



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 07:19 am BST

PDB ID : 3WQR
Title : Crystal structure of pfdxr complexed with inhibitor-12
Authors : Tanaka, N.; Umeda, T.
Deposited on : 2014-01-31
Resolution : 1.97 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

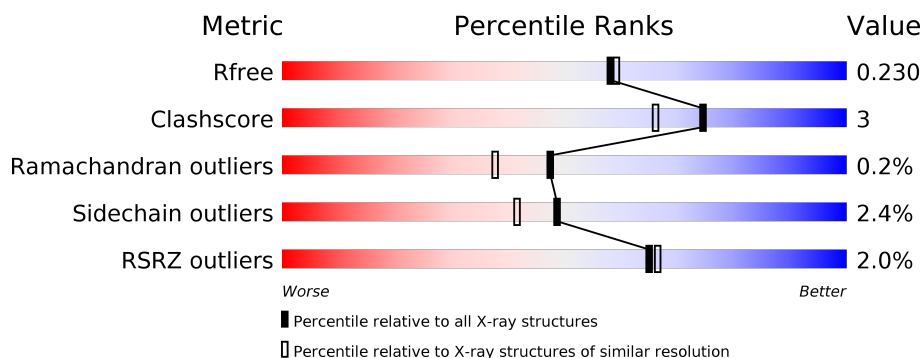
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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.



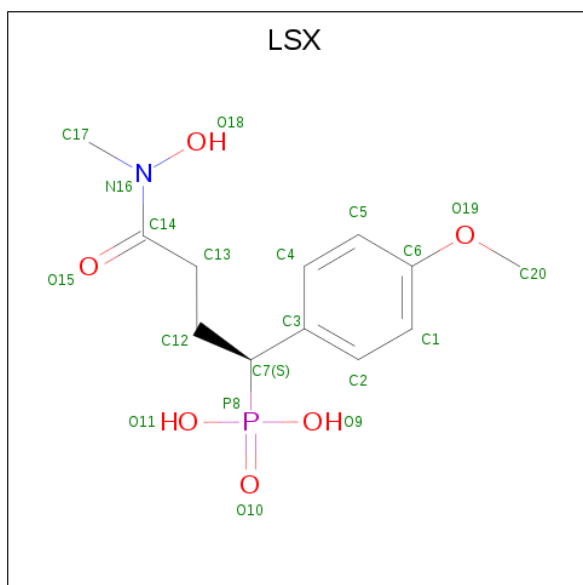
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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 on 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	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>7%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	488	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>6%</div> <div>•</div> <div>16%</div> </div> </div>

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

- Molecule 4 is [(1S)-4-[hydroxy(methyl)amino]-1-(4-methoxyphenyl)-4-oxobutyl]phosphonic acid (three-letter code: LSX) (formula: C₁₂H₁₈NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			20	12	1	6	1		
4	B	1	Total	C	N	O	P	0	0
			20	12	1	6	1		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	2	Total Ca 2 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	239	Total O 239 239	0	0
6	B	256	Total O 256 256	0	0

These plots are drawn for all protein, RNA and DNA 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.

- Chain A:
-
- 2% 76% 7% 16%
- MET LYS LYS TYR ILE TYR ILE PHE PHE ILE THR ILE THR ASN ASP LEU VAL ASN ASN THR SER LYS CYS VAL SER ILE GLU ARG LYS ASN ASN ALA TYR ILE ASN TYR GLY ILE TYR ASN GLY PRO ASP LYS ASN THR LYS ARG CYS ARG ARG

- Chain B:
-
- 77% 6% 16%
- ILE LYS LEU CYS LYS ASP LEU ASP ILE GLY ALA ILE LYS P77 Y106 K116 R126 T135 K138 Y141 T158 L159 C160 E163 G164 M165 C169 Y183 L202 I208 S257 T262 N263 K264 S269 T286 N289 H293 P294

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.08Å 76.55Å 104.09Å 90.00° 90.68° 90.00°	Depositor
Resolution (Å)	50.00 – 1.97 46.07 – 1.97	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-1.97) 98.8 (46.07-1.97)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.180 , 0.230 0.180 , 0.230	Depositor DCC
R_{free} test set	2837 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	22.9	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7187	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% 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: NDP, CA, MG, LSX

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	0.45	0/3339	0.55	0/4509
1	B	0.48	1/3339 (0.0%)	0.55	0/4509
All	All	0.47	1/6678 (0.0%)	0.55	0/9018

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	160	CYS	CB-SG	-5.37	1.73	1.81

There are no bond angle outliers.

