Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 03:18 pm BST

PDB ID	:	1U72
Title	:	Understanding the Role of Leu22 Variants in Methotrexate Resistance: Comparison of Wild-type and Leu22Arg Variant Mouse and Human Dihydrfolate Reductase Ternary Crystal Complexes with Methotrexate and NADPH
Authors	:	Cody, V.
Deposited on	:	2004-08-02
Resolution	:	1.90 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:

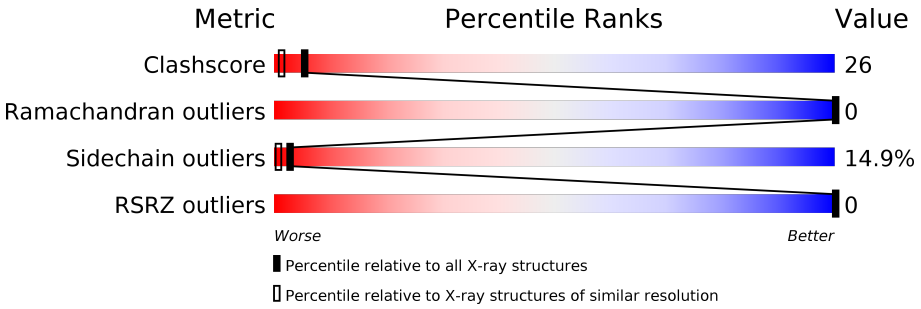
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 <=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	186	43% 40% 15% .

2 Entry composition

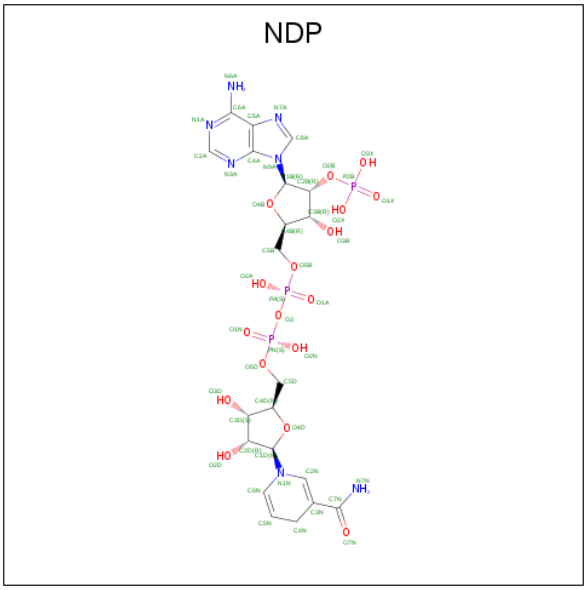
There are 4 unique types of molecules in this entry. The entry contains 1629 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Dihydrofolate reductase.

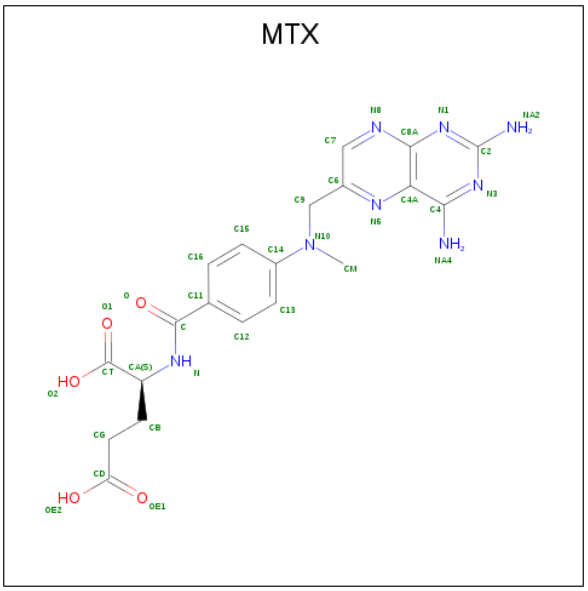
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	186	Total	C	N	O	S	0	0	0
			1502	963	253	279	7			

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



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

- Molecule 3 is METHOTREXATE (three-letter code: MTX) (formula: $C_{20}H_{22}N_8O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	33	20	8	5	0	0

- Molecule 4 is water.

