Depositor EDS
% Data completeness (in resolution range)	99.7 (55.47-1.53) 99.7 (55.47-1.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 1.53Å)	Xtriage
Refinement program		Depositor
R, R_{free}	0.183 , 0.204 0.195 , 0.213	Depositor DCC
R_{free} test set	6728 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	18.1	Xtriage
Anisotropy	0.131	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 34.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.049 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7255	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.57% 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: A1L4W, CA, MN, NDP

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	0.62	0/3356	1.04	5/4532 (0.1%)
1	B	0.67	0/3356	1.08	2/4532 (0.0%)
All	All	0.64	0/6712	1.06	7/9064 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	282	LEU	N-CA-CB	-5.49	101.77	110.22
1	A	222	HIS	CA-CB-CG	-5.38	108.42	113.80
1	A	231	ASP	CA-CB-CG	5.34	117.94	112.60
1	B	462	ASP	CA-CB-CG	5.12	117.72	112.60
1	A	286	THR	CA-CB-OG1	-5.03	102.05	109.60
1	A	459	ASN	CB-CA-C	5.01	118.01	109.75
1	A	399	PHE	CA-CB-CG	-5.00	108.80	113.80

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	3293	0	3337	15	0
1	B	3293	0	3337	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	48	0	26	3	0
2	B	48	0	26	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	25	0	0	0	0
4	B	25	0	0	0	0
5	B	3	0	0	0	0
6	A	231	0	0	10	0
6	B	287	0	0	16	0
All	All	7255	0	6726	53	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 4.

All (53) 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)
2:A:501:NDP:H5N	6:A:617:HOH:O	1.69	0.92
1:B:449:GLU:HG3	6:B:857:HOH:O	1.69	0.91
6:A:730:HOH:O	1:B:372:ASP:HB3	1.74	0.88
1:B:480:ASP:HB2	6:B:601:HOH:O	1.88	0.73
1:B:279:MET:HG3	1:B:283:LYS:HE3	1.72	0.71
1:A:191:MET:HG2	1:A:195:MET:HE3	1.73	0.70
1:B:142:GLU:HG3	6:B:830:HOH:O	1.92	0.69
1:A:138:LYS:HD3	1:A:160:CYS:SG	2.34	0.68
1:B:108:ASN:HB3	6:B:823:HOH:O	1.94	0.67
1:A:336:LYS:HE3	6:A:763:HOH:O	1.95	0.67
2:A:501:NDP:C5N	6:A:617:HOH:O	2.35	0.64
1:B:217:LYS:NZ	1:B:458:GLU:O	2.31	0.63
1:B:403:LYS:HE3	1:B:407:GLN:NE2	2.14	0.63
1:B:480:ASP:CB	6:B:601:HOH:O	2.44	0.63
1:A:340:ILE:HG12	1:A:355:MET:HG2	1.80	0.63
1:B:184:PHE:HA	6:B:798:HOH:O	2.02	0.59
1:A:143:GLU:O	1:A:147:LEU:HD23	2.03	0.58
1:B:449:GLU:CG	6:B:857:HOH:O	2.39	0.57
1:A:115:ASN:HD22	1:A:136:HIS:HB3	1.71	0.56
1:B:126:ARG:HD3	6:B:851:HOH:O	2.07	0.54
1:B:459:ASN:OD1	1:B:462:ASP:OD2	2.25	0.54
1:B:355:MET:CE	6:B:710:HOH:O	2.56	0.54
1:B:355:MET:HE2	6:B:710:HOH:O	2.07	0.53
1:A:79:ASN:HD22	1:A:108:ASN:HB2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:ILE:HD12	6:A:620:HOH:O	2.09	0.51
1:B:403:LYS:HE3	1:B:407:GLN:HE21	1.74	0.51
1:A:138:LYS:CD	1:A:160:CYS:SG	2.99	0.50
1:A:191:MET:CG	1:A:195:MET:HE3	2.41	0.50
1:B:411:LYS:HG3	6:B:731:HOH:O	2.11	0.50
1:B:403:LYS:CD	6:B:620:HOH:O	2.61	0.49
1:B:148:VAL:HG12	6:B:606:HOH:O	2.12	0.48
1:B:279:MET:O	1:B:283:LYS:HG3	2.13	0.48
1:B:295:LYS:HD3	6:B:638:HOH:O	2.14	0.48
1:B:115:ASN:HD22	1:B:136:HIS:HB3	1.79	0.47
1:B:254:ASP:O	1:B:255:ASN:HB2	2.14	0.47
1:B:166:LYS:HE2	1:B:192:TYR:CZ	2.50	0.47
6:A:797:HOH:O	1:B:375:LYS:HE2	2.14	0.46
1:B:480:ASP:OD1	6:B:601:HOH:O	2.21	0.46
6:A:641:HOH:O	1:B:393:LYS:CE	2.64	0.45
1:A:138:LYS:HA	1:A:160:CYS:SG	2.56	0.45
1:A:393:LYS:HE3	6:A:807:HOH:O	2.16	0.45
1:B:480:ASP:CG	6:B:601:HOH:O	2.57	0.45
1:A:292:LYS:HA	1:A:292:LYS:HE2	2.00	0.43
6:A:730:HOH:O	1:B:372:ASP:CB	2.50	0.43
1:B:369:THR:O	1:B:370:TRP:C	2.61	0.43
1:B:292:LYS:O	1:B:293:HIS:C	2.61	0.43
2:A:501:NDP:C4N	6:A:617:HOH:O	2.62	0.42
1:B:214:PHE:CZ	1:B:218:LEU:HD11	2.54	0.42
1:B:118:VAL:HG23	1:B:144:LEU:HD13	2.01	0.42
1:A:129:LEU:HD22	1:A:129:LEU:N	2.34	0.41
1:A:333:ILE:HD11	1:A:391:PHE:HB3	2.02	0.41
1:B:295:LYS:HE2	1:B:295:LYS:HB3	1.94	0.41
1:B:129:LEU:N	1:B:130:PRO:CD	2.84	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	410/488 (84%)	399 (97%)	11 (3%)	0	100	100
1	B	410/488 (84%)	398 (97%)	11 (3%)	1 (0%)	44	25
All	All	820/976 (84%)	797 (97%)	22 (3%)	1 (0%)	48	26

