



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 05:00 PM BST

PDB ID : 6IUD
Title : Structure of Helicobacter pylori Soj-ADP complex bound to DNA
Authors : Yen, C.Y.; Chu, C.H.; Sun, Y.J.
Deposited on : 2018-11-28
Resolution : 2.51 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 : 2.13.1
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) : 2.13.1

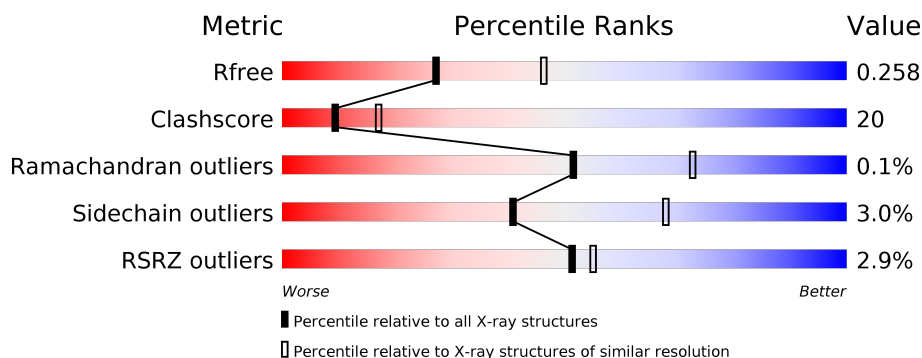
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	276	<div> <div>2%</div> <div> <div></div> <div>61%</div> <div>30%</div> <div>• • •</div> </div> </div>
1	B	276	<div> <div>3%</div> <div> <div></div> <div>63%</div> <div>30%</div> <div>• •</div> </div> </div>
1	C	276	<div> <div>2%</div> <div> <div></div> <div>66%</div> <div>28%</div> <div>• • •</div> </div> </div>
1	D	276	<div> <div>3%</div> <div> <div></div> <div>61%</div> <div>30%</div> <div>• • •</div> </div> </div>
2	E	24	<div> <div>4%</div> <div> <div></div> <div>46%</div> <div>42%</div> <div>13%</div> </div> </div>
3	F	24	<div> <div>17%</div> <div> <div></div> <div>29%</div> <div>58%</div> <div>13%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9308 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 SpoOJ regulator (Soj).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	0	0
			2053	1328	337	380	8			
1	B	264	Total	C	N	O	S	0	0	0
			2053	1328	337	380	8			
1	C	264	Total	C	N	O	S	0	0	0
			2053	1328	337	380	8			
1	D	264	Total	C	N	O	S	0	0	0
			2053	1328	337	380	8			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP O25759
A	-10	ARG	-	expression tag	UNP O25759
A	-9	GLY	-	expression tag	UNP O25759
A	-8	SER	-	expression tag	UNP O25759
A	-7	HIS	-	expression tag	UNP O25759
A	-6	HIS	-	expression tag	UNP O25759
A	-5	HIS	-	expression tag	UNP O25759
A	-4	HIS	-	expression tag	UNP O25759
A	-3	HIS	-	expression tag	UNP O25759
A	-2	HIS	-	expression tag	UNP O25759
A	-1	GLY	-	expression tag	UNP O25759
A	0	SER	-	expression tag	UNP O25759
B	-11	MET	-	initiating methionine	UNP O25759
B	-10	ARG	-	expression tag	UNP O25759
B	-9	GLY	-	expression tag	UNP O25759
B	-8	SER	-	expression tag	UNP O25759
B	-7	HIS	-	expression tag	UNP O25759
B	-6	HIS	-	expression tag	UNP O25759
B	-5	HIS	-	expression tag	UNP O25759
B	-4	HIS	-	expression tag	UNP O25759
B	-3	HIS	-	expression tag	UNP O25759

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	expression tag	UNP O25759
B	-1	GLY	-	expression tag	UNP O25759
B	0	SER	-	expression tag	UNP O25759
C	-11	MET	-	initiating methionine	UNP O25759
C	-10	ARG	-	expression tag	UNP O25759
C	-9	GLY	-	expression tag	UNP O25759
C	-8	SER	-	expression tag	UNP O25759
C	-7	HIS	-	expression tag	UNP O25759
C	-6	HIS	-	expression tag	UNP O25759
C	-5	HIS	-	expression tag	UNP O25759
C	-4	HIS	-	expression tag	UNP O25759
C	-3	HIS	-	expression tag	UNP O25759
C	-2	HIS	-	expression tag	UNP O25759
C	-1	GLY	-	expression tag	UNP O25759
C	0	SER	-	expression tag	UNP O25759
D	-11	MET	-	initiating methionine	UNP O25759
D	-10	ARG	-	expression tag	UNP O25759
D	-9	GLY	-	expression tag	UNP O25759
D	-8	SER	-	expression tag	UNP O25759
D	-7	HIS	-	expression tag	UNP O25759
D	-6	HIS	-	expression tag	UNP O25759
D	-5	HIS	-	expression tag	UNP O25759
D	-4	HIS	-	expression tag	UNP O25759
D	-3	HIS	-	expression tag	UNP O25759
D	-2	HIS	-	expression tag	UNP O25759
D	-1	GLY	-	expression tag	UNP O25759
D	0	SER	-	expression tag	UNP O25759

- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*CP*CP*CP*TP*GP*TP*TP*TP*CP*AP*CP*GP*TP*GP*GP*AP*AP*CP*AP*CP*CP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	24	Total	C	N	O	P	0	0	0
			483	231	81	147	24			

- Molecule 3 is a DNA chain called DNA (5'-D(P*AP*GP*GP*GP*TP*GP*TP*TP*CP*CP*AP*CP*GP*TP*GP*AP*AP*AP*CP*AP*GP*GP*GP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	24	Total	C	N	O	P	0	0	0
			501	236	100	141	24			

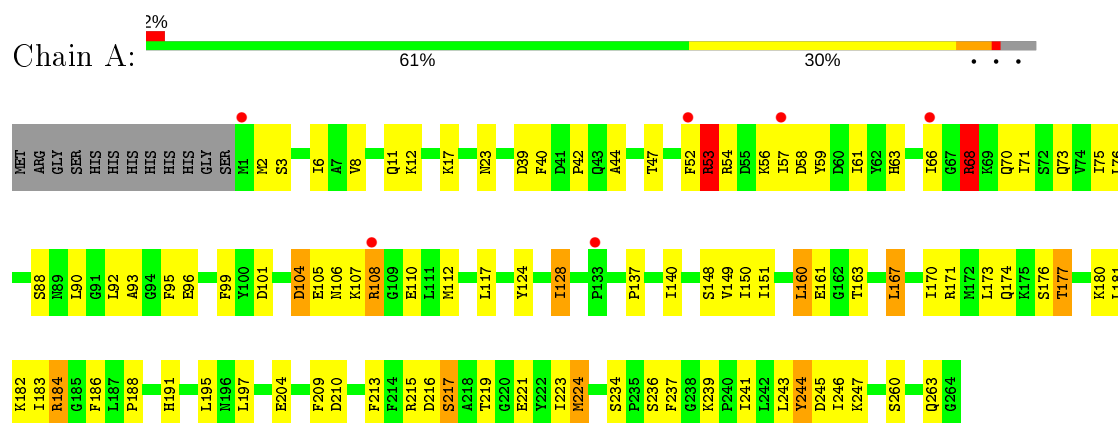
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Mg 1 1	0	0
5	A	1	Total Mg 1 1	0	0
5	D	1	Total Mg 1 1	0	0
5	C	1	Total Mg 1 1	0	0

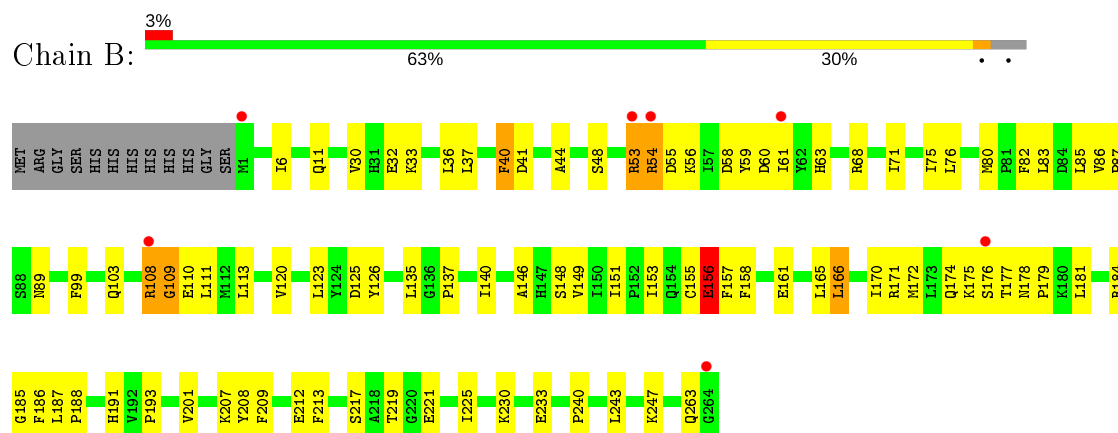
3 Residue-property plots

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.

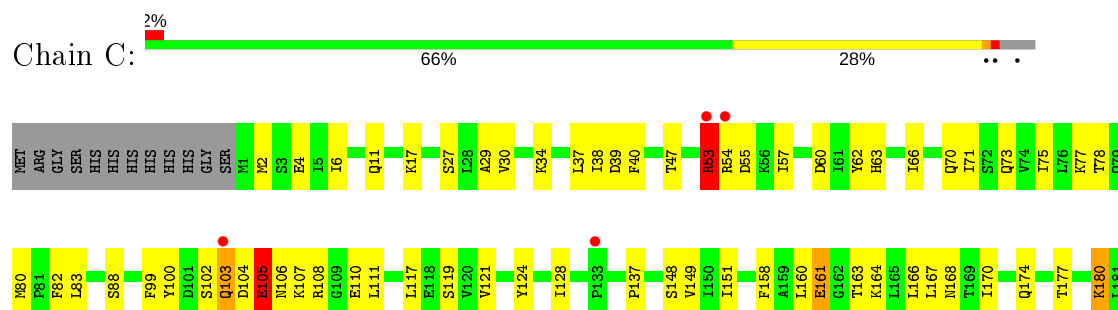
- Molecule 1: SpoOJ regulator (Soj)



- Molecule 1: SpoOJ regulator (Soj)

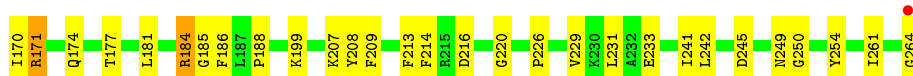


- Molecule 1: SpoOJ regulator (Soj)





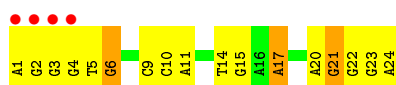
• Molecule 1: SpoOJ regulator (Soj)



• Molecule 2: DNA (5'-D(P*TP*CP*CP*CP*TP*GP*TP*TP*TP*CP*AP*CP*GP*TP*GP*GP*AP*AP*CP*AP*CP*CP*CP*T)-3')