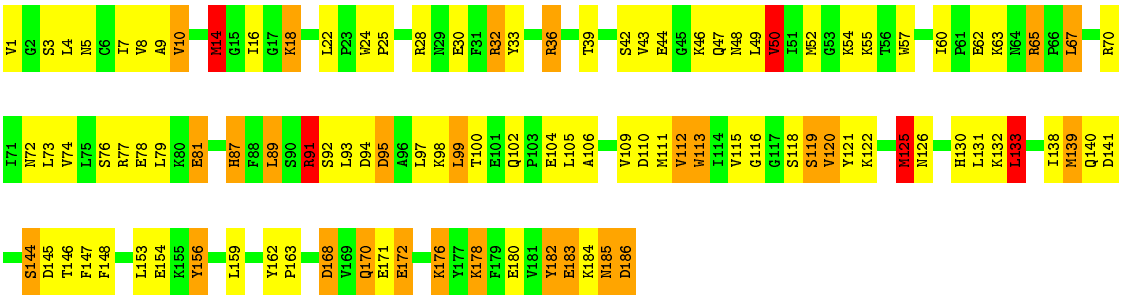
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	46	46	46	0	0

3 Residue-property plots (i)

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.

- Molecule 1: Dihydrofolate reductase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	87.38Å 87.38Å 76.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.90 53.88 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-1.90) 37.2 (53.88-1.90)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.18 (at 1.90Å)	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.159 , 0.213 0.157 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	24.9	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 78.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.064 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1629	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 7.42% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, MTX

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	0.96	0/1537	2.32	72/2073 (3.5%)

There are no bond length outliers.

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	91	ARG	NE-CZ-NH2	-14.75	112.92	120.30
1	A	32	ARG	NE-CZ-NH1	14.59	127.60	120.30
1	A	91	ARG	NE-CZ-NH1	13.66	127.13	120.30
1	A	145	ASP	CB-CG-OD1	13.28	130.25	118.30
1	A	65	ARG	NE-CZ-NH1	12.16	126.38	120.30
1	A	133	LEU	CA-CB-CG	11.77	142.36	115.30
1	A	172	GLU	CA-CB-CG	10.81	137.18	113.40
1	A	125	MET	CA-CB-CG	10.21	130.66	113.30
1	A	77	ARG	NE-CZ-NH1	9.64	125.12	120.30
1	A	162	TYR	CB-CG-CD1	-9.13	115.52	121.00
1	A	182	TYR	CB-CG-CD1	-9.07	115.56	121.00
1	A	162	TYR	CB-CG-CD2	8.79	126.27	121.00
1	A	95	ASP	CB-CG-OD1	-8.61	110.56	118.30
1	A	36	ARG	NE-CZ-NH2	8.27	124.43	120.30
1	A	168	ASP	CB-CG-OD2	-8.16	110.95	118.30
1	A	141	ASP	CB-CG-OD1	7.84	125.36	118.30
1	A	156	TYR	CB-CG-CD1	-7.71	116.37	121.00
1	A	156	TYR	CB-CG-CD2	7.55	125.53	121.00
1	A	140	GLN	N-CA-CB	7.51	124.11	110.60
1	A	126	ASN	CA-CB-CG	7.25	129.34	113.40
1	A	18	LYS	N-CA-CB	7.22	123.60	110.60
1	A	33	TYR	CB-CG-CD2	-7.22	116.67	121.00
1	A	110	ASP	CB-CG-OD1	7.14	124.73	118.30
1	A	186	ASP	CA-C-O	-7.07	105.25	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	67	LEU	O-C-N	7.02	133.94	122.70
1	A	145	ASP	OD1-CG-OD2	-6.87	110.24	123.30
1	A	154	GLU	CA-CB-CG	6.58	127.87	113.40
1	A	180	GLU	CG-CD-OE2	-6.42	105.47	118.30
1	A	132	LYS	O-C-N	6.40	132.94	122.70
1	A	180	GLU	CG-CD-OE1	6.38	131.07	118.30
1	A	145	ASP	CA-CB-CG	6.32	127.29	113.40
1	A	32	ARG	NE-CZ-NH2	-6.29	117.16	120.30
1	A	120	VAL	O-C-N	6.22	132.65	122.70
1	A	65	ARG	NE-CZ-NH2	-6.19	117.20	120.30
1	A	91	ARG	CD-NE-CZ	6.18	132.25	123.60
1	A	186	ASP	CB-CG-OD2	-6.17	112.75	118.30
1	A	78	GLU	CG-CD-OE1	6.08	130.46	118.30
1	A	168	ASP	OD1-CG-OD2	6.01	134.72	123.30
1	A	10	VAL	CB-CA-C	-5.96	100.08	111.40
1	A	113	TRP	C-N-CA	5.87	136.37	121.70
1	A	163	PRO	C-N-CA	5.83	134.55	122.30
1	A	119	SER	O-C-N	5.82	132.01	122.70
1	A	9	ALA	C-N-CA	5.81	136.22	121.70
1	A	183	GLU	CG-CD-OE1	5.67	129.63	118.30
1	A	32	ARG	CD-NE-CZ	5.65	131.51	123.60
1	A	48	ASN	CB-CG-OD1	-5.64	110.33	121.60
1	A	7	ILE	CB-CA-C	5.61	122.81	111.60
1	A	87	HIS	O-C-N	5.55	131.58	122.70
1	A	115	VAL	O-C-N	5.55	132.63	123.20
1	A	14	MET	CG-SD-CE	-5.43	91.52	100.20
1	A	50	VAL	CB-CA-C	5.40	121.67	111.40
1	A	139	MET	CA-C-N	5.40	129.09	117.20
1	A	79	LEU	CA-CB-CG	5.35	127.61	115.30
1	A	138	ILE	CB-CG1-CD1	5.32	128.78	113.90
1	A	118	SER	CB-CA-C	-5.31	100.01	110.10
1	A	170	GLN	CG-CD-OE1	5.31	132.22	121.60
1	A	115	VAL	CB-CA-C	5.30	121.47	111.40
1	A	77	ARG	CB-CA-C	5.28	120.96	110.40
1	A	3	SER	CA-CB-OG	-5.24	97.06	111.20
1	A	183	GLU	N-CA-CB	5.21	119.98	110.60
1	A	42	SER	CB-CA-C	-5.17	100.27	110.10
1	A	81	GLU	OE1-CD-OE2	-5.16	117.11	123.30
1	A	138	ILE	N-CA-C	-5.14	97.11	111.00
1	A	182	TYR	CB-CG-CD2	5.12	124.07	121.00
1	A	115	VAL	CA-CB-CG2	5.12	118.58	110.90
1	A	50	VAL	CA-CB-CG2	5.11	118.56	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	36	ARG	NH1-CZ-NH2	-5.11	113.78	119.40
1	A	144	SER	O-C-N	5.11	130.87	122.70
1	A	62	GLU	OE1-CD-OE2	5.08	129.40	123.30
1	A	126	ASN	CB-CG-OD1	5.03	131.65	121.60
1	A	176	LYS	CB-CA-C	-5.01	100.37	110.40
1	A	183	GLU	CG-CD-OE2	-5.01	108.28	118.30