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	3276	0	3322	25	0
1	B	3276	0	3322	18	0
2	A	48	0	26	0	0
2	B	48	0	26	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	20	0	16	0	0
4	B	20	0	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	2	0	0	0	0
6	A	239	0	0	5	0
6	B	256	0	0	1	0
All	All	7187	0	6728	43	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 3.

All (43) 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:165:MET:CE	1:B:169:CYS:SG	2.51	0.98
1:B:165:MET:HE2	1:B:169:CYS:SG	2.08	0.93
1:B:165:MET:HE3	1:B:169:CYS:SG	2.29	0.72
1:B:480:ASP:OD2	6:B:843:HOH:O	2.15	0.65
1:B:202:LEU:HD23	1:B:208:ILE:HD11	1.84	0.60
1:B:289:ASN:OD1	1:B:289:ASN:N	2.32	0.60
1:A:139:SER:HB2	6:A:819:HOH:O	2.01	0.59
1:B:138:LYS:HG2	1:B:160:CYS:SG	2.42	0.59
1:A:269:SER:HB2	1:A:312:LYS:HE3	1.86	0.57
1:B:116:LYS:HA	1:B:135:ILE:HD11	1.86	0.56
1:B:286:THR:OG1	1:B:289:ASN:OD1	2.19	0.54
1:B:340:ILE:HG12	1:B:355:MET:HG2	1.88	0.54
1:A:165:MET:HE3	1:A:192:TYR:HB2	1.88	0.54
1:A:266:PHE:HB2	1:A:343:CYS:HB2	1.90	0.54
1:B:269:SER:HB2	1:B:312:LYS:HE3	1.90	0.52
1:A:99:GLU:HG2	6:A:683:HOH:O	2.08	0.52
1:B:257:SER:HB2	1:B:262:ILE:HB	1.92	0.51
1:A:340:ILE:HG12	1:A:355:MET:HE2	1.93	0.50
1:A:86:THR:HG23	1:A:114:VAL:HG11	1.93	0.50
1:A:269:SER:CB	1:A:312:LYS:HE3	2.42	0.50
1:A:165:MET:HE2	1:A:169:CYS:SG	2.54	0.48
1:A:165:MET:CE	1:A:169:CYS:SG	3.03	0.47
1:B:264:LYS:HG3	1:B:345:GLU:HB3	1.96	0.47
1:A:114:VAL:HG22	1:A:121:LEU:HD22	1.97	0.47
1:A:362:ILE:HB	1:A:363:PRO:HD3	1.97	0.47
1:A:93:ALA:HA	1:A:364:ILE:HG21	1.97	0.46
1:B:141:TYR:HE1	1:B:158:ILE:HG22	1.81	0.46
1:B:340:ILE:HG12	1:B:355:MET:CG	2.47	0.45
1:A:433:ASN:ND2	6:A:695:HOH:O	2.45	0.45
1:A:128:PHE:O	6:A:781:HOH:O	2.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:MET:CE	1:A:192:TYR:HB2	2.47	0.43
1:A:296:TRP:HD1	1:A:298:MET:HE1	1.83	0.43
1:A:166:LYS:HD3	1:A:192:TYR:CE1	2.53	0.43
1:B:269:SER:CB	1:B:312:LYS:HE3	2.48	0.43
1:A:429:LEU:HB3	1:A:435:ILE:HG12	2.01	0.42
1:A:242:ASP:HB3	1:A:244:ASN:OD1	2.19	0.42
1:A:197:ASN:HA	1:A:225:ALA:HB2	2.02	0.41
1:A:421:ALA:HB3	1:A:474:ALA:HB3	2.03	0.41
1:B:421:ALA:HB1	1:B:475:LYS:HG3	2.03	0.41
1:A:213:PHE:HB2	6:A:699:HOH:O	2.20	0.41
1:A:340:ILE:HD12	1:A:391:PHE:HZ	1.85	0.41
1:B:340:ILE:HD12	1:B:391:PHE:HZ	1.87	0.40
1:A:216:LYS:HB3	1:A:216:LYS:HE3	1.89	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	408/488 (84%)	394 (97%)	14 (3%)	0	100	100
1	B	408/488 (84%)	390 (96%)	16 (4%)	2 (0%)	29	16
All	All	816/976 (84%)	784 (96%)	30 (4%)	2 (0%)	47	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	294	PRO
1	B	295	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	377/449 (84%)	369 (98%)	8 (2%)	53	47
1	B	377/449 (84%)	367 (97%)	10 (3%)	44	35
All	All	754/898 (84%)	736 (98%)	18 (2%)	49	41