• Molecule 3: DNA (5'-D(P*AP*GP*GP*GP*TP*GP*TP*TP*CP*CP*AP*CP*GP*TP*GP*A P*AP*AP*CP*AP*GP*GP*GP*A)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	74.77Å 74.69Å 80.75Å 71.54° 71.59° 67.73°	Depositor
Resolution (Å)	29.95 – 2.51 29.95 – 2.51	Depositor EDS
% Data completeness (in resolution range)	95.7 (29.95-2.51) 91.5 (29.95-2.51)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.205 , 0.258 0.206 , 0.258	Depositor DCC
R_{free} test set	2443 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.457 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9308	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.37% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ADP

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	0.70	2/2091 (0.1%)	1.11	16/2826 (0.6%)
1	B	0.88	8/2091 (0.4%)	1.10	11/2826 (0.4%)
1	C	0.71	5/2091 (0.2%)	1.04	10/2826 (0.4%)
1	D	0.78	5/2091 (0.2%)	1.10	12/2826 (0.4%)
2	E	1.22	2/538 (0.4%)	1.25	4/826 (0.5%)
3	F	1.32	4/564 (0.7%)	1.26	3/870 (0.3%)
All	All	0.84	26/9466 (0.3%)	1.11	56/13000 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	1
1	C	0	2
1	D	0	1
All	All	0	7

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	108	ARG	CG-CD	17.66	1.96	1.51
1	B	108	ARG	NE-CZ	10.21	1.46	1.33
1	B	108	ARG	CZ-NH1	8.31	1.43	1.33
1	D	54	ARG	CG-CD	-7.50	1.33	1.51
1	D	59	TYR	CE2-CZ	-7.35	1.28	1.38
1	A	177	THR	CB-CG2	-7.35	1.28	1.52
3	F	17	DA	C3'-O3'	-7.29	1.34	1.44
1	C	103	GLN	CG-CD	-6.38	1.36	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	68	ARG	CG-CD	-6.27	1.36	1.51
1	D	199	LYS	CG-CD	6.11	1.73	1.52
1	C	161	GLU	CD-OE2	-5.79	1.19	1.25
1	C	161	GLU	CB-CG	-5.77	1.41	1.52
1	B	108	ARG	N-CA	-5.73	1.34	1.46
1	C	103	GLN	CB-CG	-5.61	1.37	1.52
3	F	14	DT	C3'-O3'	-5.42	1.36	1.44
1	B	161	GLU	CG-CD	5.30	1.59	1.51
1	B	109	GLY	CA-C	5.29	1.60	1.51
1	D	60	ASP	CB-CG	-5.27	1.40	1.51
1	C	105	GLU	CG-CD	-5.25	1.44	1.51
2	E	15	DG	C3'-O3'	-5.20	1.37	1.44
1	B	149	VAL	CB-CG1	-5.19	1.42	1.52
3	F	6	DG	C3'-O3'	5.13	1.50	1.44
2	E	12	DC	C1'-N1	5.12	1.55	1.49
1	D	199	LYS	CD-CE	5.08	1.64	1.51
3	F	15	DG	C3'-O3'	-5.08	1.37	1.44
1	B	108	ARG	CB-CG	5.01	1.66	1.52

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	108	ARG	NE-CZ-NH1	19.45	130.03	120.30
1	C	53	ARG	NE-CZ-NH2	-18.07	111.27	120.30
1	C	53	ARG	NE-CZ-NH1	14.04	127.32	120.30
1	A	108	ARG	CG-CD-NE	-13.57	83.31	111.80
1	B	53	ARG	CB-CG-CD	-13.52	76.44	111.60
1	D	54	ARG	NE-CZ-NH2	-13.14	113.73	120.30
1	D	68	ARG	NE-CZ-NH2	-11.48	114.56	120.30
1	D	60	ASP	CB-CG-OD2	11.42	128.58	118.30
1	A	68	ARG	NE-CZ-NH2	-10.80	114.90	120.30
1	D	60	ASP	CB-CG-OD1	-10.77	108.61	118.30
1	A	180	LYS	CB-CG-CD	-10.44	84.47	111.60
1	C	180	LYS	CB-CG-CD	10.32	138.44	111.60
1	A	68	ARG	CA-CB-CG	10.22	135.89	113.40
1	A	68	ARG	CB-CG-CD	9.69	136.78	111.60
1	D	171	ARG	CG-CD-NE	-8.99	92.92	111.80
1	D	54	ARG	CB-CG-CD	-8.62	89.19	111.60
1	C	53	ARG	CB-CG-CD	8.53	133.76	111.60
1	B	108	ARG	CG-CD-NE	-8.40	94.16	111.80
1	A	167	LEU	CA-CB-CG	-8.39	96.00	115.30
1	A	68	ARG	NE-CZ-NH1	8.30	124.45	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	180	LYS	CG-CD-CE	-8.01	87.87	111.90
2	E	3	DC	O4'-C1'-N1	7.99	113.59	108.00
1	D	68	ARG	N-CA-CB	-7.98	96.24	110.60
3	F	21	DG	O4'-C1'-N9	7.85	113.49	108.00
1	A	104	ASP	CB-CG-OD2	-7.82	111.27	118.30
1	C	53	ARG	CD-NE-CZ	-7.70	112.82	123.60
1	C	103	GLN	N-CA-CB	-7.53	97.04	110.60
1	A	53	ARG	CA-CB-CG	-7.04	97.91	113.40
1	D	108	ARG	NE-CZ-NH1	-6.69	116.95	120.30
1	A	68	ARG	CG-CD-NE	-6.68	97.78	111.80
1	B	108	ARG	NE-CZ-NH2	-6.67	116.97	120.30
1	A	53	ARG	NE-CZ-NH1	-6.49	117.06	120.30
1	A	53	ARG	CD-NE-CZ	6.47	132.66	123.60
1	B	108	ARG	C-N-CA	-6.38	108.90	122.30
2	E	14	DT	OP2-P-O3'	6.13	118.70	105.20
1	D	60	ASP	CB-CA-C	-5.99	98.41	110.40
1	A	180	LYS	CA-CB-CG	5.99	126.58	113.40
1	C	53	ARG	CB-CA-C	-5.92	98.56	110.40
1	B	230	LYS	CD-CE-NZ	-5.90	98.12	111.70
1	B	108	ARG	NH1-CZ-NH2	-5.82	113.00	119.40
1	B	166	LEU	CB-CG-CD1	5.77	120.81	111.00
1	B	54	ARG	NE-CZ-NH1	-5.71	117.44	120.30
3	F	21	DG	C1'-O4'-C4'	-5.67	104.43	110.10
1	D	53	ARG	NE-CZ-NH2	-5.57	117.52	120.30
1	C	256	LYS	CD-CE-NZ	-5.47	99.12	111.70
3	F	14	DT	OP2-P-O3'	5.44	117.17	105.20
1	D	57	ILE	CG1-CB-CG2	-5.43	99.46	111.40
1	A	128	ILE	CG1-CB-CG2	5.42	123.31	111.40
2	E	14	DT	N3-C4-O4	5.40	123.14	119.90
1	A	68	ARG	CD-NE-CZ	5.39	131.15	123.60
1	C	105	GLU	OE1-CD-OE2	5.26	129.61	123.30
1	B	108	ARG	CA-C-N	5.23	126.66	116.20
2	E	1	DT	O4'-C1'-C2'	-5.15	101.78	105.90
1	B	41	ASP	CB-CG-OD1	-5.07	113.73	118.30
1	D	242	LEU	CA-CB-CG	5.01	126.83	115.30
1	A	217	SER	N-CA-CB	5.01	118.02	110.50

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	105	GLU	Peptide

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Mol	Chain	Res	Type	Group
1	A	53	ARG	Sidechain
1	A	68	ARG	Sidechain
1	B	156	GLU	Sidechain
1	C	105	GLU	Peptide
1	C	53	ARG	Mainchain
1	D	60	ASP	Sidechain

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	2053	0	2133	86	2
1	B	2053	0	2133	83	1
1	C	2053	0	2133	83	1
1	D	2053	0	2133	92	2
2	E	483	0	272	15	0
3	F	501	0	269	24	0
4	A	27	0	12	0	0
4	B	27	0	12	0	0
4	C	27	0	12	0	0
4	D	27	0	12	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
All	All	9308	0	9121	359	3

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 20.