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	1502	0	1511	79	0
2	A	48	0	26	6	0
3	A	33	0	20	3	0
4	A	46	0	0	3	0
All	All	1629	0	1557	82	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 26.

All (82) 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:43:VAL:HG11	1:A:46:LYS:HD2	1.21	1.09
1:A:99:LEU:HD22	1:A:105:LEU:HD12	1.33	1.09
1:A:1:VAL:CG2	1:A:100:THR:HG22	1.88	1.01
1:A:43:VAL:CG1	1:A:46:LYS:HD2	1.90	1.01
1:A:1:VAL:HG22	1:A:100:THR:HG22	1.40	1.01
1:A:99:LEU:CD2	1:A:105:LEU:HD12	2.00	0.91
1:A:130:HIS:ND1	1:A:184:LYS:O	2.04	0.91
1:A:168:ASP:O	1:A:170:GLN:NE2	2.06	0.86
1:A:99:LEU:HD22	1:A:105:LEU:CD1	2.05	0.85
1:A:43:VAL:HG11	1:A:46:LYS:CD	2.07	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:ASN:H	1:A:87:HIS:HD2	1.26	0.83
1:A:4:LEU:HD23	1:A:131:LEU:CD1	2.09	0.82
1:A:93:LEU:O	1:A:97:LEU:HG	1.79	0.81
1:A:4:LEU:HD12	1:A:112:VAL:HG22	1.68	0.76
1:A:73:LEU:HD23	1:A:73:LEU:C	2.06	0.76
1:A:94:ASP:O	1:A:98:LYS:HG3	1.90	0.72
1:A:159:LEU:O	4:A:212:HOH:O	2.06	0.72
1:A:36:ARG:HG2	1:A:36:ARG:NH1	2.05	0.70
1:A:184:LYS:HG2	1:A:185:ASN:N	2.07	0.68
1:A:99:LEU:HA	1:A:102:GLN:HG2	1.78	0.66
1:A:1:VAL:HG21	1:A:100:THR:HG22	1.75	0.66
1:A:36:ARG:HH11	1:A:36:ARG:HG2	1.60	0.65
1:A:91:ARG:HB3	4:A:221:HOH:O	1.97	0.64
1:A:4:LEU:HD23	1:A:131:LEU:HD13	1.80	0.63
1:A:50:VAL:HG23	1:A:52:MET:HE2	1.81	0.63
1:A:72:ASN:N	1:A:72:ASN:HD22	1.99	0.61
1:A:14:MET:O	1:A:147:PHE:HD2	1.84	0.61
1:A:36:ARG:HH11	1:A:36:ARG:CG	2.15	0.60
1:A:121:TYR:O	1:A:125:MET:HB2	2.02	0.59
1:A:24:TRP:HB2	1:A:25:PRO:HD2	1.86	0.58
2:A:187:NDP:H52A	2:A:187:NDP:H8A	1.86	0.57
1:A:120:VAL:HG22	2:A:187:NDP:N7A	2.20	0.56
1:A:73:LEU:HD23	1:A:74:VAL:N	2.21	0.56
1:A:133:LEU:HD22	1:A:156:TYR:CE2	2.40	0.56
1:A:50:VAL:HA	1:A:113:TRP:O	2.06	0.56
1:A:130:HIS:HE1	1:A:183:GLU:CG	2.19	0.56
1:A:50:VAL:HG21	1:A:67:LEU:HD12	1.88	0.55
1:A:171:GLU:HA	1:A:176:LYS:HA	1.88	0.55
1:A:72:ASN:H	1:A:87:HIS:CD2	2.16	0.55
1:A:50:VAL:HG23	1:A:52:MET:CE	2.38	0.54