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	140	VAL
1	A	165	MET
1	A	213	PHE
1	A	252	LEU
1	A	298	MET
1	A	328	ASN
1	A	429	LEU
1	A	484	LYS
1	B	126	ARG
1	B	160	CYS
1	B	163	GLU
1	B	165	MET
1	B	264	LYS
1	B	289	ASN
1	B	296	TRP
1	B	434	LYS
1	B	449	GLU
1	B	484	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	136	HIS
1	A	284	ASN
1	A	392	HIS
1	A	433	ASN

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Mol	Chain	Res	Type
1	B	407	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 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	B	501	-	45,52,52	1.53	4 (8%)	53,80,80	1.32	5 (9%)
4	LSX	B	505	3	17,20,20	1.07	1 (5%)	18,28,28	1.27	1 (5%)
4	LSX	A	503	3	17,20,20	1.05	2 (11%)	18,28,28	1.31	2 (11%)
2	NDP	A	501	-	45,52,52	1.56	4 (8%)	53,80,80	1.32	5 (9%)

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	B	501	-	-	3/30/77/77	0/5/5/5
4	LSX	B	505	3	-	2/21/21/21	0/1/1/1
4	LSX	A	503	3	-	2/21/21/21	0/1/1/1
2	NDP	A	501	-	-	3/30/77/77	0/5/5/5

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NDP	O7N-C7N	6.74	1.40	1.24
2	B	501	NDP	O7N-C7N	6.69	1.40	1.24
2	A	501	NDP	C2A-N3A	3.88	1.38	1.32
2	A	501	NDP	C6N-C5N	3.83	1.40	1.33
2	B	501	NDP	C2A-N3A	3.65	1.38	1.32
2	B	501	NDP	C6N-C5N	3.46	1.39	1.33
2	B	501	NDP	C2A-N1A	2.73	1.39	1.33
2	A	501	NDP	C2A-N1A	2.50	1.38	1.33
4	A	503	LSX	P8-O11	-2.37	1.51	1.54
4	B	505	LSX	P8-O11	-2.29	1.51	1.54
4	A	503	LSX	P8-O9	-2.24	1.51	1.54

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	NDP	N3A-C2A-N1A	-5.97	119.34	128.68
2	B	501	NDP	N3A-C2A-N1A	-5.81	119.60	128.68
4	A	503	LSX	O10-P8-C7	-3.34	104.01	113.35
4	A	503	LSX	O11-P8-O9	3.11	115.98	107.64
4	B	505	LSX	O10-P8-C7	-3.08	104.74	113.35
2	B	501	NDP	C3N-C7N-N7N	3.00	122.99	117.67
2	A	501	NDP	C1B-N9A-C4A	-2.96	121.43	126.64
2	B	501	NDP	C1B-N9A-C4A	-2.56	122.14	126.64
2	B	501	NDP	PN-O3-PA	-2.39	124.62	132.83
2	A	501	NDP	C3N-C7N-N7N	2.39	121.91	117.67
2	B	501	NDP	O7N-C7N-C3N	-2.19	116.77	120.90
2	A	501	NDP	PN-O3-PA	-2.16	125.42	132.83
2	A	501	NDP	O4D-C1D-N1N	2.06	112.09	108.06

There are no chirality outliers.