All (359) 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:108:ARG:CG	1:B:108:ARG:CD	1.96	1.41
1:C:237:PHE:HE2	1:C:244:TYR:CE2	1.45	1.33
1:C:237:PHE:CE2	1:C:244:TYR:CE2	2.25	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:60:ASP:OD2	1:D:62:TYR:HB3	1.46	1.14
1:B:60:ASP:OD2	1:B:89:ASN:HB3	1.52	1.08
2:E:23:DC:N3	3:F:2:DG:N1	2.16	0.94
1:C:78:THR:HG22	1:C:80:MET:H	1.33	0.94
1:C:161:GLU:OE2	1:D:54:ARG:NH1	2.01	0.92
1:C:161:GLU:OE2	1:D:54:ARG:NH2	2.04	0.90
2:E:24:DT:H3	3:F:1:DA:H61	1.17	0.90
2:E:23:DC:N4	3:F:2:DG:O6	2.06	0.89
1:C:161:GLU:OE2	1:D:54:ARG:CZ	2.22	0.87
1:B:54:ARG:HD3	1:B:89:ASN:HA	1.56	0.86
1:A:217:SER:OG	1:A:263:GLN:NE2	2.08	0.86
1:A:110:GLU:OE1	1:A:177:THR:HG21	1.77	0.84
1:D:23:ASN:HD21	1:D:241:ILE:H	1.23	0.83
2:E:24:DT:O4	3:F:1:DA:N6	2.12	0.82
1:B:151:ILE:HD12	1:B:166:LEU:HD21	1.60	0.82
1:D:105:GLU:HB3	1:D:106:ASN:OD1	1.79	0.82
1:C:237:PHE:CD2	1:C:244:TYR:CD2	2.67	0.82
1:A:6:ILE:HB	1:A:128:ILE:HD13	1.63	0.80
1:D:59:TYR:HA	1:D:63:HIS:CE1	2.16	0.80
1:D:53:ARG:HB2	1:D:55:ASP:OD2	1.81	0.79
1:A:173:LEU:HA	1:A:176:SER:HB3	1.61	0.79
1:C:237:PHE:HE2	1:C:244:TYR:HE2	1.29	0.78
1:C:237:PHE:HD2	1:C:244:TYR:CD2	2.03	0.76
1:A:217:SER:OG	1:A:263:GLN:CD	2.24	0.76
1:D:36:LEU:HB3	1:D:127:ILE:HD13	1.66	0.76
1:A:176:SER:OG	1:A:177:THR:HG23	1.85	0.75
1:A:219:THR:HG23	1:A:221:GLU:H	1.52	0.75
1:D:3:SER:HB2	1:D:124:TYR:O	1.87	0.74
1:A:161:GLU:OE2	1:B:54:ARG:NH2	2.20	0.73
1:C:219:THR:HB	1:C:221:GLU:HG3	1.69	0.73
1:A:167:LEU:HD22	1:A:171:ARG:HH12	1.54	0.73
1:B:174:GLN:HB2	1:B:175:LYS:HE2	1.71	0.73
1:D:59:TYR:CD2	1:D:63:HIS:CE1	2.76	0.73
1:C:99:PHE:CE1	1:C:103:GLN:NE2	2.57	0.72
1:B:108:ARG:CG	1:B:108:ARG:NE	2.51	0.72
1:B:171:ARG:HD2	1:B:175:LYS:HE3	1.72	0.72
1:C:237:PHE:CD2	1:C:244:TYR:CE2	2.77	0.72
1:A:106:ASN:HB3	1:A:108:ARG:HE	1.55	0.72
1:B:103:GLN:OE1	1:B:109:GLY:N	2.24	0.71
1:A:70:GLN:H	1:A:73:GLN:NE2	1.89	0.71
1:A:54:ARG:HA	1:A:57:ILE:HD12	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:170:ILE:O	1:B:174:GLN:HG3	1.91	0.70
1:A:6:ILE:HB	1:A:128:ILE:CD1	2.20	0.70
1:C:106:ASN:HB2	1:C:108:ARG:HG3	1.74	0.70
1:C:237:PHE:HE2	1:C:244:TYR:CZ	2.07	0.69
1:C:233:GLU:O	1:C:236:SER:HB3	1.92	0.69
1:C:53:ARG:HB2	1:C:55:ASP:OD2	1.92	0.69
1:D:111:LEU:HD22	1:D:114:LYS:HD3	1.74	0.69
1:D:102:SER:HB3	1:D:108:ARG:HD2	1.73	0.68
1:A:6:ILE:HG12	1:A:148:SER:OG	1.93	0.68
1:C:237:PHE:CE2	1:C:244:TYR:CZ	2.80	0.68
1:C:100:TYR:O	1:C:103:GLN:HB2	1.94	0.68
1:C:70:GLN:OE1	1:C:73:GLN:NE2	2.27	0.68
1:D:102:SER:CB	1:D:108:ARG:HD2	2.24	0.67
1:D:110:GLU:OE2	1:D:177:THR:HG21	1.95	0.66
1:D:207:LYS:HE2	1:D:208:TYR:CZ	2.30	0.66
1:A:54:ARG:HA	1:A:57:ILE:CD1	2.25	0.66
1:C:11:GLN:OE1	1:C:166:LEU:HB2	1.95	0.66
1:D:59:TYR:HD2	1:D:63:HIS:CE1	2.11	0.66
1:C:54:ARG:HA	1:C:57:ILE:HD13	1.77	0.66
1:B:148:SER:HB2	1:B:184:ARG:HB2	1.76	0.65
1:C:106:ASN:CB	1:C:108:ARG:HG3	2.26	0.65
1:B:108:ARG:NH1	1:B:111:LEU:HD12	2.12	0.65
3:F:4:DG:H2"	3:F:5:DT:H5'	1.78	0.65
1:A:260:SER:HA	1:A:263:GLN:NE2	2.13	0.64
1:D:53:ARG:N	1:D:53:ARG:HD3	2.11	0.64
1:C:105:GLU:HG3	1:C:106:ASN:ND2	2.13	0.64
1:A:39:ASP:OD2	1:A:44:ALA:HA	1.98	0.64
1:D:148:SER:HB2	1:D:184:ARG:HB2	1.80	0.64
2:E:24:DT:C4	3:F:1:DA:N6	2.66	0.63
2:E:20:DA:H2"	2:E:21:DC:H5"	1.80	0.63
1:D:36:LEU:HD11	1:D:86:VAL:HG23	1.82	0.62
1:A:70:GLN:HB2	1:A:73:GLN:HE21	1.63	0.62
1:C:70:GLN:N	1:C:70:GLN:OE1	2.32	0.62
1:C:6:ILE:HG12	1:C:148:SER:OG	2.00	0.62
1:A:210:ASP:OD1	1:A:215:ARG:NH2	2.32	0.62
1:B:54:ARG:HG2	1:B:89:ASN:OD1	2.00	0.61
1:B:33:LYS:HD2	1:B:126:TYR:HE1	1.65	0.61
1:A:161:GLU:CD	1:B:54:ARG:HH22	2.03	0.61
3:F:10:DC:H2'	3:F:11:DA:C8	2.35	0.61
1:A:170:ILE:HG23	1:A:181:LEU:HD23	1.80	0.61
1:A:70:GLN:H	1:A:73:GLN:HE21	1.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156:GLU:OE1	1:B:157:PHE:N	2.34	0.61
1:D:37:LEU:HD21	1:D:46:ALA:HB1	1.80	0.61
1:D:59:TYR:HA	1:D:63:HIS:HE1	1.66	0.60
1:D:171:ARG:HG2	1:D:174:GLN:OE1	2.00	0.60
1:B:191:HIS:HE1	1:B:193:PRO:HB3	1.67	0.60
1:A:58:ASP:OD2	1:A:59:TYR:CD2	2.55	0.60
1:B:36:LEU:HD11	1:B:86:VAL:HG23	1.84	0.59
1:B:120:VAL:HA	1:B:123:LEU:HD12	1.83	0.59
1:D:23:ASN:ND2	1:D:241:ILE:H	1.98	0.59
1:C:99:PHE:CG	1:C:137:PRO:HB3	2.37	0.59
1:C:4:GLU:OE2	1:C:184:ARG:NH1	2.35	0.59
1:B:53:ARG:O	1:B:56:LYS:HG2	2.02	0.59
1:C:39:ASP:HB3	1:C:88:SER:HB2	1.84	0.59
1:D:23:ASN:ND2	1:D:241:ILE:HG22	2.18	0.59
1:D:54:ARG:HA	1:D:57:ILE:HG12	1.84	0.59
1:D:51:GLY:O	1:D:53:ARG:NE	2.36	0.58
1:C:196:ASN:OD1	1:C:199:LYS:HE3	2.03	0.58
1:A:71:ILE:O	1:A:75:ILE:HG13	2.03	0.58
1:C:111:LEU:HD21	1:C:177:THR:CG2	2.33	0.58
3:F:5:DT:H2"	3:F:6:DG:C8	2.39	0.58
2:E:24:DT:H3	3:F:1:DA:N6	1.96	0.58
1:D:11:GLN:HE21	1:D:135:LEU:HG	1.69	0.58
1:D:80:MET:HB2	1:D:83:LEU:HB3	1.85	0.58
1:C:106:ASN:CB	1:C:108:ARG:HE	2.17	0.58
3:F:20:DA:H2'	3:F:20:DA:OP2	2.04	0.58
1:B:171:ARG:CD	1:B:175:LYS:HE3	2.34	0.57
1:C:78:THR:HB	1:C:83:LEU:O	2.04	0.57
1:C:110:GLU:OE1	1:C:177:THR:OG1	2.21	0.57
1:C:62:TYR:CZ	1:C:66:ILE:HD11	2.38	0.57
3:F:22:DG:H1'	3:F:23:DG:H5'	1.87	0.57
1:D:63:HIS:O	1:D:68:ARG:HB2	2.06	0.56
1:D:99:PHE:CG	1:D:137:PRO:HB3	2.40	0.56
1:A:188:PRO:HG2	1:A:224:MET:SD	2.45	0.56
1:D:151:ILE:HD12	1:D:166:LEU:CD2	2.36	0.56
1:A:246:ILE:HG23	1:A:247:LYS:HG2	1.87	0.56
1:B:240:PRO:HD2	1:B:243:LEU:HD12	1.88	0.56
1:C:237:PHE:CE2	1:C:244:TYR:CD2	2.85	0.56
1:D:16:GLY:O	1:D:20:THR:HG23	2.07	0.55
2:E:21:DC:H2"	2:E:22:DC:H5"	1.88	0.55
3:F:21:DG:H2"	3:F:22:DG:H8	1.70	0.55
1:D:11:GLN:NE2	1:D:135:LEU:HG	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:170:ILE:O	1:C:174:GLN:HG3	2.07	0.55
1:C:27:SER:HA	1:C:242:LEU:HD11	1.87	0.55
3:F:4:DG:H2'	3:F:5:DT:C6	2.42	0.55
1:D:184:ARG:NH2	1:D:261:ILE:HG23	2.22	0.54
1:A:66:ILE:HG22	1:A:68:ARG:HB2	1.88	0.54
1:B:99:PHE:CG	1:B:137:PRO:HB3	2.43	0.54
1:B:217:SER:OG	1:B:263:GLN:NE2	2.40	0.54
2:E:22:DC:H2'	2:E:23:DC:O4'	2.08	0.54
1:A:191:HIS:CD2	1:A:224:MET:HE3	2.42	0.53
1:A:66:ILE:CG2	1:A:68:ARG:HB2	2.39	0.53
1:D:61:ILE:HG23	1:D:92:LEU:HD13	1.89	0.53
1:A:216:ASP:CG	1:A:219:THR:HG22	2.29	0.53
1:B:33:LYS:HD2	1:B:126:TYR:CE1	2.44	0.53
1:A:42:PRO:O	1:A:90:LEU:HD13	2.09	0.53
1:A:151:ILE:HD12	1:A:186:PHE:HE1	1.72	0.53
1:A:171:ARG:HG2	1:A:174:GLN:OE1	2.09	0.53
1:B:59:TYR:HA	1:B:63:HIS:CE1	2.43	0.53
1:A:101:ASP:O	1:A:104:ASP:HB2	2.09	0.53
1:A:59:TYR:HD1	1:A:63:HIS:ND1	2.06	0.53
1:D:20:THR:HB	1:D:254:TYR:HE1	1.74	0.53
1:C:71:ILE:O	1:C:75:ILE:HG13	2.09	0.52
1:C:54:ARG:NH1	1:D:161:GLU:CD	2.62	0.52
1:B:207:LYS:HE3	1:B:208:TYR:CE1	2.44	0.52
1:D:150:ILE:HD11	1:D:261:ILE:HD11	1.91	0.52
1:C:245:ASP:OD2	1:C:245:ASP:C	2.45	0.52
1:B:146:ALA:O	1:B:178:ASN:ND2	2.42	0.52
1:D:186:PHE:HE1	1:D:209:PHE:CG	2.27	0.52
1:A:137:PRO:HA	1:A:140:ILE:HG22	1.91	0.52
1:B:188:PRO:HG3	1:B:213:PHE:HE1	1.75	0.52
1:A:11:GLN:OE1	1:A:11:GLN:N	2.42	0.51
1:A:8:VAL:HG22	1:A:150:ILE:HB	1.93	0.51
1:A:148:SER:HB2	1:A:184:ARG:HB2	1.91	0.51
1:A:223:ILE:C	1:A:224:MET:HG2	2.31	0.51
1:A:239:LYS:HB3	1:A:243:LEU:HD12	1.93	0.51
1:A:99:PHE:CG	1:A:137:PRO:HB3	2.46	0.51
1:C:106:ASN:CG	1:C:108:ARG:HE	2.14	0.51
1:D:149:VAL:HG23	1:D:181:LEU:HD11	1.91	0.51
1:D:60:ASP:OD2	1:D:62:TYR:CB	2.38	0.51
1:D:154:GLN:HG2	1:D:156:GLU:HG3	1.93	0.51
1:A:246:ILE:HG13	1:A:246:ILE:O	2.11	0.51
1:D:151:ILE:HD12	1:D:166:LEU:HD21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:ALA:HB3	1:B:54:ARG:NE	2.26	0.50
1:A:216:ASP:OD2	1:A:219:THR:HG22	2.11	0.50
1:C:184:ARG:NH2	1:C:261:ILE:O	2.45	0.50
1:A:95:PHE:HE1	1:A:112:MET:SD	2.34	0.50
1:A:23:ASN:HD21	1:A:241:ILE:H	1.59	0.50
1:C:99:PHE:CD1	1:C:137:PRO:HG3	2.47	0.50
1:C:151:ILE:HD12	1:C:186:PHE:HE2	1.77	0.50
1:D:60:ASP:H	1:D:63:HIS:CE1	2.29	0.50
1:D:71:ILE:O	1:D:74:VAL:HG22	2.12	0.50
1:D:58:ASP:O	1:D:59:TYR:CD2	2.65	0.50
3:F:1:DA:H2"	3:F:2:DG:H8	1.76	0.50
1:A:163:THR:HG22	1:A:167:LEU:HD12	1.94	0.49
1:A:219:THR:HG21	1:A:221:GLU:OE1	2.11	0.49
1:D:120:VAL:HA	1:D:123:LEU:HD12	1.94	0.49
