



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:32 PM UTC

PDB ID : 1FNN / pdb_00001fnn
Title : CRYSTAL STRUCTURE OF CDC6P FROM PYROBACULUM AEROPHILUM
Authors : Liu, J.; Smith, C.L.; DeRyckere, D.; DeAngelis, K.; Martin, G.S.; Berger, J.M.
Deposited on : 2000-08-22
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

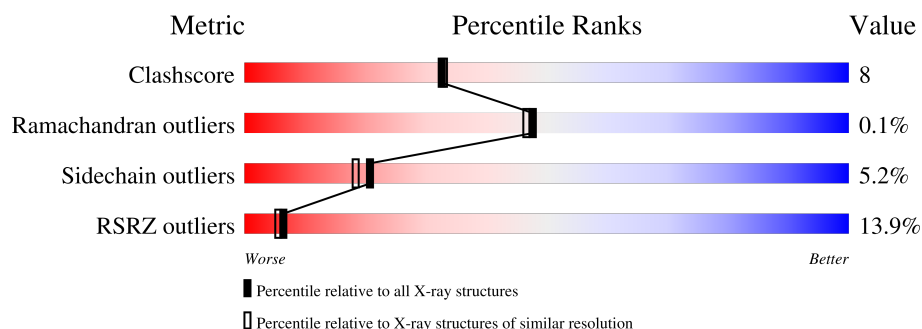
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	389	13% 70% 23% ...
1	B	389	14% 74% 19% ...

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6471 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.

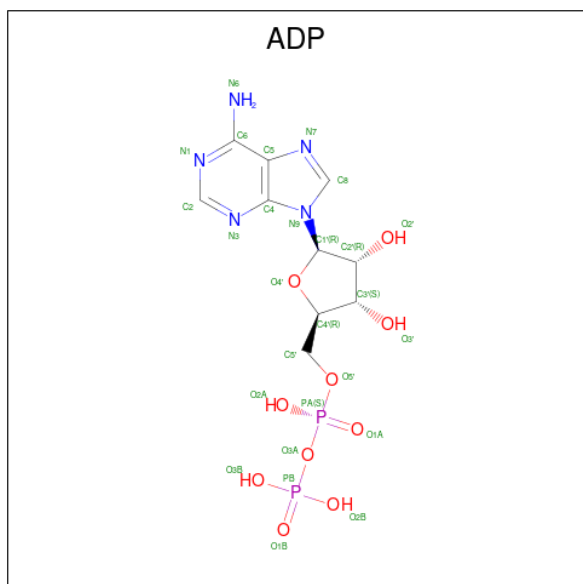
- Molecule 1 is a protein called CELL DIVISION CONTROL PROTEIN 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	0	0
			3044	1949	533	558	4			
1	B	379	Total	C	N	O	S	0	0	0
			3044	1949	533	558	4			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

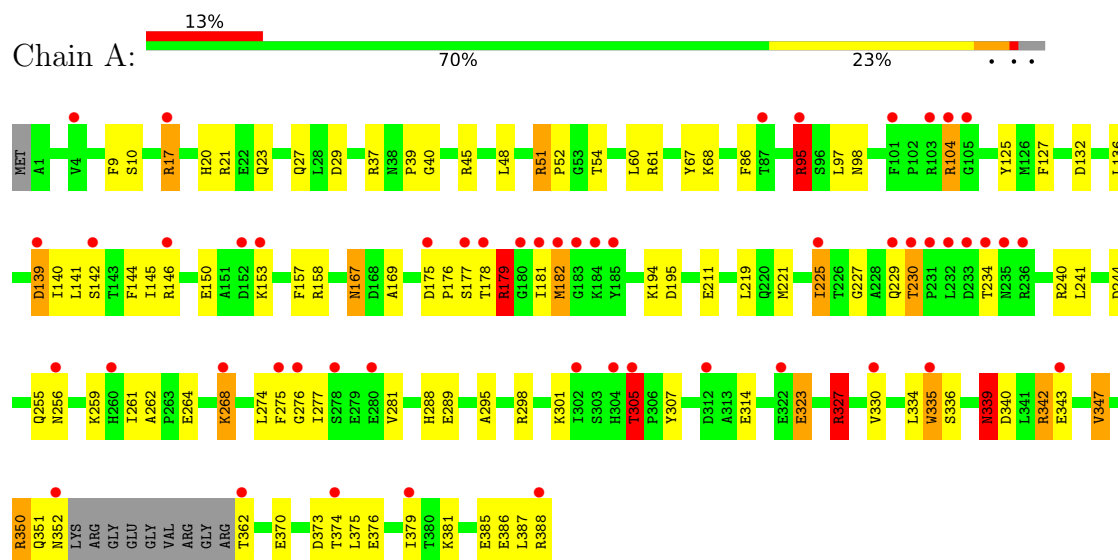
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	156	Total	O	0	0
			156	156		
4	B	171	Total	O	0	0
			171	171		