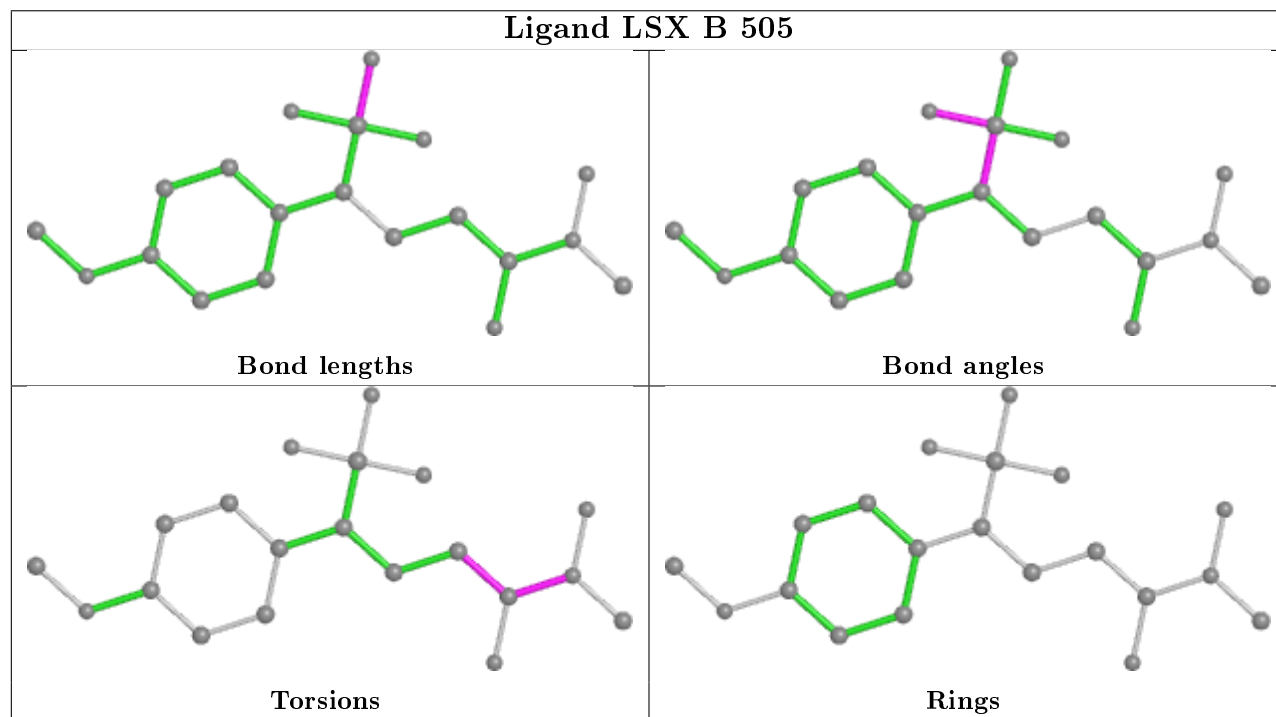
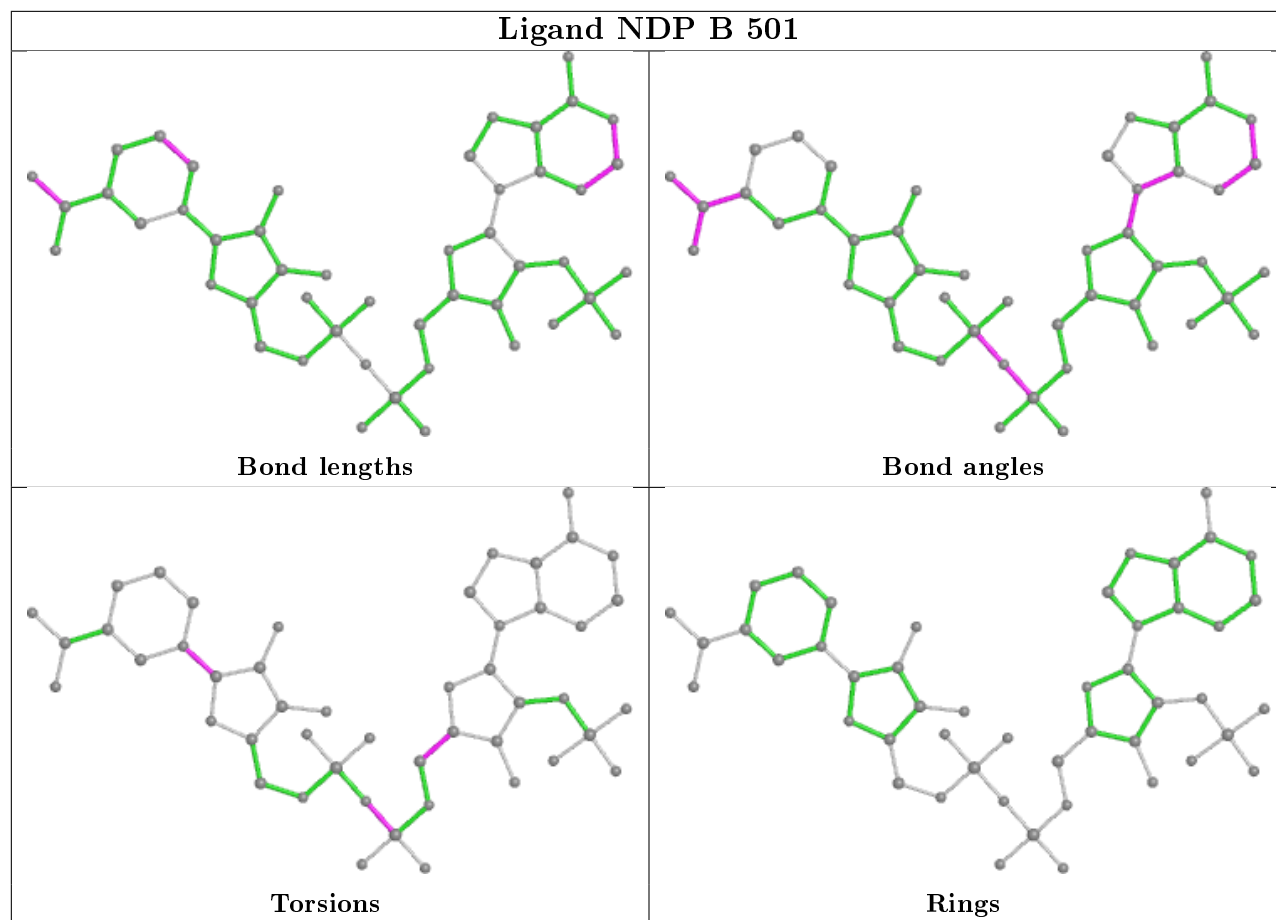
All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	NDP	O4D-C1D-N1N-C6N
2	B	501	NDP	O4D-C1D-N1N-C6N
2	B	501	NDP	PN-O3-PA-O1A
2	A	501	NDP	PN-O3-PA-O1A
4	B	505	LSX	C12-C13-C14-N16
4	A	503	LSX	C12-C13-C14-N16
2	B	501	NDP	O4B-C4B-C5B-O5B
2	A	501	NDP	O4B-C4B-C5B-O5B
4	B	505	LSX	O15-C14-N16-O18
4	A	503	LSX	O15-C14-N16-O18