1:A:110:GLU:OE1	1:A:177:THR:CG2	2.56	0.49
1:A:95:PHE:CE1	1:A:112:MET:SD	3.05	0.49
1:D:58:ASP:O	1:D:59:TYR:HD2	1.95	0.49
1:A:161:GLU:CD	1:B:54:ARG:NH2	2.64	0.49
1:D:102:SER:OG	1:D:108:ARG:HD2	2.13	0.49
1:A:161:GLU:OE1	1:B:54:ARG:NH2	2.44	0.49
1:A:151:ILE:HD12	1:A:186:PHE:CE1	2.48	0.49
1:B:108:ARG:HH21	1:B:110:GLU:N	2.11	0.49
1:B:108:ARG:HH21	1:B:110:GLU:H	1.61	0.49
1:C:148:SER:HB2	1:C:184:ARG:HB2	1.93	0.49
1:D:229:VAL:O	1:D:233:GLU:HG2	2.13	0.49
1:A:186:PHE:HE2	1:A:209:PHE:CG	2.31	0.48
2:E:14:DT:H2"	2:E:15:DG:C8	2.48	0.48
3:F:21:DG:H2"	3:F:22:DG:C8	2.47	0.48
1:A:106:ASN:O	1:A:107:LYS:HG2	2.13	0.48
1:A:59:TYR:HA	1:A:63:HIS:ND1	2.28	0.48
1:A:236:SER:HA	1:B:157:PHE:CE1	2.48	0.48
1:D:170:ILE:O	1:D:174:GLN:HG3	2.13	0.48
1:A:151:ILE:HB	1:A:186:PHE:HD1	1.78	0.48
1:A:61:ILE:HG23	1:A:92:LEU:HD13	1.95	0.48
1:B:108:ARG:NE	1:B:108:ARG:O	2.43	0.48
1:C:149:VAL:HG13	1:C:183:ILE:HA	1.95	0.48
1:B:151:ILE:HD12	1:B:166:LEU:CD2	2.38	0.48
1:A:245:ASP:OD2	1:A:245:ASP:C	2.52	0.48
1:A:197:LEU:HB2	1:B:233:GLU:HG2	1.96	0.48
1:D:163:THR:O	1:D:167:LEU:HG	2.14	0.48
1:C:39:ASP:OD1	1:C:47:THR:OG1	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:GLU:HG2	1:B:140:ILE:HG21	1.97	0.47
1:C:38:ILE:HD11	1:C:117:LEU:HD21	1.96	0.47
1:A:149:VAL:HG12	1:A:182:LYS:O	2.13	0.47
1:B:80:MET:HB2	1:B:83:LEU:HB3	1.95	0.47
1:D:36:LEU:HB3	1:D:127:ILE:CD1	2.41	0.47
1:B:186:PHE:HE2	1:B:209:PHE:CG	2.33	0.47
1:C:151:ILE:HD12	1:C:186:PHE:CE2	2.49	0.47
1:B:76:LEU:HD11	1:B:87:PRO:HG3	1.96	0.47
3:F:2:DG:H2'	3:F:3:DG:C8	2.50	0.47
1:C:99:PHE:O	1:C:102:SER:HB3	2.15	0.47
2:E:21:DC:H2''	2:E:22:DC:O4'	2.15	0.47
3:F:6:DG:H3'	3:F:6:DG:OP2	2.15	0.46
1:B:30:VAL:C	1:B:32:GLU:H	2.16	0.46
1:B:108:ARG:HA	1:B:108:ARG:NE	2.30	0.46
1:D:149:VAL:CG1	1:D:151:ILE:HD11	2.45	0.46
1:A:75:ILE:O	1:A:76:LEU:HD12	2.15	0.46
1:B:247:LYS:HE3	1:B:247:LYS:HB2	1.73	0.46
1:C:54:ARG:NH1	1:D:161:GLU:OE1	2.48	0.46
1:D:10:ASN:HA	1:D:166:LEU:HD22	1.97	0.46
1:A:191:HIS:CE1	1:A:224:MET:HE1	2.51	0.46
1:A:23:ASN:ND2	1:A:241:ILE:H	2.14	0.46
1:A:137:PRO:HA	1:A:140:ILE:CG2	2.45	0.46
1:D:59:TYR:HA	1:D:63:HIS:ND1	2.30	0.46
1:A:6:ILE:HG12	1:A:148:SER:HG	1.81	0.46
1:B:44:ALA:HB3	1:B:54:ARG:CZ	2.46	0.46
1:C:158:PHE:CZ	1:D:45:ASN:HB3	2.51	0.46
1:D:216:ASP:O	1:D:220:GLY:N	2.45	0.46
2:E:24:DT:N3	3:F:1:DA:N6	2.57	0.46
1:A:188:PRO:HG3	1:A:213:PHE:HE2	1.81	0.45
1:B:71:ILE:O	1:B:75:ILE:HG13	2.17	0.45
1:D:108:ARG:HD3	1:D:112:MET:SD	2.56	0.45
1:D:170:ILE:HG22	1:D:171:ARG:HG3	1.98	0.45
1:D:20:THR:HG22	1:D:254:TYR:OH	2.16	0.45
1:A:167:LEU:CD2	1:A:183:ILE:HD11	2.47	0.45
1:A:54:ARG:HH11	1:A:90:LEU:HD21	1.80	0.45
1:C:54:ARG:HH12	1:D:161:GLU:CD	2.19	0.45
1:A:59:TYR:HD1	1:A:63:HIS:CE1	2.35	0.45
1:B:40:PHE:CZ	1:B:113:LEU:HD22	2.52	0.45
1:D:60:ASP:OD1	1:D:60:ASP:N	2.48	0.45
3:F:1:DA:C2'	3:F:2:DG:H8	2.30	0.45
1:C:53:ARG:HD3	1:C:53:ARG:HH21	1.11	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:34:LYS:HE3	1:C:124:TYR:CE1	2.52	0.45
1:C:99:PHE:CD1	1:C:103:GLN:NE2	2.85	0.45
1:D:57:ILE:HD12	1:D:57:ILE:HG23	1.74	0.45
1:A:167:LEU:HA	1:A:167:LEU:HD23	1.42	0.44
1:D:60:ASP:OD1	1:D:60:ASP:C	2.54	0.44
1:B:53:ARG:HD2	1:B:53:ARG:HA	1.42	0.44
1:C:60:ASP:OD1	1:C:63:HIS:ND1	2.49	0.44
1:D:44:ALA:HB3	1:D:54:ARG:NH1	2.32	0.44
1:C:30:VAL:HG21	1:C:242:LEU:HD13	1.98	0.44
1:B:191:HIS:CE1	1:B:193:PRO:HB3	2.50	0.44
1:B:32:GLU:HA	1:B:82:PHE:CD1	2.53	0.44
1:C:117:LEU:O	1:C:121:VAL:HG23	2.17	0.44
1:B:61:ILE:HB	1:B:86:VAL:CG1	2.48	0.44
1:D:117:LEU:HA	1:D:117:LEU:HD23	1.62	0.44
1:C:236:SER:HA	1:D:157:PHE:CE1	2.53	0.44
1:B:108:ARG:HG3	1:B:108:ARG:O	2.17	0.44
1:A:160:LEU:HD13	1:A:204:GLU:HG2	1.98	0.44
1:D:184:ARG:NH1	1:D:264:GLY:O	2.48	0.44
3:F:9:DC:H2''	3:F:10:DC:C6	2.52	0.44
2:E:5:DT:H2'	2:E:6:DG:C8	2.53	0.44
1:A:167:LEU:HD22	1:A:171:ARG:NH1	2.28	0.43
1:A:182:LYS:HB2	1:A:182:LYS:HE3	1.94	0.43
1:B:156:GLU:OE2	1:B:158:PHE:HB2	2.18	0.43
1:D:231:LEU:HD11	1:D:250:GLY:HA3	2.00	0.43
1:A:53:ARG:O	1:A:56:LYS:HB3	2.18	0.43
1:C:106:ASN:HB3	1:C:108:ARG:HG3	2.00	0.43
1:C:53:ARG:O	1:C:57:ILE:HD12	2.18	0.43
2:E:22:DC:H1'	3:F:4:DG:N2	2.33	0.43
1:B:187:LEU:HD11	1:B:225:ILE:HD11	2.01	0.43
1:C:105:GLU:HG3	1:C:106:ASN:CG	2.38	0.43
3:F:23:DG:H2''	3:F:24:DA:H5''	1.99	0.43
1:B:11:GLN:HE21	1:B:135:LEU:HG	1.84	0.43
1:C:160:LEU:CD1	1:C:204:GLU:HG2	2.48	0.43
1:D:102:SER:O	1:D:105:GLU:HB2	2.18	0.43
1:D:55:ASP:OD2	1:D:56:LYS:N	2.51	0.43
1:A:170:ILE:O	1:A:174:GLN:HG3	2.18	0.43
1:B:174:GLN:HG2	1:B:181:LEU:HB3	2.00	0.43
1:C:151:ILE:HB	1:C:186:PHE:HD2	1.83	0.43
1:B:59:TYR:CG	1:B:63:HIS:ND1	2.87	0.43
1:C:38:ILE:CD1	1:C:117:LEU:HD21	2.49	0.43
1:C:106:ASN:HB3	1:C:108:ARG:HE	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:11:GLN:HG3	1:D:43:GLN:OE1	2.19	0.43
1:D:110:GLU:OE2	1:D:177:THR:CG2	2.66	0.43
1:A:117:LEU:HD23	1:A:117:LEU:HA	1.68	0.43
1:C:242:LEU:HA	1:C:242:LEU:HD23	1.83	0.43
1:B:37:LEU:O	1:B:85:LEU:HD12	2.18	0.43
1:B:59:TYR:CG	1:B:63:HIS:CE1	3.06	0.43
1:C:37:LEU:HD12	1:C:128:ILE:O	2.19	0.43
1:C:71:ILE:HD13	1:C:117:LEU:HD23	2.00	0.43
1:D:32:GLU:HG2	1:D:82:PHE:CE2	2.53	0.43
1:B:110:GLU:OE1	1:B:177:THR:HG21	2.19	0.42
1:B:148:SER:HB2	1:B:184:ARG:HD3	2.01	0.42
1:B:32:GLU:HB3	1:B:82:PHE:CE1	2.53	0.42
1:D:12:LYS:HG2	1:D:13:GLY:N	2.34	0.42
1:A:234:SER:OG	1:A:239:LYS:O	2.37	0.42
1:D:103:GLN:NE2	1:D:107:LYS:HA	2.34	0.42
1:B:188:PRO:HG3	1:B:213:PHE:CE1	2.55	0.42
1:C:163:THR:O	1:C:167:LEU:HD22	2.19	0.42
1:C:168:ASN:N	1:C:168:ASN:HD22	2.16	0.42
1:A:47:THR:HG22	1:A:52:PHE:HB2	2.00	0.42
1:B:174:GLN:O	1:B:179:PRO:HA	2.19	0.42
1:D:71:ILE:O	1:D:75:ILE:HG13	2.19	0.42
1:B:11:GLN:NE2	1:B:135:LEU:HG	2.35	0.42
1:B:58:ASP:C	1:B:59:TYR:HD2	2.23	0.42
1:D:150:ILE:HD11	1:D:261:ILE:CD1	2.50	0.42
1:A:39:ASP:HB3	1:A:88:SER:HB2	2.02	0.42
1:B:40:PHE:CE2	1:B:113:LEU:HD22	2.54	0.42
1:B:153:ILE:O	1:B:188:PRO:HA	2.20	0.42
1:B:207:LYS:HE3	1:B:208:TYR:CZ	2.54	0.42
1:B:185:GLY:HA2	1:B:212:GLU:O	2.19	0.42
1:B:48:SER:HB2	1:B:54:ARG:NH1	2.35	0.41
3:F:3:DG:H8	3:F:3:DG:OP2	2.03	0.41
1:B:110:GLU:HG2	1:B:140:ILE:CG2	2.50	0.41
1:B:6:ILE:HA	1:B:148:SER:O	2.20	0.41
1:C:263:GLN:OE1	1:C:263:GLN:HA	2.20	0.41
1:D:151:ILE:HB	1:D:186:PHE:HD2	1.85	0.41
1:C:149:VAL:CG1	1:C:183:ILE:HA	2.51	0.41
1:D:103:GLN:C	1:D:105:GLU:H	2.24	0.41
1:D:171:ARG:CG	1:D:174:GLN:OE1	2.67	0.41
1:D:159:ALA:O	1:D:163:THR:HG23	2.20	0.41
1:D:184:ARG:NH1	1:D:264:GLY:C	2.74	0.41
1:B:176:SER:HB2	1:B:177:THR:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:SER:HB2	1:A:124:TYR:O	2.21	0.41
1:A:93:ALA:O	1:A:96:GLU:OE1	2.39	0.41
1:D:99:PHE:O	1:D:102:SER:HB2	2.20	0.41
1:A:17:LYS:HB2	1:A:17:LYS:HE2	1.80	0.41
1:B:11:GLN:HG2	1:B:165:LEU:HD23	2.02	0.41
1:C:100:TYR:HA	1:C:103:GLN:CD	2.41	0.41
1:D:226:PRO:HG3	1:D:249:ASN:HB3	2.03	0.41
1:D:188:PRO:HG3	1:D:213:PHE:HE1	1.86	0.41
2:E:2:DC:H2''	2:E:3:DC:C6	2.56	0.41
1:D:207:LYS:HE2	1:D:208:TYR:CE2	2.55	0.41
1:D:99:PHE:CD1	1:D:137:PRO:HB3	2.56	0.41
1:B:207:LYS:HB3	1:B:207:LYS:HE2	1.75	0.40
1:C:4:GLU:CD	1:C:184:ARG:HH12	2.23	0.40
1:C:54:ARG:HA	1:C:57:ILE:CD1	2.47	0.40
1:D:185:GLY:HA3	1:D:214:PHE:CE1	2.56	0.40
1:B:219:THR:OG1	1:B:221:GLU:HG2	2.21	0.40
1:A:195:LEU:CD2	3:F:17:DA:H4'	2.52	0.40
1:B:155:CYS:HA	1:B:201:VAL:HG11	2.04	0.40
1:B:156:GLU:CD	1:B:158:PHE:H	2.23	0.40
1:C:17:LYS:HE2	1:C:17:LYS:HB2	1.65	0.40
1:B:33:LYS:HD3	1:B:125:ASP:HB3	2.02	0.40
1:B:36:LEU:HD11	1:B:86:VAL:CG2	2.49	0.40
1:C:117:LEU:HA	1:C:117:LEU:HD23	1.76	0.40
1:A:237:PHE:HE1	1:A:244:TYR:CE2	2.40	0.40
1:B:148:SER:CB	1:B:184:ARG:HD3	2.51	0.40
1:C:149:VAL:HG12	1:C:182:LYS:O	2.20	0.40
1:C:184:ARG:HD3	1:C:184:ARG:HH11	1.65	0.40
1:C:29:ALA:HB1	1:C:82:PHE:HB2	2.03	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:ASP:OD2	1:D:68:ARG:NH2[1_446]	1.61	0.59
1:A:104:ASP:CG	1:D:68:ARG:NH2[1_446]	2.17	0.03
1:B:68:ARG:NH1	1:C:104:ASP:OD2[1_446]	2.18	0.02