1:A:47:GLN:O	1:A:109:VAL:HA	2.09	0.53
1:A:182:TYR:CD1	1:A:182:TYR:N	2.76	0.53
1:A:139:MET:SD	1:A:178:LYS:HD3	2.50	0.52
1:A:168:ASP:N	1:A:168:ASP:OD2	2.42	0.51
1:A:28:ARG:O	1:A:32:ARG:HG3	2.11	0.51
1:A:130:HIS:CE1	1:A:183:GLU:HG3	2.46	0.51
1:A:39:THR:HG22	1:A:39:THR:O	2.10	0.50
1:A:130:HIS:CE1	1:A:184:LYS:O	2.64	0.49
1:A:139:MET:HB2	1:A:176:LYS:O	2.12	0.49
1:A:57:TRP:O	1:A:65:ARG:HD2	2.13	0.49
1:A:184:LYS:CG	1:A:185:ASN:N	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ILE:O	2:A:187:NDP:H2N	2.14	0.47
1:A:102:GLN:O	1:A:106:ALA:N	2.44	0.46
1:A:73:LEU:CD2	1:A:73:LEU:C	2.80	0.46
1:A:60:ILE:O	1:A:65:ARG:HD3	2.16	0.46
1:A:130:HIS:HE1	1:A:183:GLU:HG3	1.82	0.45
1:A:133:LEU:HD22	1:A:156:TYR:CD2	2.52	0.45
1:A:52:MET:HA	1:A:116:GLY:O	2.17	0.44
1:A:91:ARG:HE	1:A:92:SER:HB3	1.83	0.43
1:A:120:VAL:CG2	2:A:187:NDP:N7A	2.81	0.43
1:A:49:LEU:HD23	1:A:112:VAL:HB	2.00	0.43
1:A:72:ASN:ND2	1:A:72:ASN:N	2.63	0.43
1:A:8:VAL:HG21	1:A:148:PHE:CD1	2.54	0.42
1:A:130:HIS:ND1	1:A:185:ASN:HB2	2.34	0.42
1:A:39:THR:CG2	1:A:39:THR:O	2.68	0.42
1:A:81:GLU:C	1:A:89:LEU:HD23	2.39	0.42
1:A:130:HIS:HE1	1:A:183:GLU:CD	2.22	0.42
1:A:91:ARG:NE	1:A:95:ASP:OD2	2.52	0.42
1:A:22:LEU:HD11	3:A:188:MTX:H7	2.01	0.42
3:A:188:MTX:HM1	3:A:188:MTX:H15	1.82	0.42
1:A:170:GLN:O	1:A:176:LYS:HA	2.19	0.41
1:A:24:TRP:HB2	1:A:25:PRO:CD	2.50	0.41
1:A:1:VAL:CG1	1:A:100:THR:HG21	2.50	0.41
1:A:70:ARG:O	1:A:72:ASN:ND2	2.54	0.41
1:A:4:LEU:HD23	1:A:131:LEU:HD11	1.97	0.41
1:A:55:LYS:NZ	4:A:194:HOH:O	2.37	0.41
1:A:70:ARG:HH22	3:A:188:MTX:CT	2.34	0.41
1:A:184:LYS:HG2	1:A:185:ASN:H	1.84	0.41
2:A:187:NDP:H52N	2:A:187:NDP:H6N	2.02	0.41
1:A:76:SER:OG	2:A:187:NDP:O2X	2.31	0.41
1:A:24:TRP:HA	1:A:25:PRO:HD3	1.76	0.40
1:A:184:LYS:HE2	1:A:186:ASP:CG	2.42	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	184/186 (99%)	176 (96%)	8 (4%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	168/168 (100%)	143 (85%)	25 (15%)	3 1