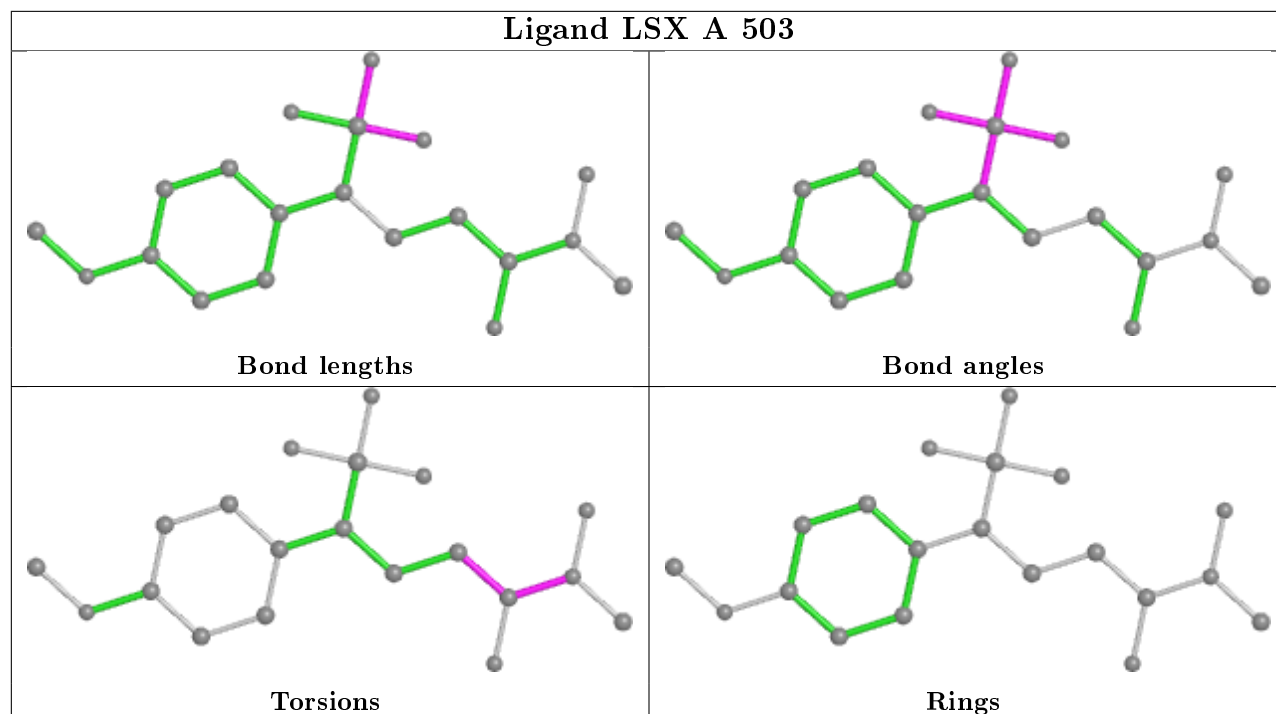
There are no ring outliers.