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	342	SER

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	379/449 (84%)	378 (100%)	1 (0%)	91	84
1	B	379/449 (84%)	375 (99%)	4 (1%)	70	48
All	All	758/898 (84%)	753 (99%)	5 (1%)	81	66

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ASP
1	B	116	LYS
1	B	163	GLU
1	B	387	SER
1	B	461	GLU

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	79	ASN
1	A	115	ASN
1	A	172	ASN
1	A	197	ASN
1	A	255	ASN

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Mol	Chain	Res	Type
1	A	260	ASN
1	A	284	ASN
1	A	407	GLN
1	A	452	ASN
1	A	483	ASN
1	B	105	ASN
1	B	115	ASN
1	B	172	ASN
1	B	253	GLN
1	B	255	ASN
1	B	261	ASN
1	B	407	GLN
1	B	428	ASN
1	B	432	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 for Mogul analysis.

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	NDP	A	501	-	45,52,52	0.89	2 (4%)	53,80,80	0.92	1 (1%)
2	NDP	B	501	-	45,52,52	0.99	1 (2%)	53,80,80	1.00	2 (3%)
4	A1L4W	A	503	3	25,26,26	1.87	5 (20%)	26,35,35	1.31	1 (3%)
4	A1L4W	B	503	3	25,26,26	1.26	1 (4%)	26,35,35	1.36	2 (7%)

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	NDP	A	501	-	-	5/30/77/77	0/5/5/5
2	NDP	B	501	-	-	3/30/77/77	0/5/5/5
4	A1L4W	A	503	3	-	1/24/24/24	0/2/2/2
4	A1L4W	B	503	3	-	1/24/24/24	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	A1L4W	P1-C7	5.00	1.88	1.82
4	A	503	A1L4W	P1-O4	4.21	1.56	1.49
2	B	501	NDP	P2B-O2B	4.07	1.67	1.59
4	A	503	A1L4W	O2-N1	3.89	1.43	1.40
2	A	501	NDP	P2B-O2B	3.77	1.66	1.59
4	A	503	A1L4W	P1-O3	-3.44	1.49	1.54
4	B	503	A1L4W	P1-O3	-3.33	1.49	1.54
4	A	503	A1L4W	C2-C1	2.25	1.42	1.39
2	A	501	NDP	C8A-N7A	-2.12	1.30	1.34

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	A1L4W	O2-N1-C11	3.17	121.53	113.59
4	B	503	A1L4W	C2-C1-C6	2.63	121.57	118.29
2	B	501	NDP	C3B-C2B-C1B	-2.60	98.00	102.89
4	B	503	A1L4W	C6-C1-C7	-2.52	116.77	120.82
2	A	501	NDP	C3B-C2B-C1B	-2.40	98.38	102.89
2	B	501	NDP	C3N-C7N-N7N	2.26	121.68	117.67

There are no chirality outliers.

All (10) torsion outliers are listed below:

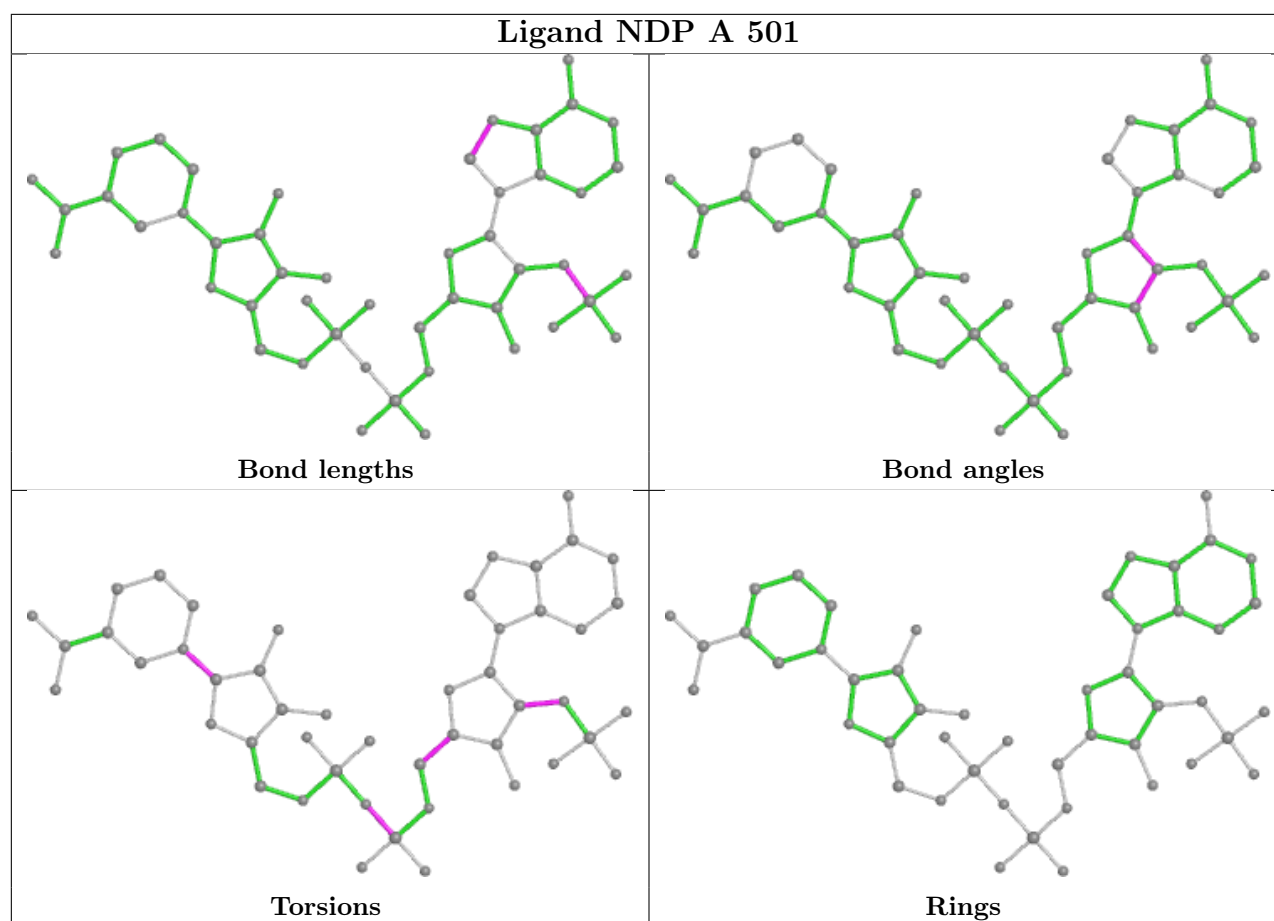
Mol	Chain	Res	Type	Atoms
2	B	501	NDP	O4D-C1D-N1N-C6N
2	A	501	NDP	O4D-C1D-N1N-C6N
2	A	501	NDP	PN-O3-PA-O1A
2	A	501	NDP	PN-O3-PA-O2A
2	B	501	NDP	PN-O3-PA-O1A
2	A	501	NDP	O4B-C4B-C5B-O5B
2	B	501	NDP	O4B-C4B-C5B-O5B
4	A	503	A1L4W	O1-C10-N1-O2
4	B	503	A1L4W	O1-C10-N1-O2
2	A	501	NDP	C1B-C2B-O2B-P2B