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	10	VAL
1	A	14	MET
1	A	18	LYS
1	A	30	GLU
1	A	44	GLU
1	A	50	VAL
1	A	54	LYS
1	A	63	LYS
1	A	89	LEU
1	A	91	ARG
1	A	99	LEU
1	A	104	GLU
1	A	111	MET
1	A	112	VAL
1	A	119	SER
1	A	122	LYS
1	A	125	MET
1	A	133	LEU
1	A	144	SER
1	A	146	THR

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Mol	Chain	Res	Type
1	A	153	LEU
1	A	172	GLU
1	A	178	LYS
1	A	185	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	185	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 carbohydrates in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NDP	A	187	-	45,52,52	2.52	13 (28%)	53,80,80	2.17	18 (33%)
3	MTX	A	188	-	29,35,35	0.90	0	38,49,49	2.35	13 (34%)

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	187	-	-	13/30/77/77	0/5/5/5
3	MTX	A	188	-	-	3/19/25/25	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	187	NDP	O4B-C4B	-9.69	1.23	1.45
2	A	187	NDP	P2B-O2B	6.34	1.71	1.59
2	A	187	NDP	C3B-C4B	4.37	1.64	1.53
2	A	187	NDP	C5A-C4A	-4.15	1.29	1.40
2	A	187	NDP	O3B-C3B	3.76	1.51	1.43
2	A	187	NDP	C6A-C5A	3.52	1.56	1.43
2	A	187	NDP	C8A-N7A	-3.23	1.28	1.34
2	A	187	NDP	O4B-C1B	3.09	1.45	1.41
2	A	187	NDP	C1D-N1N	2.76	1.54	1.46
2	A	187	NDP	PN-O1N	-2.73	1.41	1.50
2	A	187	NDP	O4D-C1D	2.64	1.48	1.42
2	A	187	NDP	P2B-O3X	-2.34	1.45	1.54
2	A	187	NDP	C4N-C3N	2.09	1.54	1.49

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	188	MTX	CA-N-C	6.99	131.35	122.34
3	A	188	MTX	CG-CB-CA	-5.73	101.47	113.04
2	A	187	NDP	O3X-P2B-O2X	5.03	126.86	107.64
3	A	188	MTX	C2-N1-C8A	4.49	120.49	115.36
2	A	187	NDP	O7N-C7N-C3N	-4.42	112.57	120.90
3	A	188	MTX	O-C-C11	-4.28	113.30	120.94
2	A	187	NDP	O4D-C4D-C3D	-4.20	96.81	105.11
2	A	187	NDP	C3N-C7N-N7N	3.90	124.59	117.67
2	A	187	NDP	O4B-C1B-C2B	-3.88	99.86	106.59
2	A	187	NDP	O3B-C3B-C4B	-3.78	100.11	111.05
2	A	187	NDP	O3D-C3D-C4D	-3.54	100.80	111.05
2	A	187	NDP	C5B-C4B-C3B	-3.53	101.95	115.18
3	A	188	MTX	N8-C8A-N1	3.51	119.82	115.82
3	A	188	MTX	O-C-N	3.50	128.90	122.45
2	A	187	NDP	C2D-C1D-N1N	3.45	121.94	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	187	NDP	PN-O3-PA	3.32	144.21	132.83
2	A	187	NDP	PN-O5D-C5D	3.23	140.63	121.68
3	A	188	MTX	C4-C4A-N5	3.22	122.80	120.33
3	A	188	MTX	N1-C2-N3	-2.75	123.56	127.22
2	A	187	NDP	O5D-C5D-C4D	-2.65	99.88	108.99
2	A	187	NDP	C2B-C3B-C4B	-2.61	96.32	101.99
2	A	187	NDP	O5D-PN-O1N	2.59	119.18	109.07
3	A	188	MTX	CB-CG-CD	-2.43	108.37	113.59
3	A	188	MTX	C4A-C4-NA4	2.32	123.88	120.35
3	A	188	MTX	C8A-C4A-N5	-2.30	119.63	122.41
3	A	188	MTX	C4A-C8A-N1	-2.29	117.99	121.71
2	A	187	NDP	O2A-PA-O1A	2.29	123.55	112.24
2	A	187	NDP	O2B-C2B-C1B	-2.21	102.16	110.10
2	A	187	NDP	C1B-N9A-C4A	2.19	130.48	126.64
2	A	187	NDP	C2A-N1A-C6A	-2.14	115.10	118.75
3	A	188	MTX	C7-C6-N5	2.01	122.16	120.85

There are no chirality outliers.