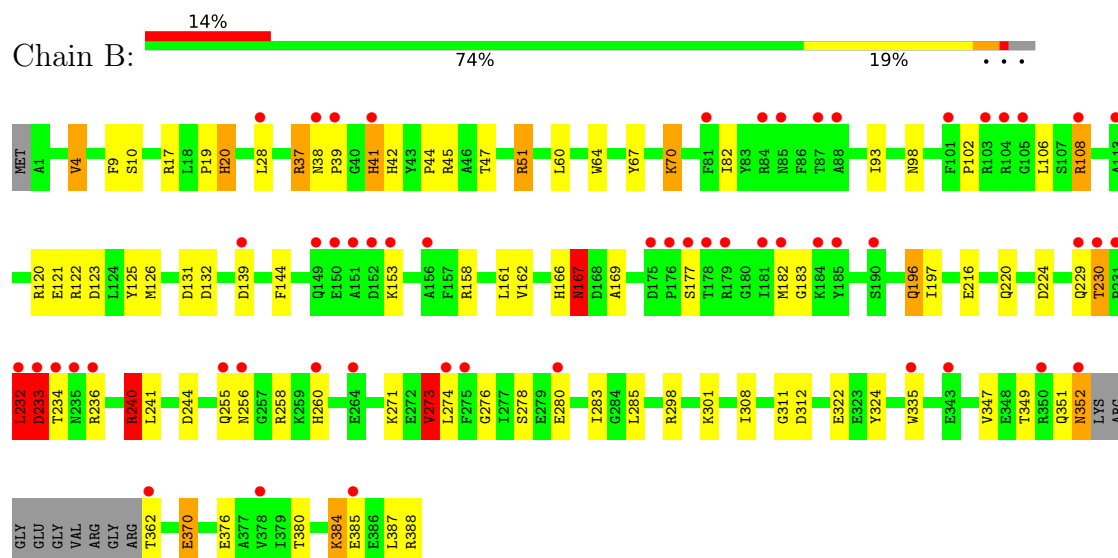
3 Residue-property plots [i](#)

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

• Molecule 1: CELL DIVISION CONTROL PROTEIN 6



• Molecule 1: CELL DIVISION CONTROL PROTEIN 6



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	132.07Å 132.07Å 82.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.4 (20.00-2.00) 98.3 (20.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.00Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.221 , 0.257 0.208 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	33.4	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 75.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.011 for -h,-k,l 0.019 for h,-h-k,-l 0.011 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6471	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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	0.83	1/3104 (0.0%)	1.67	51/4204 (1.2%)
1	B	0.92	0/3104	1.66	42/4204 (1.0%)
All	All	0.87	1/6208 (0.0%)	1.67	93/8408 (1.1%)

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	9
1	B	0	9
All	All	0	18

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	262	ALA	N-CA	5.62	1.52	1.45