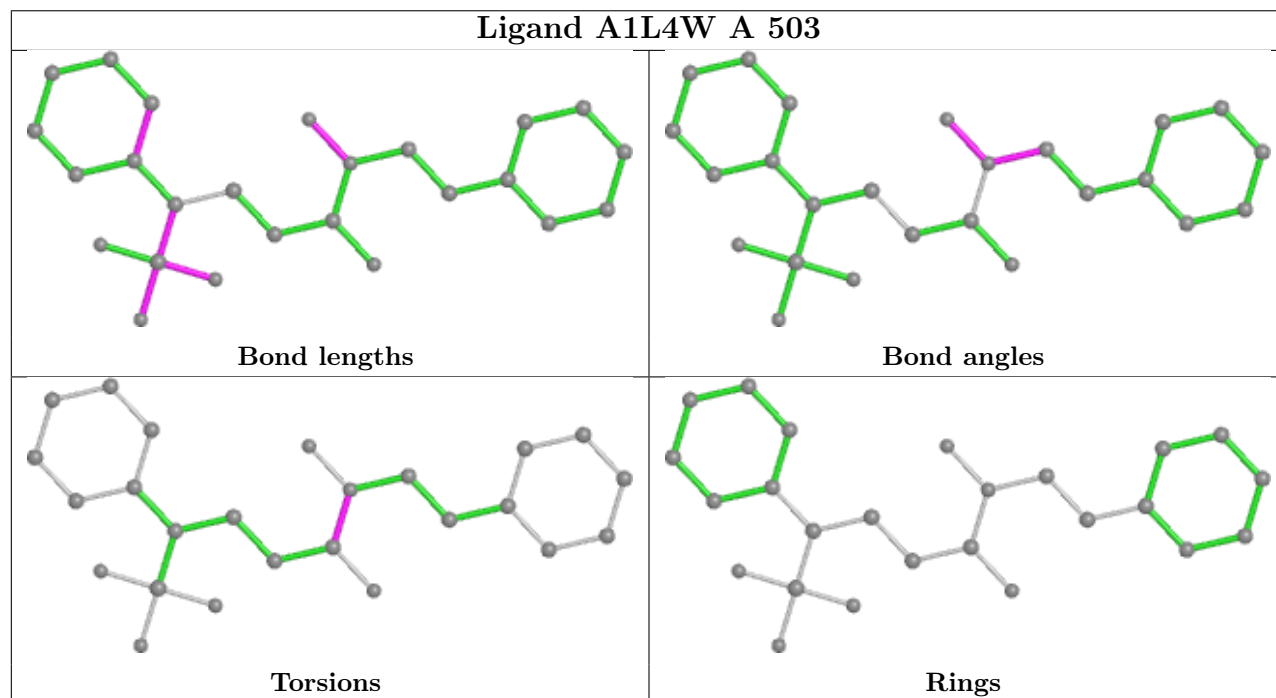
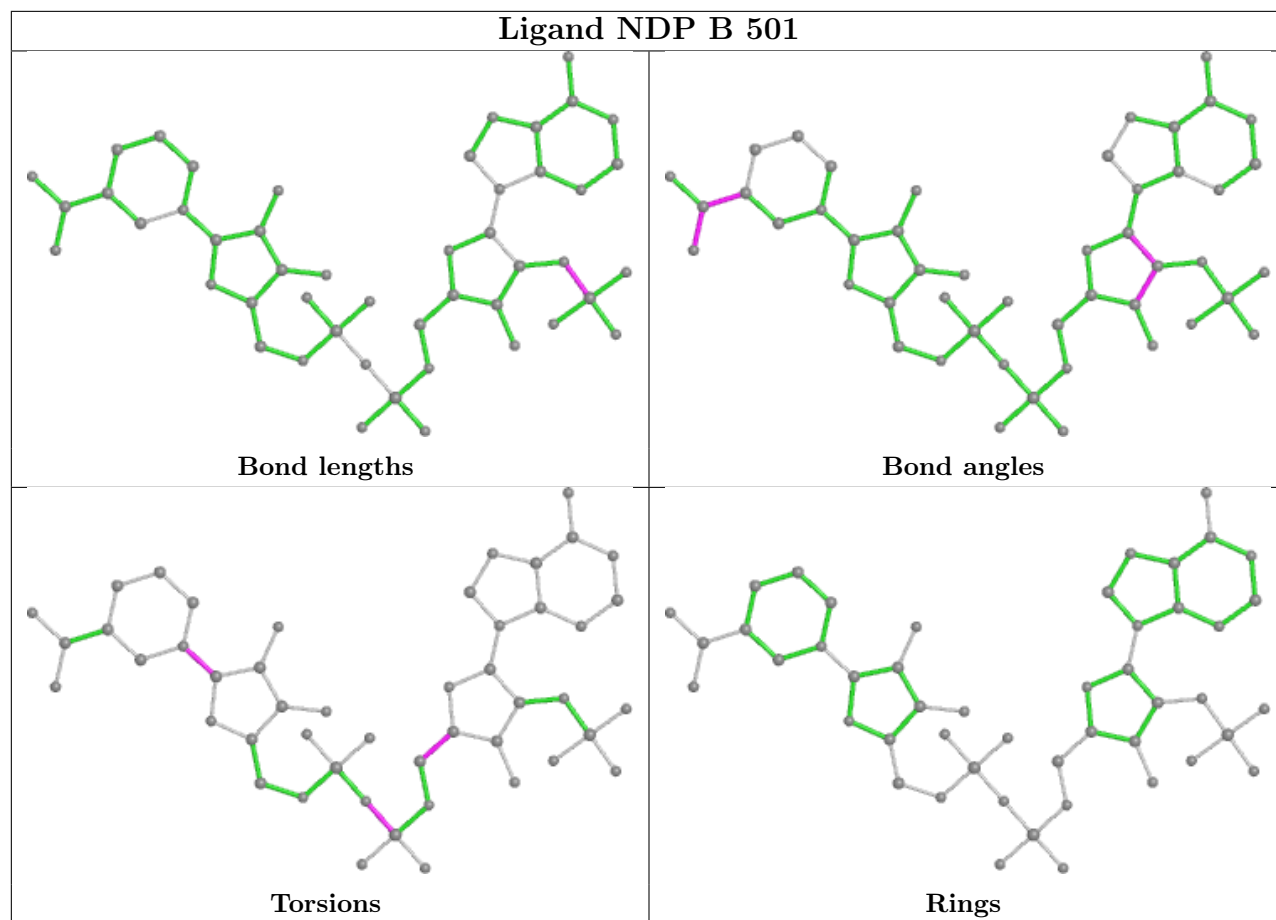
There are no ring outliers.