No monomer is involved in short contacts.

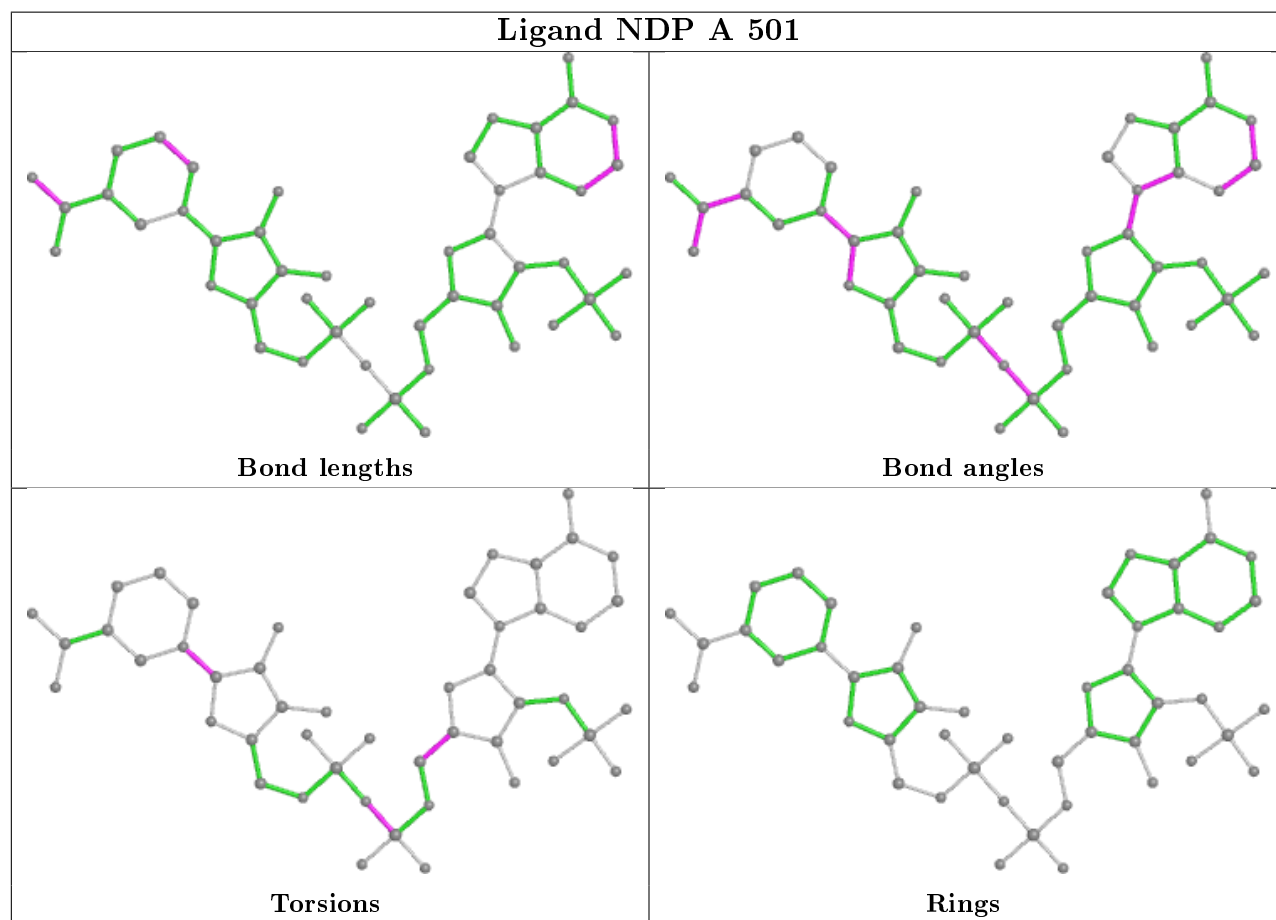
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



Ligand LSX A 503



Ligand NDP A 501



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	410/488 (84%)	0.09	9 (2%) 62 63	15, 25, 45, 58	0
1	B	410/488 (84%)	-0.00	7 (1%) 70 71	15, 22, 40, 51	0
All	All	820/976 (84%)	0.04	16 (1%) 65 66	15, 23, 43, 58	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	295	LYS	5.2
1	B	486	ASN	4.2
1	B	485	HIS	4.0
1	A	150	ASN	3.4
1	A	293	HIS	3.2
1	A	458	GLU	2.9
1	B	296	TRP	2.9
1	A	292	LYS	2.8
1	A	147	LEU	2.8
1	B	188	TYR	2.7
1	B	293	HIS	2.5
1	A	172	ASN	2.4
1	B	106	VAL	2.4
1	A	188	TYR	2.4
1	A	138	LYS	2.3
1	A	153	ASP	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 carbohydrates in this entry.