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	273	VAL	N-CA-CB	-12.31	97.68	112.33
1	B	244	ASP	CA-CB-CG	9.93	122.53	112.60
1	A	288	HIS	CA-CB-CG	-9.89	103.91	113.80
1	A	339	ASN	OD1-CG-ND2	9.49	132.09	122.60
1	A	98	ASN	CA-CB-CG	-9.26	103.34	112.60
1	B	384	LYS	CA-C-O	-9.25	110.61	120.42
1	A	179	ARG	CD-NE-CZ	9.04	137.05	124.40
1	A	98	ASN	OD1-CG-ND2	8.86	131.46	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	352	ASN	CA-CB-CG	8.70	121.30	112.60
1	A	146	ARG	CD-NE-CZ	8.59	136.42	124.40
1	A	9	PHE	CA-CB-CG	-8.56	105.24	113.80
1	B	312	ASP	CA-CB-CG	8.53	121.13	112.60
1	A	61	ARG	CD-NE-CZ	8.46	136.25	124.40
1	A	327	ARG	CD-NE-CZ	8.27	135.98	124.40
1	A	244	ASP	CA-CB-CG	7.61	120.21	112.60
1	B	240	ARG	CD-NE-CZ	7.53	134.94	124.40
1	A	275	PHE	CA-CB-CG	7.14	120.94	113.80
1	B	158	ARG	NE-CZ-NH2	7.13	125.61	119.20
1	B	224	ASP	CA-CB-CG	-7.06	105.54	112.60
1	A	347	VAL	N-CA-CB	-7.03	100.64	112.44
1	B	9	PHE	CA-CB-CG	-7.01	106.79	113.80
1	A	195	ASP	CA-CB-CG	-6.96	105.64	112.60
1	B	144	PHE	CA-CB-CG	-6.90	106.90	113.80
1	B	51	ARG	NE-CZ-NH2	6.89	125.40	119.20
1	A	350	ARG	CA-CB-CG	6.68	127.46	114.10
1	A	127	PHE	CA-CB-CG	6.45	120.25	113.80
1	A	350	ARG	CD-NE-CZ	6.43	133.41	124.40
1	B	64	TRP	CA-C-O	6.42	127.56	120.82
1	A	387	LEU	CA-C-N	6.42	133.25	121.70
1	A	387	LEU	C-N-CA	6.42	133.25	121.70
1	B	362	THR	CB-CA-C	6.42	123.22	109.10
1	B	347	VAL	CA-C-O	-6.41	114.18	121.75
1	A	339	ASN	CA-CB-CG	-6.39	106.21	112.60
1	A	342	ARG	CD-NE-CZ	6.27	133.18	124.40
1	B	37	ARG	NE-CZ-NH2	-6.11	113.70	119.20
1	B	37	ARG	CD-NE-CZ	6.10	132.94	124.40
1	A	388	ARG	CG-CD-NE	6.07	125.34	112.00
1	B	41	HIS	CA-CB-CG	-6.06	107.74	113.80
1	B	335	TRP	O-C-N	-6.06	115.83	122.07
1	B	17	ARG	CD-NE-CZ	6.06	132.88	124.40
1	A	230	THR	CB-CA-C	6.01	118.28	109.08
1	B	10	SER	CA-C-N	5.98	125.86	119.28
1	B	10	SER	C-N-CA	5.98	125.86	119.28
1	B	166	HIS	CA-CB-CG	-5.96	107.84	113.80
1	B	273	VAL	CB-CA-C	5.96	117.05	110.62