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	262/276 (95%)	252 (96%)	9 (3%)	1 (0%)	34	54
1	B	262/276 (95%)	250 (95%)	12 (5%)	0	100	100
1	C	262/276 (95%)	248 (95%)	14 (5%)	0	100	100
1	D	262/276 (95%)	249 (95%)	13 (5%)	0	100	100
All	All	1048/1104 (95%)	999 (95%)	48 (5%)	1 (0%)	51	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	160	LEU

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	228/238 (96%)	222 (97%)	6 (3%)	46	72
1	B	228/238 (96%)	224 (98%)	4 (2%)	59	81
1	C	228/238 (96%)	220 (96%)	8 (4%)	36	62
1	D	228/238 (96%)	219 (96%)	9 (4%)	32	57
All	All	912/952 (96%)	885 (97%)	27 (3%)	41	68

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	MET
1	A	12	LYS
1	A	40	PHE
1	A	184	ARG
1	A	224	MET
1	A	244	TYR
1	B	40	PHE
1	B	55	ASP
1	B	156	GLU
1	B	172	MET
1	C	2	MET
1	C	40	PHE
1	C	77	LYS
1	C	107	LYS
1	C	119	SER
1	C	164	LYS
1	C	180	LYS
1	C	184	ARG
1	D	11	GLN
1	D	20	THR
1	D	40	PHE
1	D	53	ARG
1	D	68	ARG
1	D	107	LYS
1	D	112	MET
1	D	184	ARG
1	D	245	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	31	HIS
1	A	73	GLN
1	A	178	ASN
1	A	191	HIS
1	A	263	GLN
1	B	11	GLN
1	B	45	ASN
1	B	191	HIS
1	C	79	GLN
1	C	168	ASN
1	C	174	GLN

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Mol	Chain	Res	Type
1	D	11	GLN
1	D	23	ASN
1	D	103	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
4	ADP	A	500	5	24,29,29	1.14	4 (16%)	29,45,45	1.59	5 (17%)
4	ADP	C	500	5	24,29,29	1.14	3 (12%)	29,45,45	1.74	7 (24%)
4	ADP	B	500	5	24,29,29	1.10	2 (8%)	29,45,45	1.48	5 (17%)
4	ADP	D	500	5	24,29,29	1.07	2 (8%)	29,45,45	1.37	3 (10%)

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
4	ADP	A	500	5	-	0/12/32/32	0/3/3/3
4	ADP	C	500	5	-	0/12/32/32	0/3/3/3
4	ADP	B	500	5	-	1/12/32/32	0/3/3/3
4	ADP	D	500	5	-	1/12/32/32	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	500	ADP	O4'-C1'	3.04	1.45	1.41
4	D	500	ADP	C5-C4	2.76	1.48	1.40
4	C	500	ADP	C2'-C1'	-2.58	1.49	1.53
4	B	500	ADP	C5-C4	2.55	1.47	1.40
4	A	500	ADP	C5-C4	2.48	1.47	1.40
4	A	500	ADP	C2'-C1'	-2.26	1.50	1.53
4	C	500	ADP	C5-C4	2.23	1.46	1.40
4	C	500	ADP	C6-C5	2.15	1.51	1.43
4	D	500	ADP	C2-N3	2.09	1.35	1.32
4	A	500	ADP	C6-C5	2.06	1.50	1.43
4	A	500	ADP	O4'-C1'	2.03	1.43	1.41

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	500	ADP	C4-C5-N7	-4.57	104.64	109.40
4	B	500	ADP	O3'-C3'-C4'	-3.69	100.37	111.05
4	C	500	ADP	O3'-C3'-C4'	-3.64	100.53	111.05
4	A	500	ADP	O3'-C3'-C4'	-3.28	101.56	111.05
4	C	500	ADP	O4'-C1'-C2'	-3.23	102.21	106.93
4	B	500	ADP	N3-C2-N1	-3.04	123.93	128.68
4	D	500	ADP	N3-C2-N1	-2.99	124.01	128.68
4	A	500	ADP	N3-C2-N1	-2.98	124.02	128.68
4	A	500	ADP	C4-C5-N7	-2.87	106.41	109.40
4	A	500	ADP	O2B-PB-O3A	-2.87	95.02	104.64
4	C	500	ADP	N3-C2-N1	-2.83	124.26	128.68
4	C	500	ADP	O2A-PA-O1A	2.67	125.45	112.24
4	D	500	ADP	C2'-C3'-C4'	2.60	107.70	102.64
4	D	500	ADP	O3'-C3'-C4'	-2.42	104.05	111.05
4	B	500	ADP	O3B-PB-O1B	2.16	119.14	110.68
4	B	500	ADP	C4-C5-N7	-2.15	107.15	109.40
4	A	500	ADP	O4'-C1'-C2'	-2.13	103.81	106.93
4	B	500	ADP	C2'-C3'-C4'	2.12	106.76	102.64
4	C	500	ADP	O2'-C2'-C3'	2.10	118.60	111.82
4	C	500	ADP	PA-O3A-PB	-2.02	125.90	132.83

There are no chirality outliers.