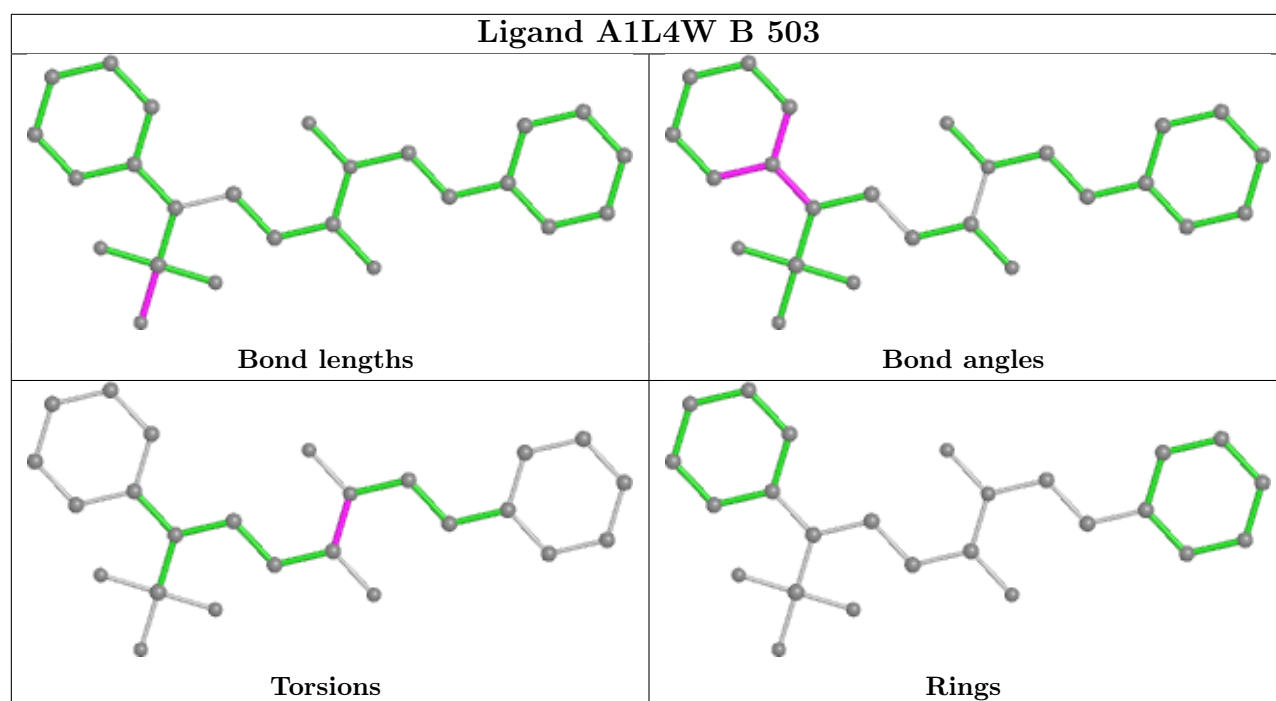
1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	NDP	3	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	411/488 (84%)	0.46	39 (9%) 15 19	10, 21, 48, 73	1 (0%)
1	B	411/488 (84%)	0.25	22 (5%) 32 41	9, 18, 39, 82	1 (0%)
All	All	822/976 (84%)	0.35	61 (7%) 22 27	9, 20, 46, 82	2 (0%)

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	294	PRO	5.4
1	B	294	PRO	5.3
1	B	293	HIS	4.7
1	B	485	HIS	4.7
1	B	296	TRP	4.6
1	A	151	ILE	4.4
1	A	296	TRP	4.1
1	A	141	TYR	3.7
1	A	184	PHE	3.7
1	B	188	TYR	3.6
1	B	76	LYS	3.4
1	B	213	PHE	3.4
1	A	77	PRO	3.3
1	B	486	ASN	3.3
1	A	158	ILE	3.3
1	A	122	TYR	3.0
1	A	293	HIS	3.0
1	B	484	LYS	3.0
1	A	157	ILE	2.9
1	A	485	HIS	2.9
1	A	292	LYS	2.9
1	B	295	LYS	2.9
1	A	213	PHE	2.8
1	A	76	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	140	VAL	2.8
1	A	147	LEU	2.8
1	B	292	LYS	2.8
1	B	377	ASN	2.7
1	A	118	VAL	2.7
1	A	106	VAL	2.7
1	A	152	LYS	2.7
1	A	148	VAL	2.5
1	A	295	LYS	2.5
1	A	155	LYS	2.5
1	B	148	VAL	2.4
1	A	160	CYS	2.4
1	A	129	LEU	2.4
1	B	172	ASN	2.4
1	A	133	LEU	2.3
1	A	252	LEU	2.3
1	B	141	TYR	2.3
1	B	192	TYR	2.3
1	A	146	GLU	2.2
1	B	291	LEU	2.2
1	A	113	TYR	2.2
1	A	150	ASN	2.2
1	A	144	LEU	2.2
1	A	172	ASN	2.2
1	A	119	ASN	2.2
1	B	150	ASN	2.1
1	A	291	LEU	2.1
1	A	149	LYS	2.1
1	A	154	TYR	2.1
1	A	192	TYR	2.1
1	B	105	ASN	2.1
1	A	145	LYS	2.1
1	A	126	ARG	2.1
1	B	480	ASP	2.1
1	B	149	LYS	2.0
1	B	255	ASN	2.0
1	A	159	LEU	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 ⓘ