1	B	308	ILE	O-C-N	-5.95	116.60	122.97
1	A	334	LEU	CA-C-O	5.93	126.83	120.55
1	B	196	GLN	OE1-CD-NE2	-5.90	116.70	122.60
1	A	323	GLU	CB-CA-C	-5.87	101.67	110.88
1	A	144	PHE	CA-CB-CG	-5.86	107.94	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	384	LYS	O-C-N	5.84	128.81	122.15
1	A	20	HIS	CA-CB-CG	-5.82	107.98	113.80
1	B	324	TYR	CA-CB-CG	-5.82	103.43	113.90
1	A	86	PHE	CA-CB-CG	-5.78	108.02	113.80
1	B	121	GLU	N-CA-C	5.78	118.52	111.82
1	A	51	ARG	NE-CZ-NH2	5.76	124.38	119.20
1	B	20	HIS	CA-CB-CG	-5.62	108.18	113.80
1	A	37	ARG	CA-C-N	5.58	127.19	122.28
1	A	37	ARG	C-N-CA	5.58	127.19	122.28
1	B	311	GLY	O-C-N	-5.51	116.89	122.19
1	B	362	THR	CA-C-O	-5.49	111.47	120.80
1	B	93	ILE	CA-C-O	5.49	126.98	121.17
1	A	385	GLU	CA-CB-CG	5.47	125.04	114.10
1	A	67	TYR	CA-C-N	5.45	127.84	120.38
1	A	67	TYR	C-N-CA	5.45	127.84	120.38
1	B	298	ARG	NE-CZ-NH2	-5.43	114.32	119.20
1	B	229	GLN	N-CA-CB	5.42	118.65	110.30
1	A	158	ARG	NE-CZ-NH2	5.41	124.07	119.20
1	A	261	ILE	CA-C-O	-5.39	114.89	121.04
1	A	21	ARG	CG-CD-NE	5.35	123.77	112.00
1	A	240	ARG	CD-NE-CZ	5.34	131.88	124.40
1	A	386	GLU	CA-CB-CG	5.32	124.74	114.10
1	A	29	ASP	CA-C-O	5.30	126.17	120.55
1	A	95	ARG	CD-NE-CZ	5.26	131.77	124.40
1	A	262	ALA	O-C-N	-5.20	117.40	121.14
1	B	123	ASP	CA-C-O	-5.19	115.70	122.14
1	A	305	THR	CB-CA-C	5.17	117.42	109.15
1	A	261	ILE	CA-C-N	-5.16	114.52	124.01
1	A	261	ILE	C-N-CA	-5.16	114.52	124.01
1	B	370	GLU	CA-C-N	5.15	125.07	119.76
1	B	370	GLU	C-N-CA	5.15	125.07	119.76
1	A	45	ARG	CD-NE-CZ	5.13	131.59	124.40
1	A	51	ARG	NE-CZ-NH1	-5.13	116.37	121.50
1	B	233	ASP	N-CA-C	-5.09	101.98	109.62
1	B	64	TRP	O-C-N	-5.08	116.83	122.07
1	B	122	ARG	N-CA-C	-5.06	106.69	112.92
1	A	132	ASP	CA-CB-CG	-5.06	107.54	112.60
1	A	182	MET	N-CA-C	5.06	119.50	113.23
1	B	70	LYS	CA-C-O	-5.05	113.83	119.34
1	B	19	PRO	O-C-N	-5.04	116.94	123.03
1	A	335	TRP	CA-CB-CG	-5.03	104.04	113.60
1	A	336	SER	CA-C-O	-5.03	115.09	120.42