All (16) torsion outliers are listed below:

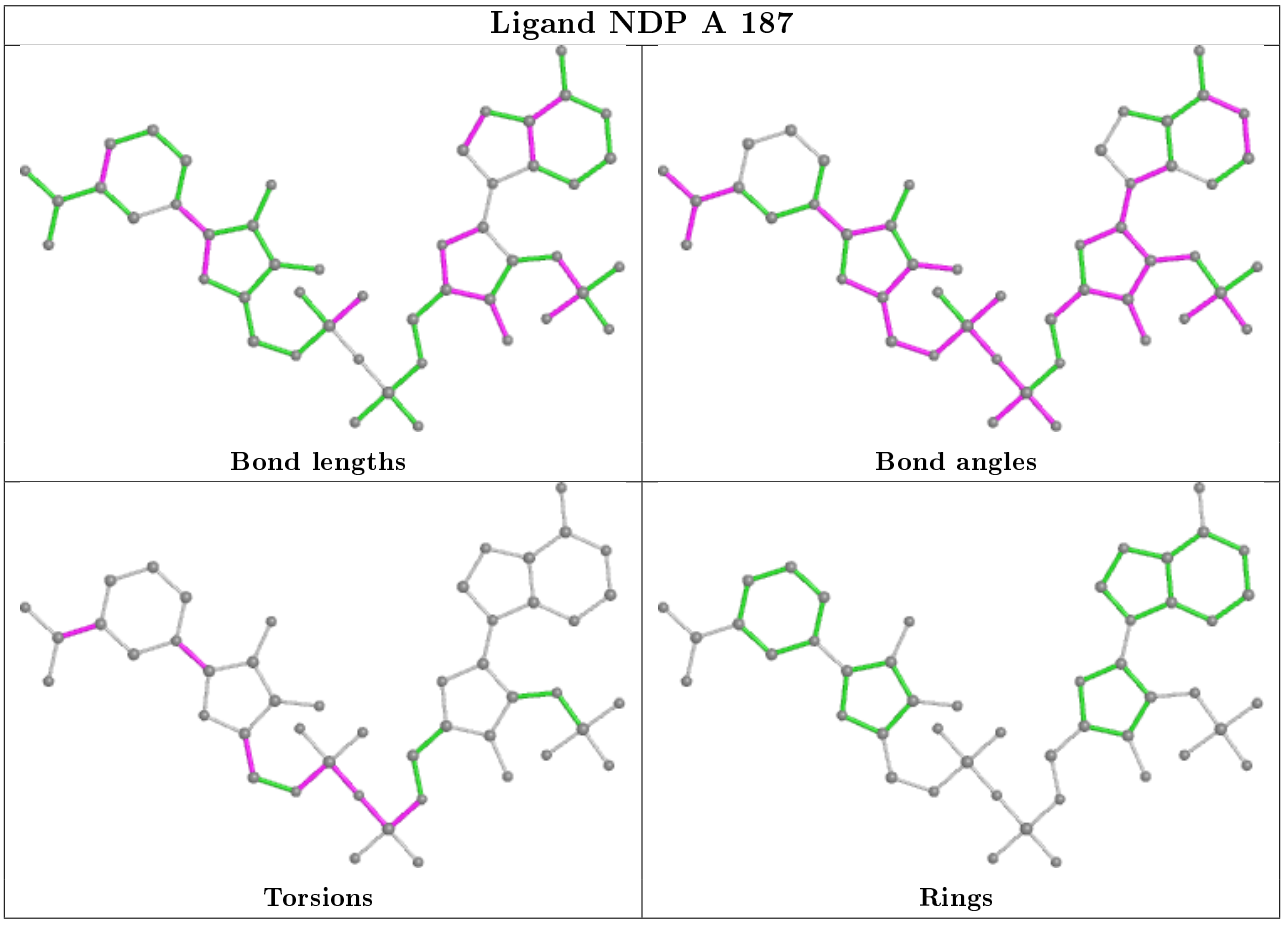
Mol	Chain	Res	Type	Atoms
2	A	187	NDP	C5D-O5D-PN-O3
2	A	187	NDP	C3D-C4D-C5D-O5D
3	A	188	MTX	CT-CA-CB-CG
3	A	188	MTX	N-CA-CB-CG
2	A	187	NDP	O4D-C4D-C5D-O5D
2	A	187	NDP	C2D-C1D-N1N-C2N
2	A	187	NDP	C5D-O5D-PN-O1N
2	A	187	NDP	C5D-O5D-PN-O2N
3	A	188	MTX	C6-C9-N10-CM
2	A	187	NDP	O4D-C1D-N1N-C2N
2	A	187	NDP	C2D-C1D-N1N-C6N
2	A	187	NDP	O4D-C1D-N1N-C6N
2	A	187	NDP	C5B-O5B-PA-O3
2	A	187	NDP	PN-O3-PA-O1A
2	A	187	NDP	PA-O3-PN-O2N
2	A	187	NDP	C2N-C3N-C7N-N7N