6.4 Ligands [i](#)

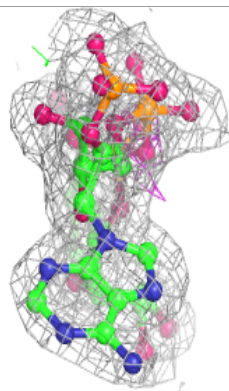
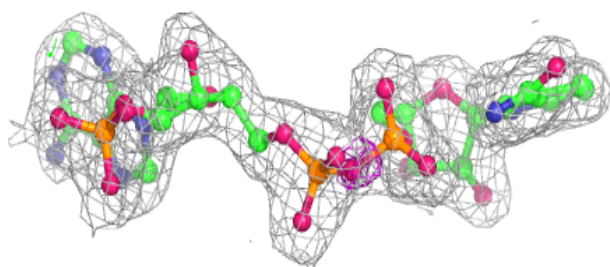
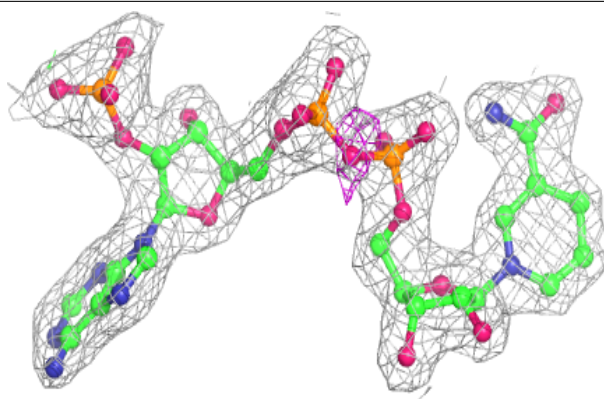
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NDP	A	501	48/48	0.97	0.09	19,25,31,32	0
2	NDP	B	501	48/48	0.98	0.07	16,18,20,21	0
4	LSX	B	505	20/20	0.98	0.08	14,17,23,23	0
4	LSX	A	503	20/20	0.98	0.09	17,20,22,23	0
5	CA	B	503	1/1	0.99	0.07	20,20,20,20	0
5	CA	B	504	1/1	0.99	0.03	26,26,26,26	0
3	MG	B	502	1/1	0.99	0.12	10,10,10,10	0
3	MG	A	502	1/1	1.00	0.15	10,10,10,10	0

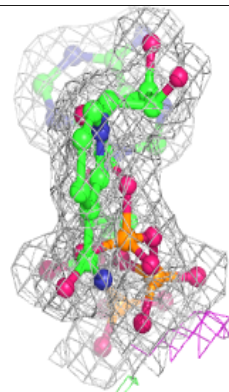
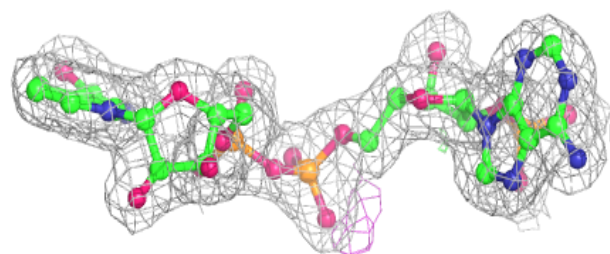
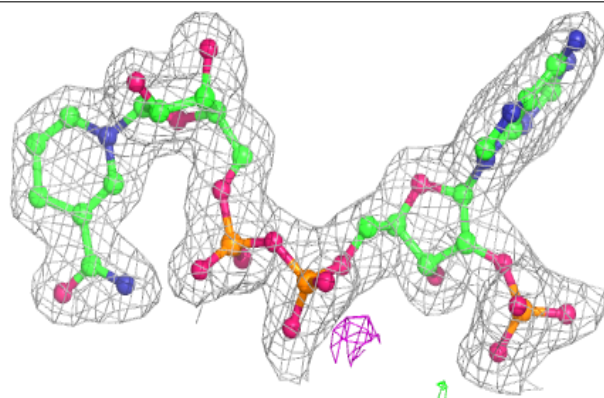
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