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	197	ILE	CA-C-O	5.02	126.17	120.95

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	211	GLU	Mainchain
1	A	225	ILE	Mainchain
1	A	227	GLY	Mainchain
1	A	259	LYS	Mainchain
1	A	281	VAL	Mainchain
1	A	295	ALA	Mainchain
1	A	305	THR	Mainchain
1	A	314	GLU	Mainchain
1	A	381	LYS	Mainchain
1	B	126	MET	Mainchain
1	B	167	ASN	Mainchain
1	B	232	LEU	Mainchain
1	B	271	LYS	Mainchain
1	B	285	LEU	Mainchain
1	B	349	THR	Mainchain
1	B	4	VAL	Mainchain
1	B	70	LYS	Mainchain
1	B	82	ILE	Mainchain

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	3044	0	3100	56	0
1	B	3044	0	3100	42	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	27	0	12	0	0
3	B	27	0	12	1	0
4	A	156	0	0	4	0
4	B	171	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6471	0	6224	98	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 8.

All (98) 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:232:LEU:HD13	1:B:234:THR:OG1	1.63	0.97
1:A:194:LYS:NZ	1:A:229:GLN:HE21	1.66	0.93
1:A:194:LYS:HZ1	1:A:229:GLN:HE21	1.23	0.83
1:A:342:ARG:NH2	1:A:343:GLU:OE1	2.17	0.78
1:A:145:ILE:HG23	1:A:182:MET:HE3	1.65	0.78
1:A:241:LEU:HD21	1:A:274:LEU:HD21	1.66	0.77
1:A:104:ARG:HB2	1:A:104:ARG:HH11	1.51	0.74
1:A:375:LEU:O	1:A:379:ILE:HG13	1.93	0.68
1:B:241:LEU:HD21	1:B:274:LEU:HD21	1.74	0.68
1:B:258:ARG:HH11	1:B:258:ARG:HG3	1.57	0.68
1:B:278:SER:OG	1:B:280:GLU:HG2	1.94	0.66
1:A:145:ILE:HG12	1:A:182:MET:HE3	1.76	0.66
1:A:145:ILE:HG23	1:A:182:MET:CE	2.25	0.66
1:B:241:LEU:HD11	1:B:273:VAL:HG13	1.80	0.64
1:A:234:THR:HG22	1:A:234:THR:O	1.96	0.64
1:B:233:ASP:OD1	1:B:236:ARG:HB2	1.98	0.64
1:B:60:LEU:HD21	1:B:162:VAL:HG11	1.84	0.60
1:A:167:ASN:HD22	1:A:169:ALA:H	1.48	0.60
1:A:150:GLU:OE1	1:A:153:LYS:HD2	2.00	0.60
1:B:47:THR:OG1	1:B:182:MET:HG2	2.01	0.60
1:A:176:PRO:HA	1:A:179:ARG:NH1	2.17	0.60
1:A:277:ILE:N	1:A:370:GLU:OE2	2.27	0.59
1:B:220:GLN:HG2	4:B:547:HOH:O	2.04	0.58
1:B:255:GLN:HG2	1:B:255:GLN:O	2.02	0.58
1:B:240:ARG:HH11	1:B:240:ARG:HG2	1.69	0.57
1:A:264:GLU:O	1:A:268:LYS:HG3	2.04	0.57
1:A:373:ASP:HB2	4:A:506:HOH:O	2.04	0.57
1:B:258:ARG:HG3	1:B:258:ARG:NH1	2.20	0.57
1:B:4:VAL:HG12	1:B:4:VAL:O	2.05	0.57
1:A:139:ASP:OD1	1:A:140:ILE:N	2.38	0.56
1:A:301:LYS:HE3	1:A:376:GLU:OE2	2.06	0.56
1:B:276:GLY:HA3	1:B:370:GLU:OE2	2.06	0.56
1:A:339:ASN:OD1	1:A:342:ARG:NH1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:THR:CG2	1:A:307:TYR:O	2.54	0.54
1:B:167:ASN:HD22	1:B:169:ALA:H	1.56	0.54
1:B:230:THR:O	1:B:233:ASP:HB3	2.08	0.54
1:A:23:GLN:HG2	1:A:27:GLN:HE21	1.72	0.54
1:A:181:ILE:HG22	1:A:182:MET:HE2	1.90	0.54
1:A:95:ARG:HH11	1:A:95:ARG:HB3	1.73	0.53
1:A:194:LYS:NZ	1:A:229:GLN:NE2	2.48	0.53
1:A:194:LYS:HZ2	1:A:229:GLN:HE21	1.51	0.52