There are no ring outliers.

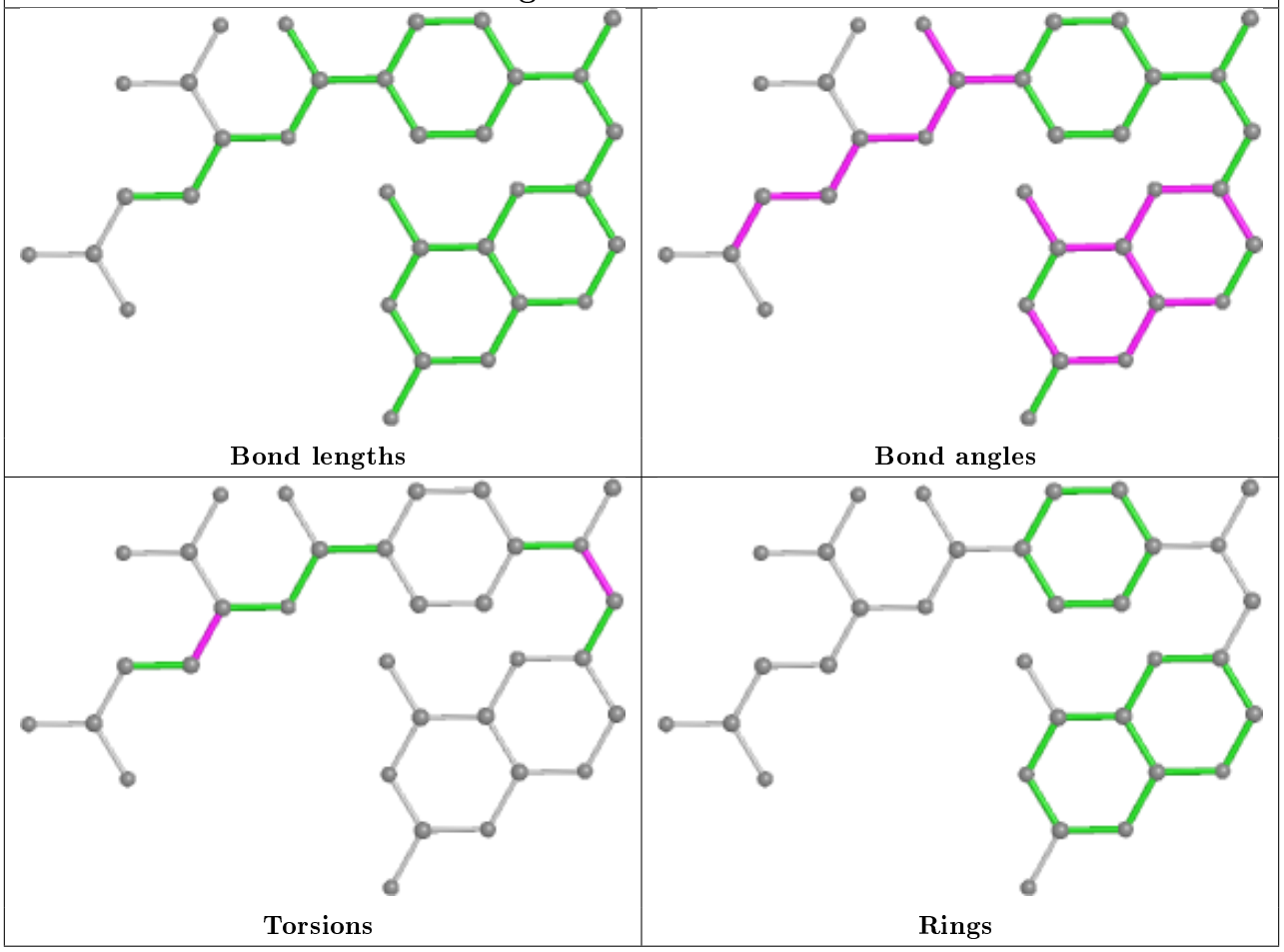
2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	187	NDP	6	0
3	A	188	MTX	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 then 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 MTX A 188



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, 95^{th} 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	186/186 (100%)	-0.75	0 100 100	16, 25, 41, 49	0

There are no RSRZ outliers to report.