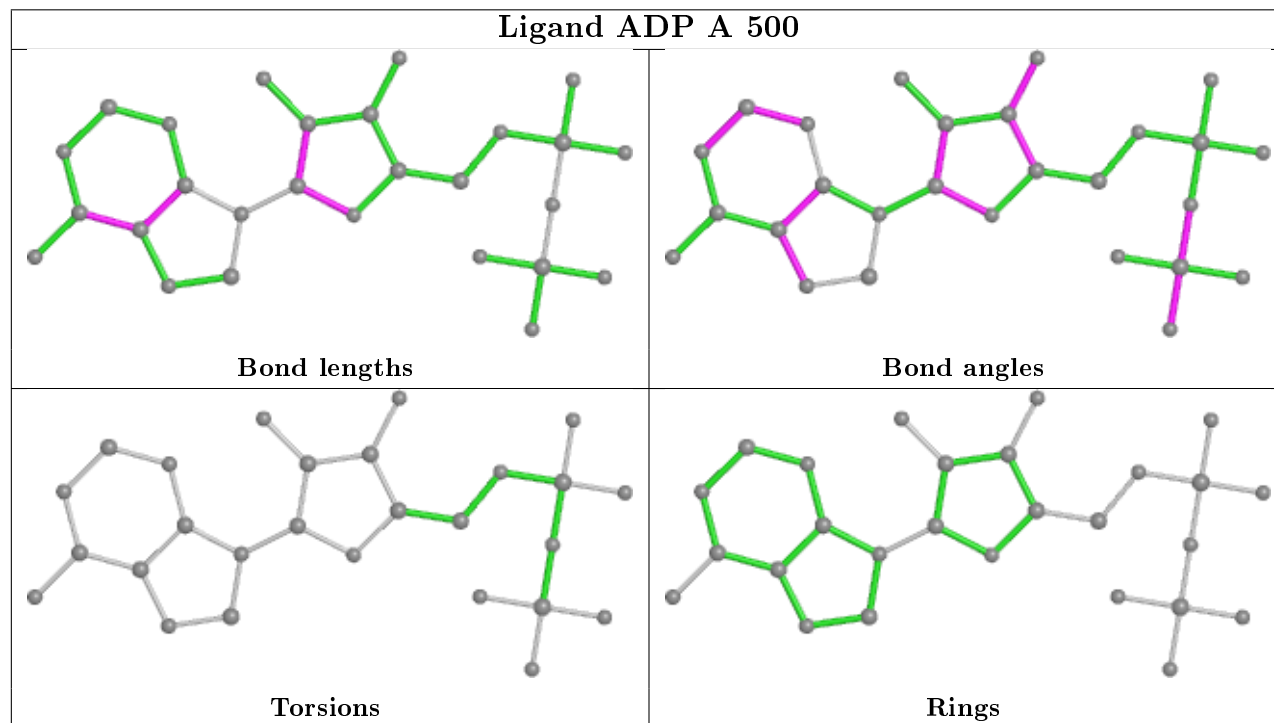
All (2) torsion outliers are listed below:

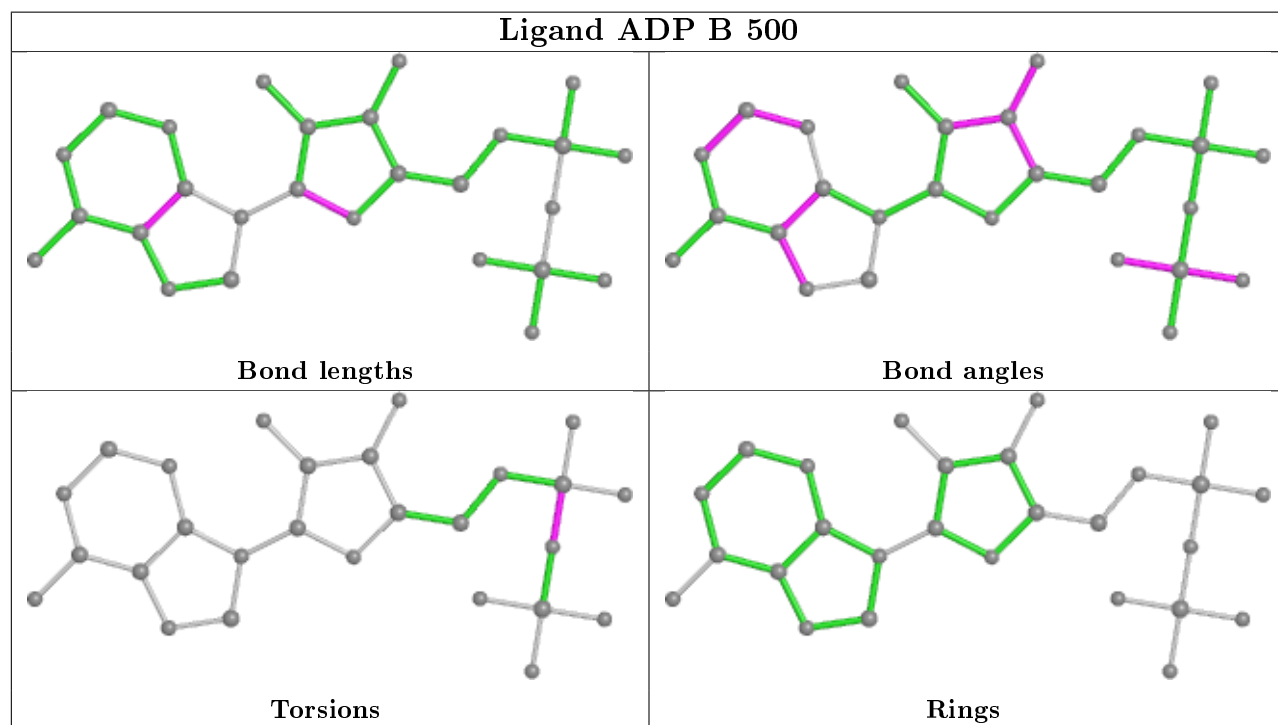
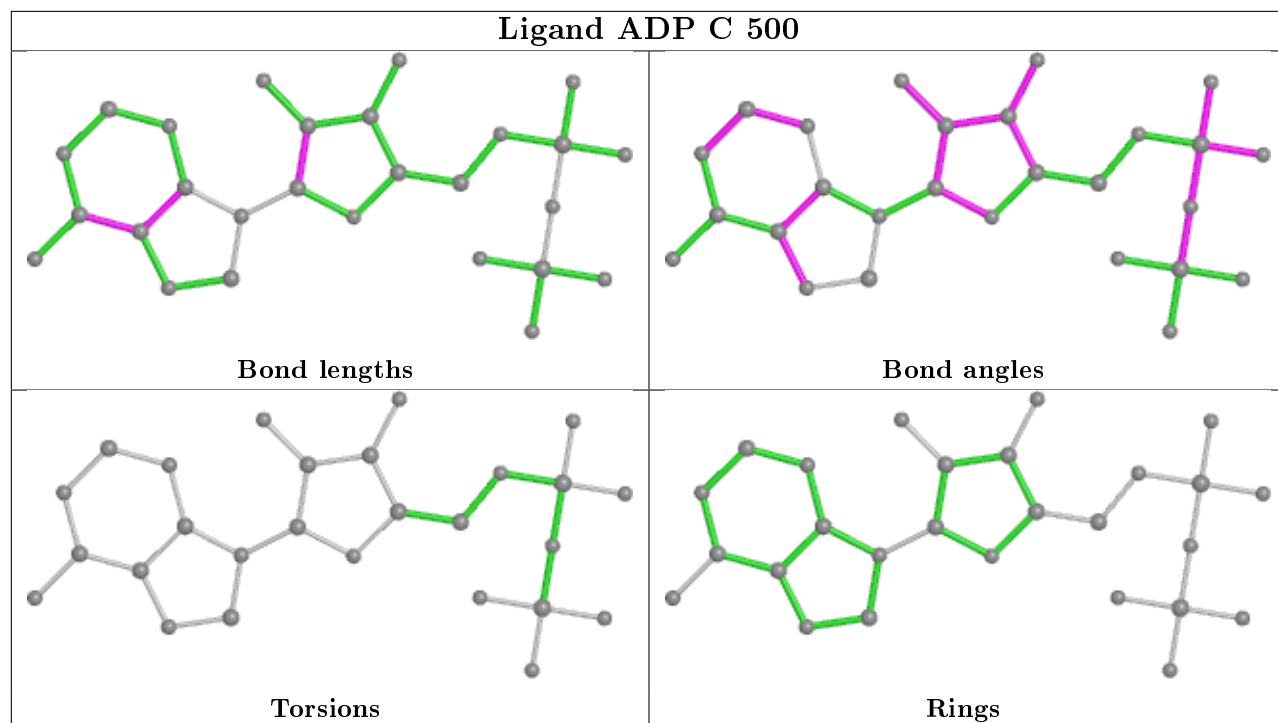
Mol	Chain	Res	Type	Atoms
4	B	500	ADP	PB-O3A-PA-O2A
4	D	500	ADP	PA-O3A-PB-O2B

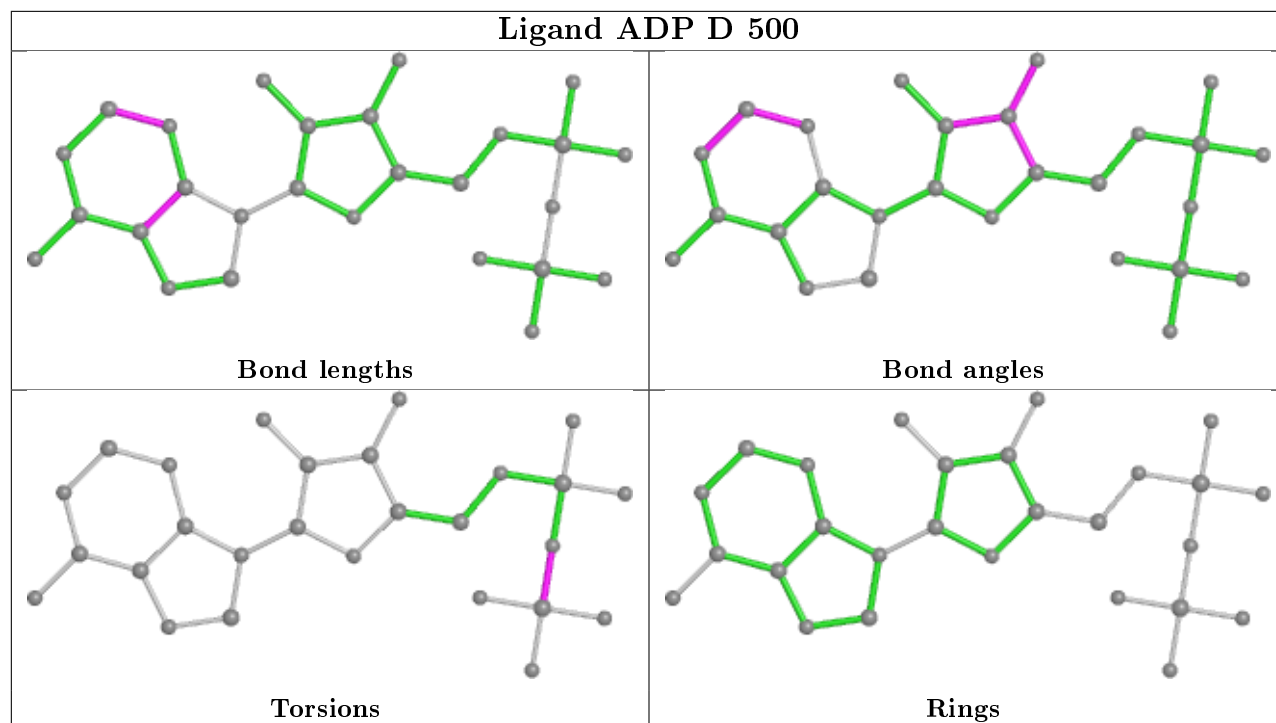
There are no ring outliers.