1:A:40:GLY:HA2	1:A:157:PHE:O	2.10	0.52
1:A:277:ILE:HB	1:A:370:GLU:HG3	1.92	0.51
1:A:48:LEU:HD11	1:A:60:LEU:HG	1.92	0.50
1:A:23:GLN:HG2	1:A:27:GLN:NE2	2.27	0.50
1:B:108:ARG:NH2	1:B:139:ASP:OD2	2.45	0.49
1:A:305:THR:HG23	1:A:307:TYR:O	2.12	0.49
1:A:298:ARG:HH12	1:A:323:GLU:CD	2.20	0.49
1:B:4:VAL:O	1:B:4:VAL:CG1	2.60	0.49
1:A:51:ARG:HB2	1:A:52:PRO:CD	2.43	0.48
1:A:51:ARG:HB2	1:A:52:PRO:HD2	1.95	0.48
1:B:20:HIS:CG	1:B:196:GLN:HG2	2.49	0.47
1:B:167:ASN:HD22	1:B:167:ASN:C	2.21	0.47
1:B:37:ARG:NH2	1:B:67:TYR:OH	2.47	0.47
1:B:322:GLU:HG3	4:B:491:HOH:O	2.14	0.47
1:B:131:ASP:O	1:B:132:ASP:C	2.58	0.47
1:B:38:ASN:OD1	1:B:41:HIS:CD2	2.68	0.46
1:A:234:THR:O	1:A:234:THR:CG2	2.63	0.46
1:B:102:PRO:HG3	1:B:106:LEU:HD21	1.97	0.46
1:B:120:ARG:NH1	1:B:153:LYS:O	2.48	0.46
1:A:255:GLN:O	1:A:255:GLN:HG2	2.16	0.46
1:A:10:SER:HB3	1:B:98:ASN:HD21	1.81	0.46
1:A:175:ASP:OD1	1:A:178:THR:OG1	2.29	0.45
1:A:194:LYS:HZ2	1:A:229:GLN:NE2	2.13	0.45
1:B:380:THR:HG22	1:B:384:LYS:HD2	1.99	0.45
1:A:175:ASP:OD1	1:A:178:THR:CB	2.65	0.44
1:B:258:ARG:HD2	1:B:260:HIS:O	2.17	0.44
1:B:351:GLN:O	1:B:352:ASN:HB3	2.18	0.44
1:A:374:THR:HB	4:A:539:HOH:O	2.18	0.44
1:B:45:ARG:HA	1:B:161:LEU:O	2.17	0.44
1:A:104:ARG:HB2	1:A:104:ARG:NH1	2.28	0.43
1:A:327:ARG:H	1:A:327:ARG:HG2	1.57	0.43
1:B:301:LYS:HE3	1:B:376:GLU:OE2	2.18	0.43
1:A:145:ILE:CG2	1:A:182:MET:HE3	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:PRO:HB2	1:B:125:TYR:CD2	2.53	0.43
1:A:51:ARG:HG3	1:A:54:THR:HG23	2.01	0.43
1:A:17:ARG:HG2	4:A:434:HOH:O	2.19	0.43
1:A:298:ARG:NH1	1:A:323:GLU:OE2	2.52	0.43
1:A:264:GLU:O	1:A:268:LYS:CG	2.67	0.42
1:A:176:PRO:HA	1:A:179:ARG:HH11	1.83	0.42
1:A:194:LYS:HE3	1:A:229:GLN:HG3	2.00	0.42
1:A:221:MET:O	1:A:225:ILE:HG13	2.19	0.42
1:A:39:PRO:HB2	1:A:125:TYR:CD2	2.54	0.42
1:A:351:GLN:HE21	1:A:362:THR:HB	1.83	0.42
1:A:142:SER:OG	1:A:178:THR:HG21	2.19	0.42
1:B:385:GLU:CD	1:B:388:ARG:HE	2.28	0.41
1:B:240:ARG:HG2	1:B:240:ARG:NH1	2.35	0.41
1:A:17:ARG:HG3	4:A:527:HOH:O	2.21	0.41
1:B:216:GLU:O	1:B:220:GLN:HG3	2.21	0.41
1:B:28:LEU:HD23	1:B:28:LEU:HA	1.87	0.41
1:B:233:ASP:OD1	1:B:233:ASP:C	2.64	0.41
1:B:233:ASP:OD1	1:B:233:ASP:O	2.39	0.40
1:A:276:GLY:HA3	1:A:370:GLU:OE2	2.21	0.40
1:A:289:GLU:OE1	1:A:340:ASP:OD2	2.40	0.40
1:B:42:HIS:O	1:B:44:PRO:HD3	2.22	0.40
1:B:167:ASN:ND2	1:B:169:ALA:H	2.17	0.40
1:B:387:LEU:HA	1:B:387:LEU:HD23	1.89	0.40
3:B:399:ADP:O5'	3:B:399:ADP:H2'	2.21	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	375/389 (96%)	373 (100%)	2 (0%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	375/389 (96%)	368 (98%)	6 (2%)	1 (0%)	36	35
All	All	750/778 (96%)	741 (99%)	8 (1%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	183	GLY