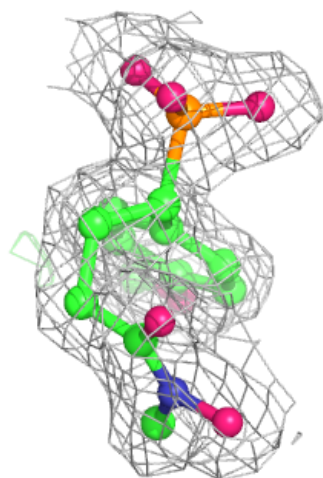
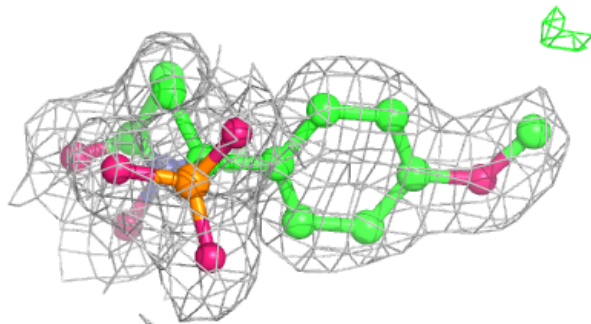
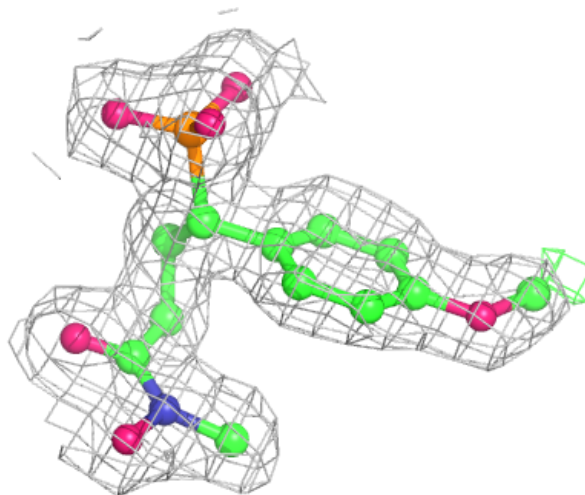
**Electron density around NDP B 501:**

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



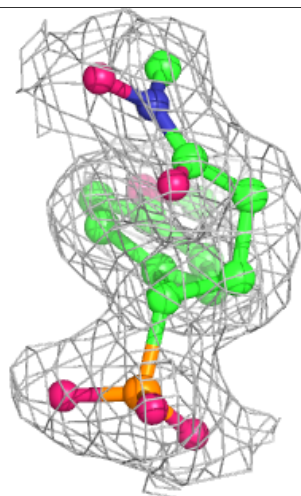
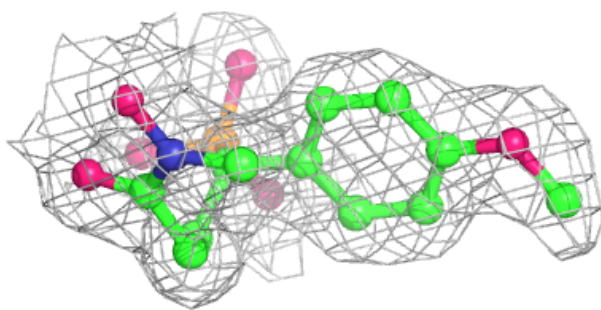
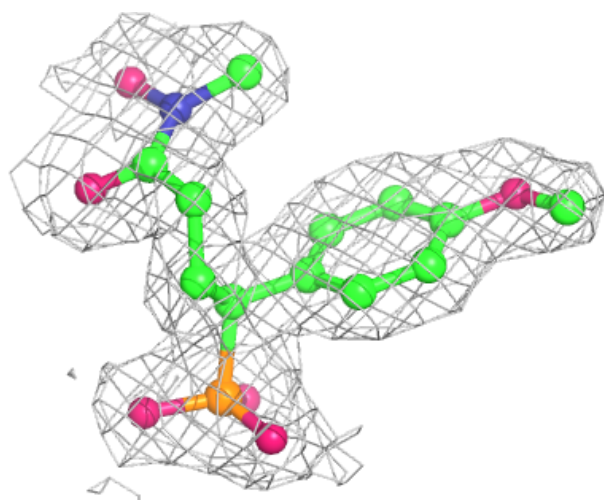
Electron density around LSX B 505:

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



Electron density around LSX 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)



6.5 Other polymers ⓘ

There are no such residues in this entry.