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 carbohydrates in this entry.

6.4 Ligands

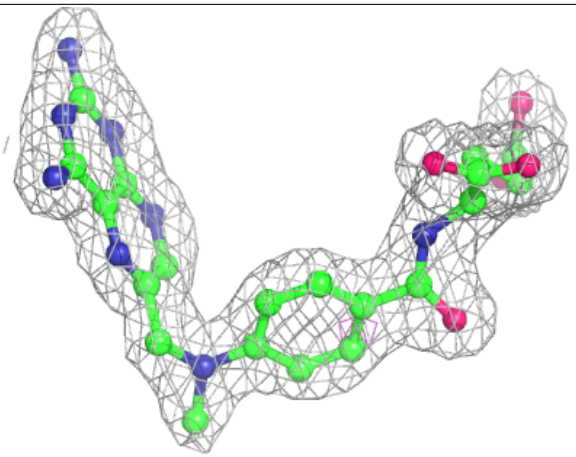
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

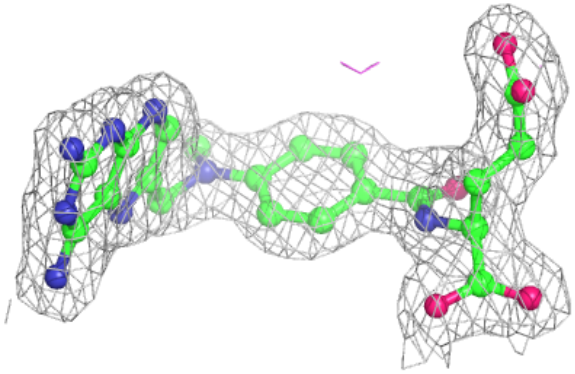
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MTX	A	188	33/33	0.98	0.07	15,19,28,28	0
2	NDP	A	187	48/48	0.99	0.06	16,23,28,28	0

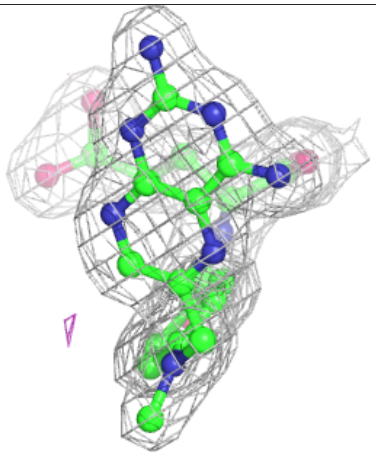
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around MTX A 188:

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

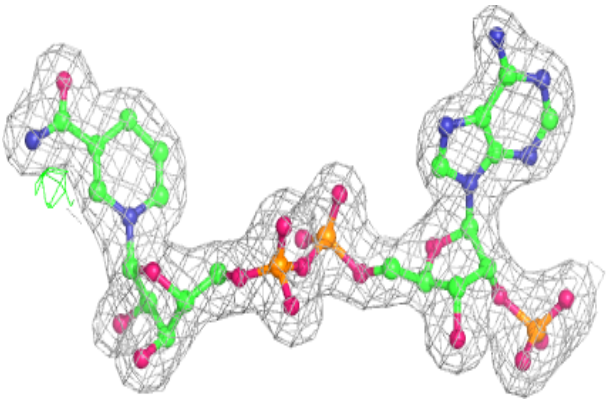


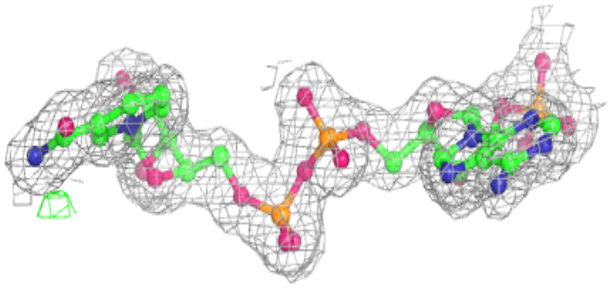




Electron density around NDP A 187:

$2mF_o$-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.