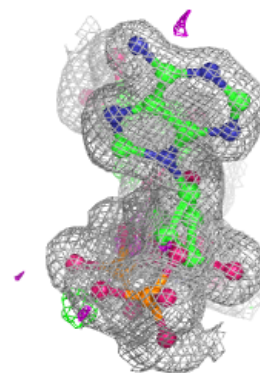
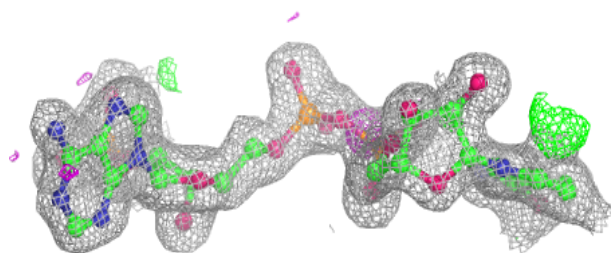
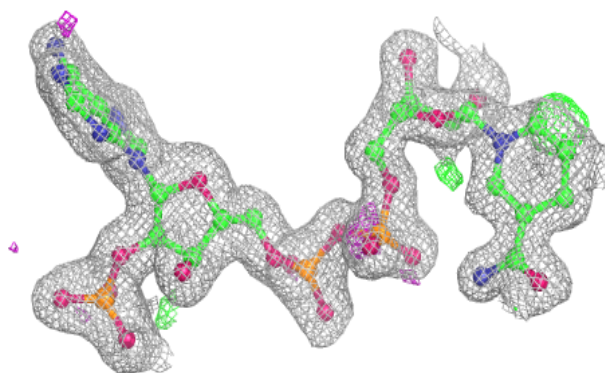
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NDP	A	501	48/48	0.94	0.09	23,26,31,32	0
2	NDP	B	501	48/48	0.97	0.06	13,16,19,22	0
4	A1L4W	A	503	25/25	0.98	0.05	14,16,23,24	0
4	A1L4W	B	503	25/25	0.98	0.06	11,13,19,22	0
5	CA	B	505	1/1	0.98	0.08	22,22,22,22	0
5	CA	B	504	1/1	0.99	0.04	15,15,15,15	0
5	CA	B	506	1/1	0.99	0.06	25,25,25,25	0
3	MN	B	502	1/1	1.00	0.01	11,11,11,11	0
3	MN	A	502	1/1	1.00	0.02	13,13,13,13	0

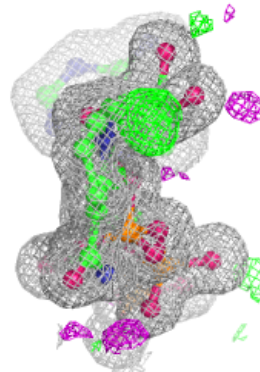
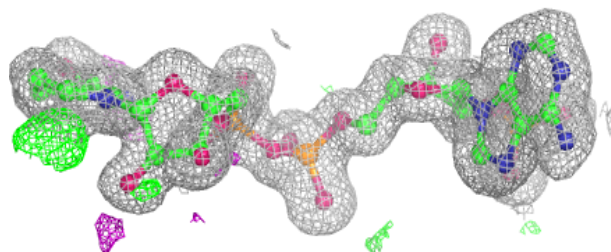
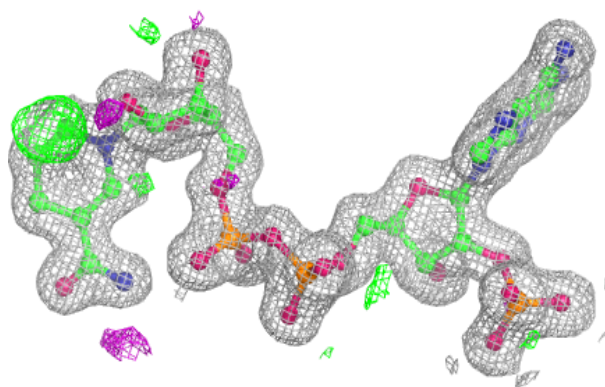
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NDP A 501:

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

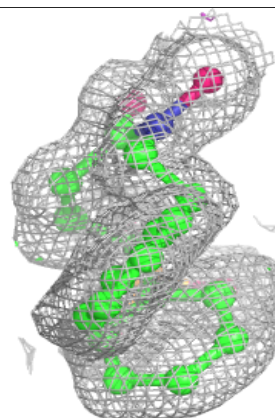
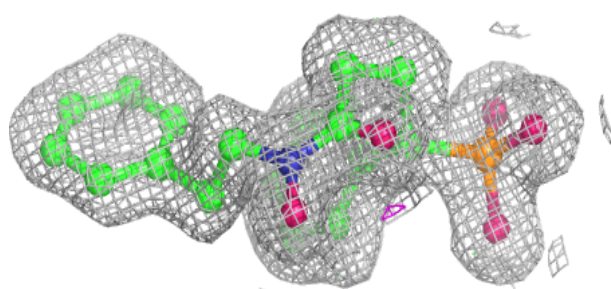
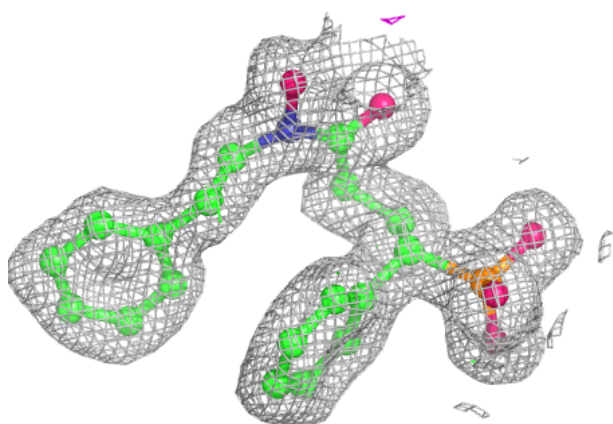
**Electron density around NDP B 501:**

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

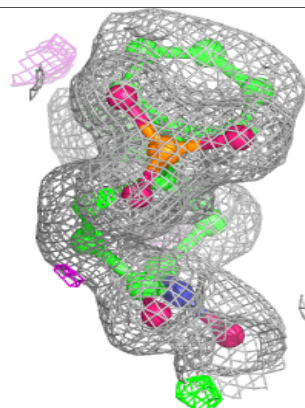
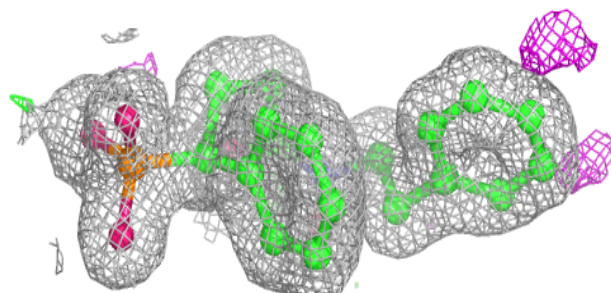
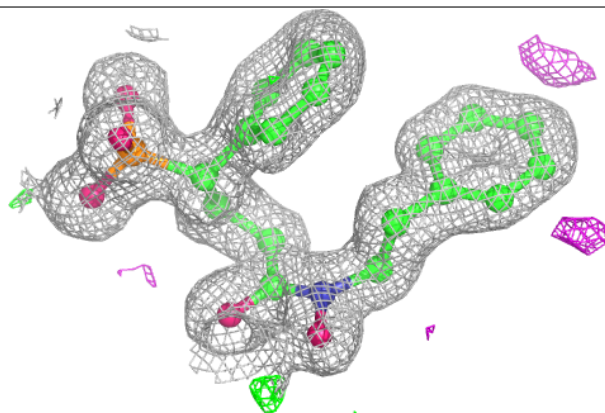


Electron density around A1L4W A 503:

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

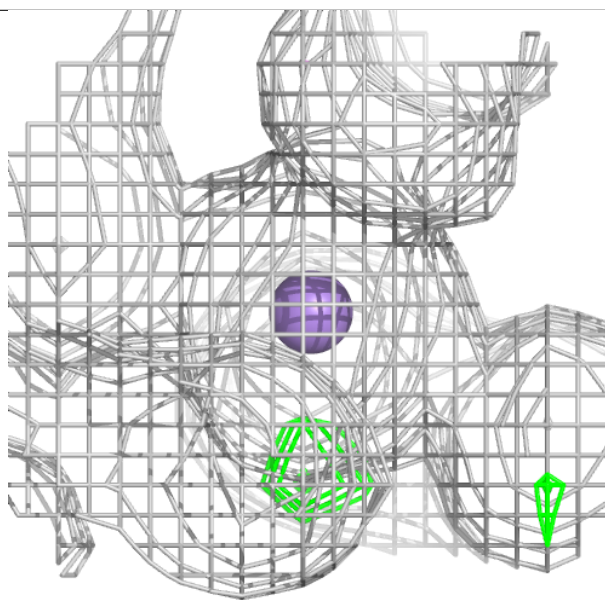
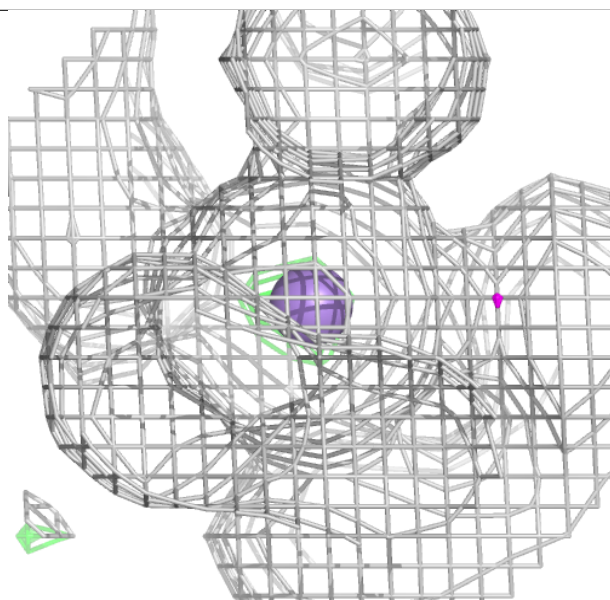
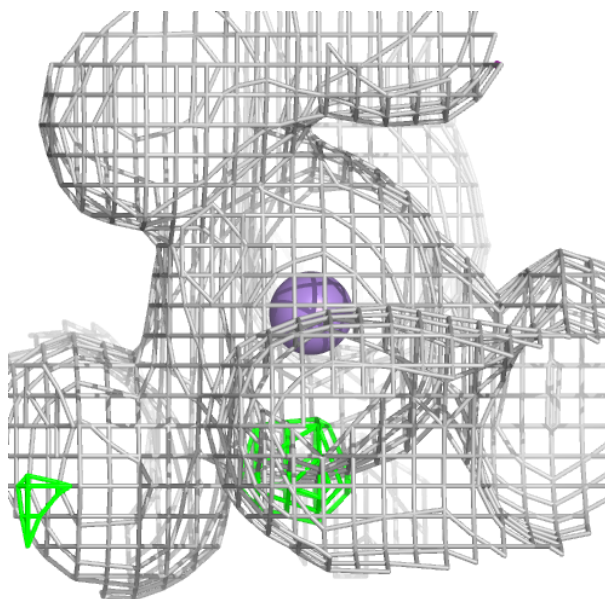
**Electron density around A1L4W B 503:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