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.







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	264/276 (95%)	-0.04	6 (2%) 60 63	32, 52, 86, 118	0
1	B	264/276 (95%)	0.04	7 (2%) 54 58	31, 52, 95, 124	0
1	C	264/276 (95%)	0.03	5 (1%) 66 69	30, 53, 85, 133	0
1	D	264/276 (95%)	0.06	9 (3%) 45 48	34, 53, 100, 124	0
2	E	24/24 (100%)	0.09	1 (4%) 36 39	42, 72, 170, 174	0
3	F	24/24 (100%)	0.17	4 (16%) 1 1	43, 76, 159, 169	0
All	All	1104/1152 (95%)	0.02	32 (2%) 51 55	30, 53, 101, 174	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	264	GLY	6.4
1	D	264	GLY	5.5
1	B	1	MET	5.4
1	D	105	GLU	4.8
1	D	1	MET	4.6
1	A	108	ARG	3.9
1	B	54	ARG	3.3
1	A	1	MET	3.3
1	C	53	ARG	3.3
1	D	71	ILE	3.2
3	F	2	DG	3.1
1	C	54	ARG	2.9
1	D	66	ILE	2.8
1	A	133	PRO	2.8
1	D	106	ASN	2.7
1	B	108	ARG	2.6
1	A	57	ILE	2.6
3	F	4	DG	2.6
2	E	2	DC	2.5

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Mol	Chain	Res	Type	RSRZ
3	F	3	DG	2.5
1	D	55	ASP	2.4
3	F	1	DA	2.4
1	C	103	GLN	2.4
1	B	61	ILE	2.4
1	B	53	ARG	2.2
1	D	54	ARG	2.2
1	A	52	PHE	2.1
1	C	244	TYR	2.1
1	B	176	SER	2.1
1	C	133	PRO	2.1
1	D	98	THR	2.1
1	A	66	ILE	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 monosaccharides 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.

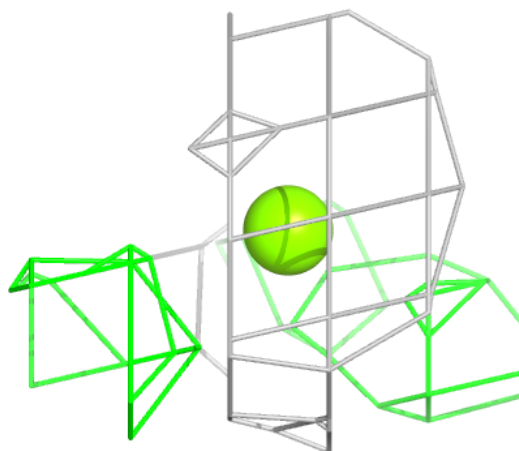
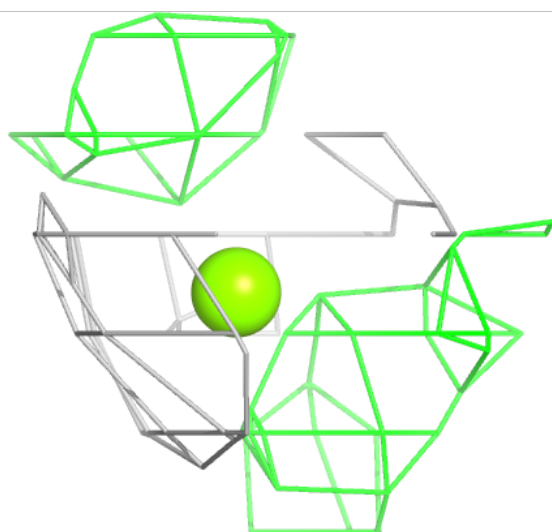
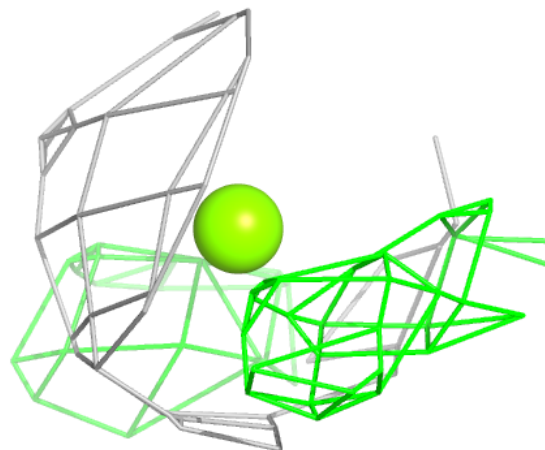
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MG	B	501	1/1	0.84	0.20	64,64,64,64	0
5	MG	A	501	1/1	0.91	0.33	56,56,56,56	0
5	MG	D	501	1/1	0.93	0.31	59,59,59,59	0
5	MG	C	501	1/1	0.94	0.33	50,50,50,50	0
4	ADP	C	500	27/27	0.97	0.14	35,37,42,43	0
4	ADP	B	500	27/27	0.97	0.14	40,42,51,55	0
4	ADP	D	500	27/27	0.98	0.14	37,39,42,43	0
4	ADP	A	500	27/27	0.98	0.15	36,39,40,41	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.

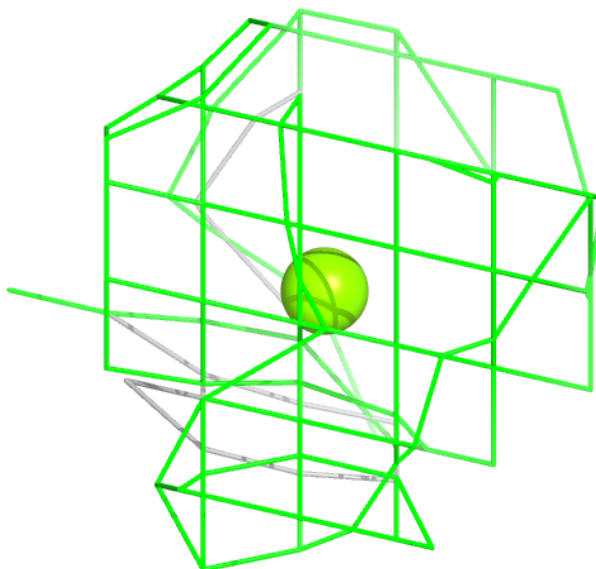
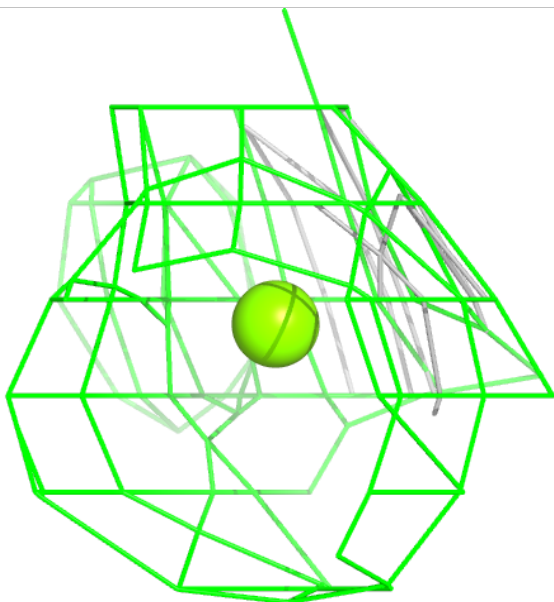
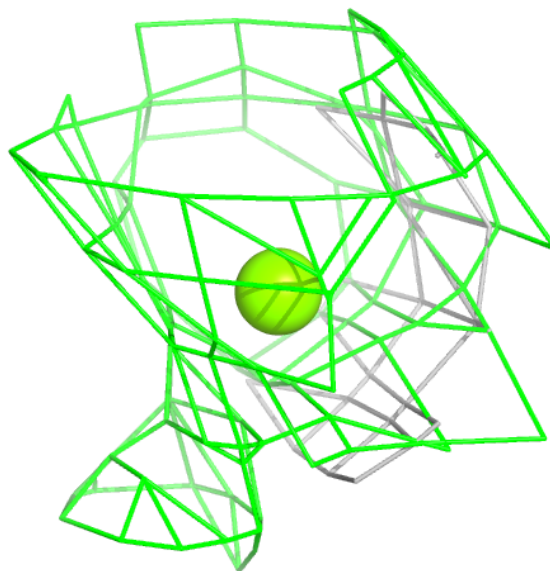
Electron density around MG B 501:

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



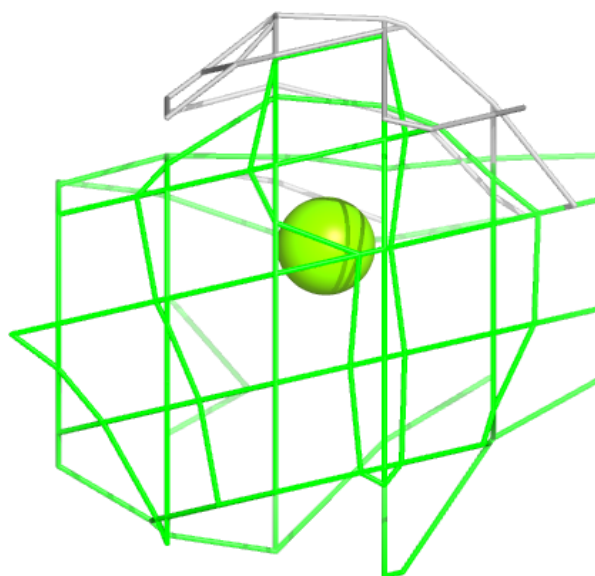
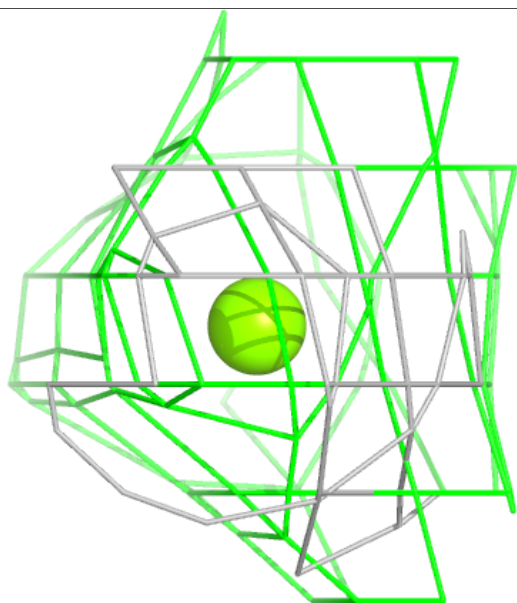
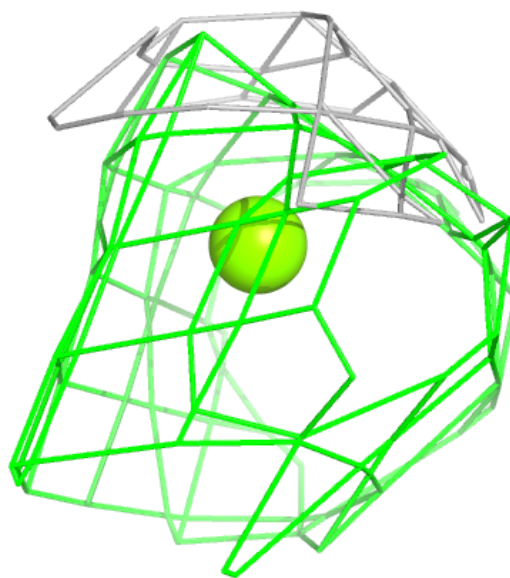
Electron density around MG A 501:

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



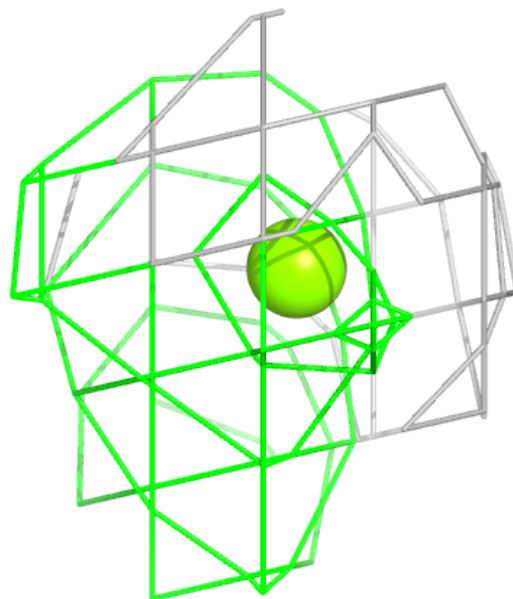
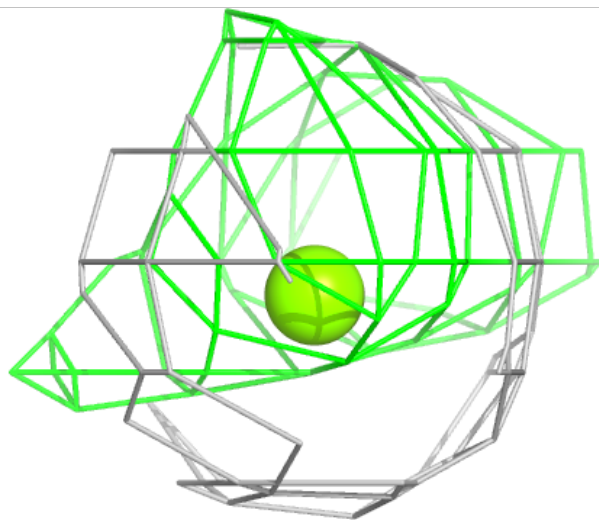
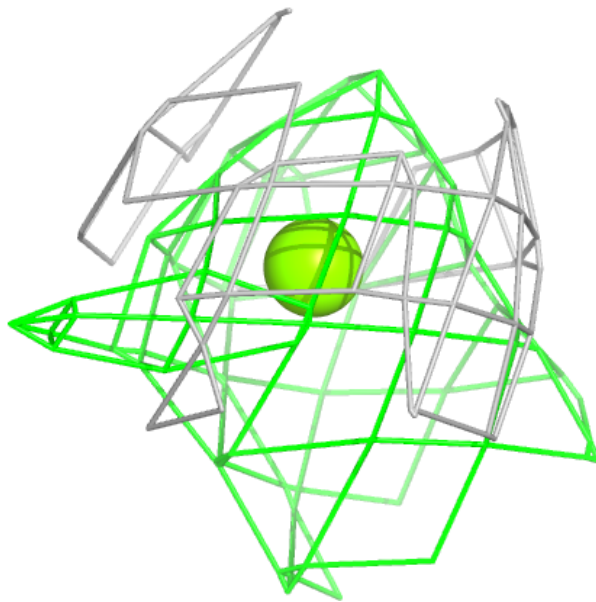
Electron density around MG D 501:

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



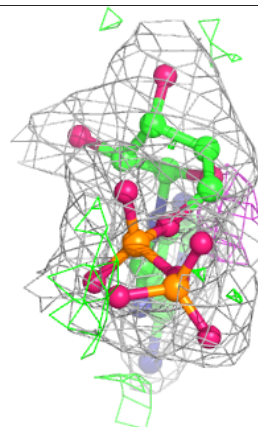
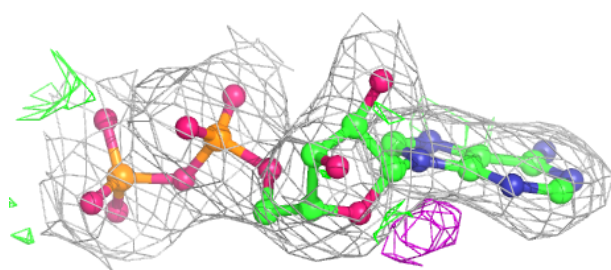
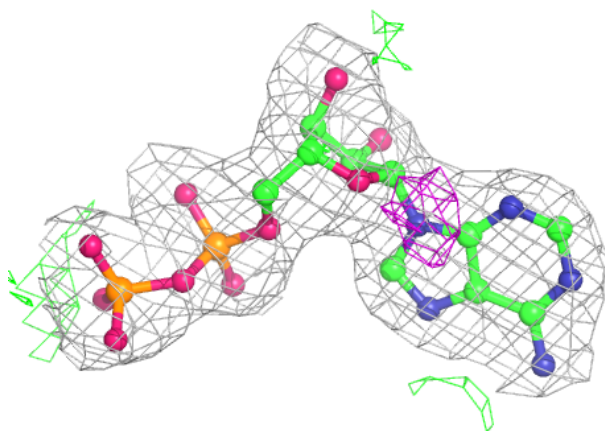
Electron density around MG C 501:

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

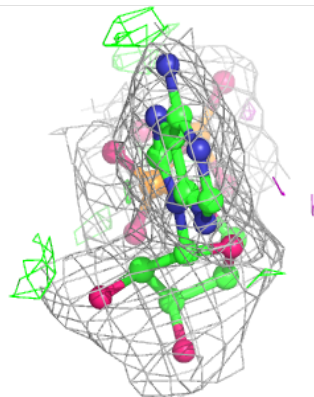
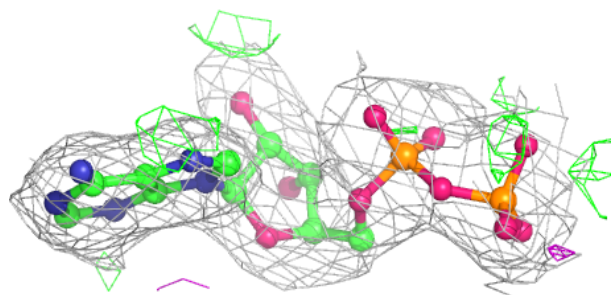
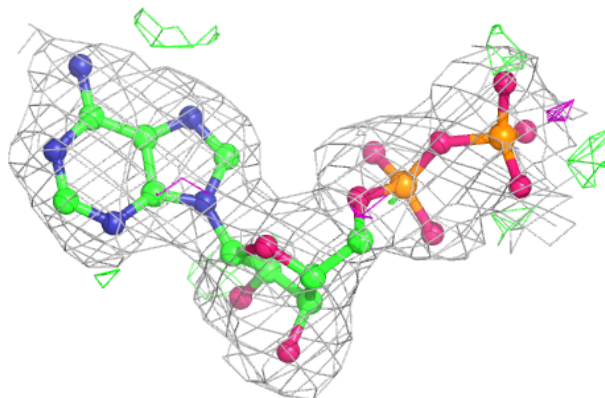


Electron density around ADP C 500:

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

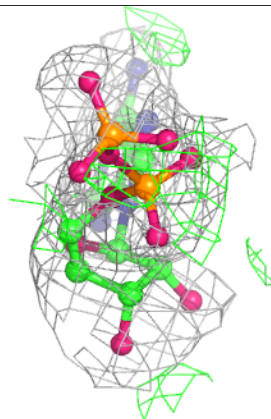
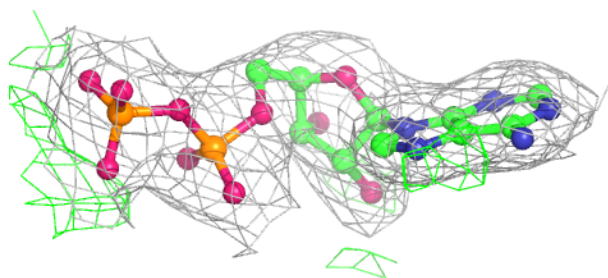
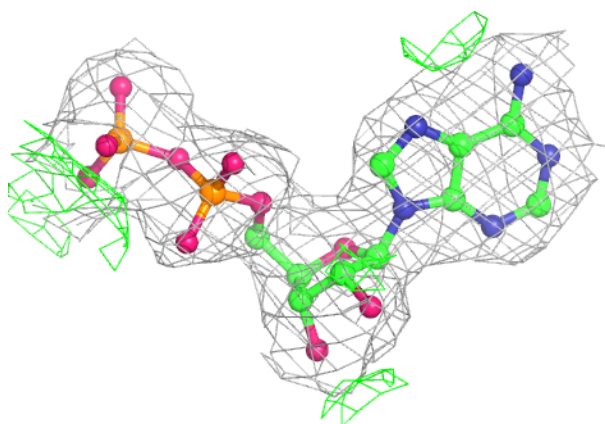
**Electron density around ADP B 500:**

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



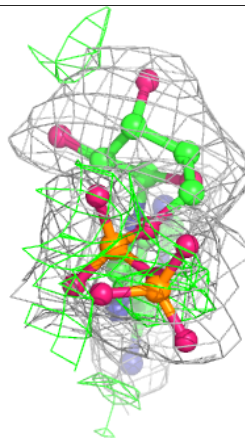
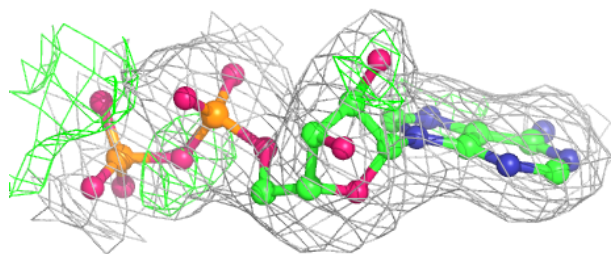
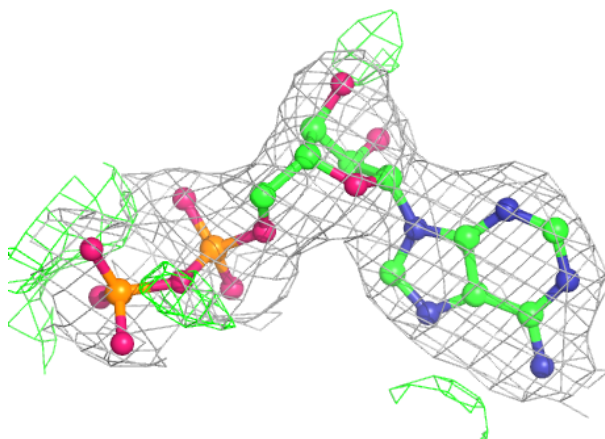
Electron density around ADP D 500:

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



Electron density around ADP 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.