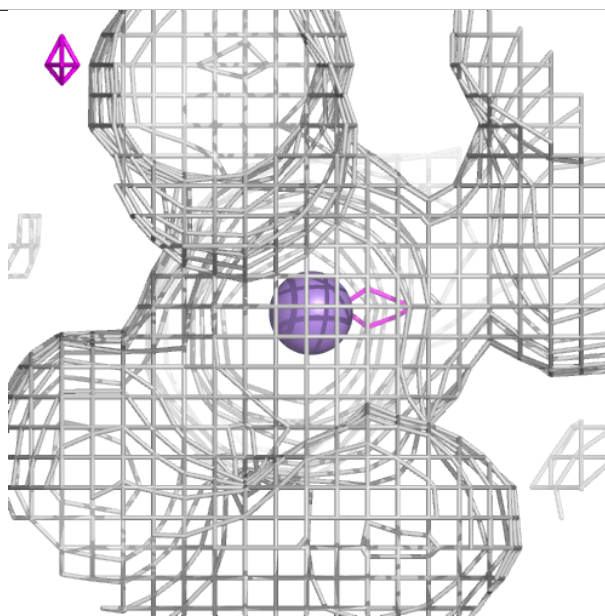
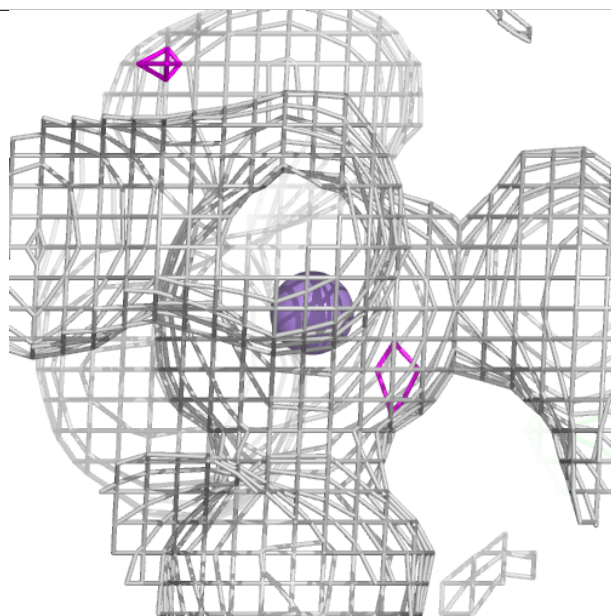
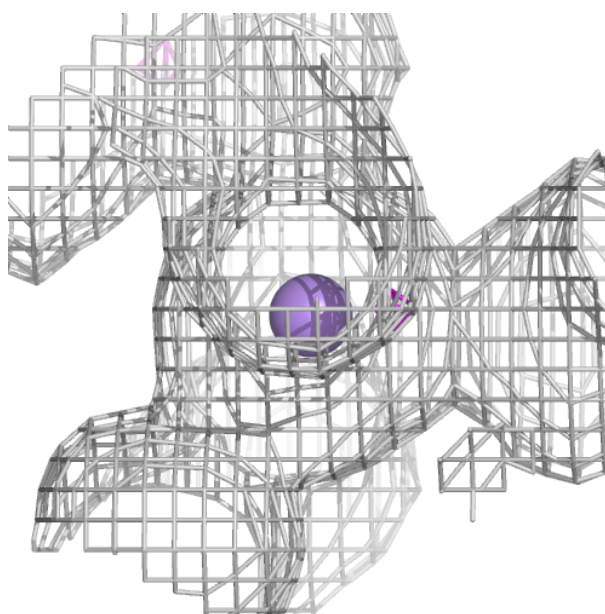
Electron density around MN B 502:

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



Electron density around MN A 502:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.