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	329/336 (98%)	307 (93%)	22 (7%)	15	11
1	B	329/336 (98%)	317 (96%)	12 (4%)	31	31
All	All	658/672 (98%)	624 (95%)	34 (5%)	21	18

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ARG
1	A	68	LYS
1	A	95	ARG
1	A	97	LEU
1	A	104	ARG
1	A	136	LEU
1	A	139	ASP
1	A	141	LEU
1	A	167	ASN
1	A	177	SER
1	A	179	ARG
1	A	219	LEU
1	A	230	THR
1	A	256	ASN
1	A	268	LYS

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Mol	Chain	Res	Type
1	A	305	THR
1	A	327	ARG
1	A	330	VAL
1	A	335	TRP
1	A	339	ASN
1	A	347	VAL
1	A	350	ARG
1	B	51	ARG
1	B	108	ARG
1	B	167	ASN
1	B	177	SER
1	B	230	THR
1	B	232	LEU
1	B	233	ASP
1	B	240	ARG
1	B	256	ASN
1	B	273	VAL
1	B	283	ILE
1	B	352	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	A	38	ASN
1	A	166	HIS
1	A	167	ASN
1	A	173	ASN
1	A	229	GLN
1	A	351	GLN
1	B	26	GLN
1	B	41	HIS
1	B	166	HIS
1	B	167	ASN
1	B	220	GLN
1	B	260	HIS
1	B	304	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
3	ADP	A	398	2	28,29,29	1.53	3 (10%)	43,45,45	0.97	2 (4%)
3	ADP	B	399	2	28,29,29	1.76	3 (10%)	43,45,45	0.99	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	A	398	2	-	2/16/32/32	0/3/3/3
3	ADP	B	399	2	-	1/16/32/32	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	399	ADP	PA-O3A	-7.66	1.51	1.59
3	A	398	ADP	PA-O3A	-5.18	1.53	1.59
3	A	398	ADP	PB-O2B	-3.27	1.42	1.54
3	B	399	ADP	PB-O3B	-2.84	1.44	1.54
3	A	398	ADP	PB-O3B	-2.27	1.46	1.54
3	B	399	ADP	PB-O2B	-2.12	1.46	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	398	ADP	O3B-PB-O1B	-2.42	101.42	110.83
3	A	398	ADP	C2'-C1'-N9	-2.25	107.72	113.30
3	B	399	ADP	O2A-PA-O3A	2.22	113.26	107.27

There are no chirality outliers.

All (3) torsion outliers are listed below:

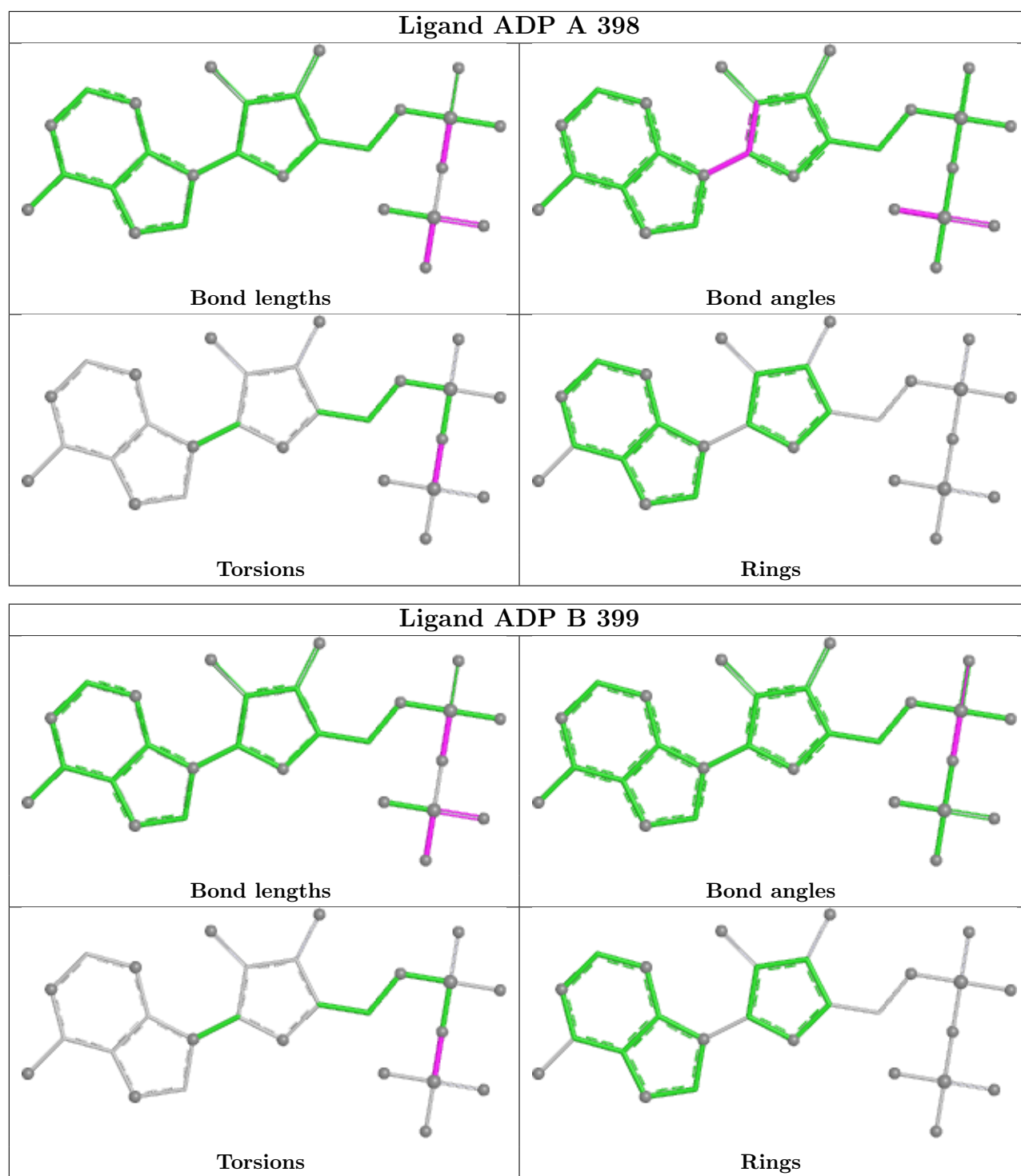
Mol	Chain	Res	Type	Atoms
3	A	398	ADP	PA-O3A-PB-O1B
3	A	398	ADP	PA-O3A-PB-O2B
3	B	399	ADP	PA-O3A-PB-O2B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	399	ADP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	379/389 (97%)	0.87	51 (13%) 7 6	32, 43, 71, 103	0
1	B	379/389 (97%)	0.72	54 (14%) 6 5	26, 41, 72, 96	0
All	All	758/778 (97%)	0.80	105 (13%) 6 5	26, 42, 72, 103	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	233	ASP	7.7
1	B	232	LEU	6.9
1	A	230	THR	6.5
1	A	275	PHE	6.1
1	A	232	LEU	5.9
1	B	177	SER	5.8
1	B	231	PRO	5.6
1	B	230	THR	5.5
1	B	275	PHE	5.5
1	A	229	GLN	5.1
1	A	302	ILE	5.0
1	A	184	LYS	4.6
1	B	362	THR	4.6
1	A	335	TRP	4.3
1	B	38	ASN	4.2
1	B	352	ASN	4.0
1	B	182	MET	4.0
1	A	362	THR	4.0
1	A	233	ASP	4.0
1	A	139	ASP	3.9
1	A	181	ILE	3.9
1	B	264	GLU	3.8
1	A	312	ASP	3.7
1	A	352	ASN	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	235	ASN	3.7
1	A	235	ASN	3.6
1	B	178	THR	3.6
1	A	183	GLY	3.6
1	B	152	ASP	3.5
1	A	231	PRO	3.4
1	B	101	PHE	3.4
1	A	175	ASP	3.3
1	B	255	GLN	3.3
1	A	185	TYR	3.2
1	A	234	THR	3.2
1	B	280	GLU	3.2
1	B	185	TYR	3.1
1	B	104	ARG	3.1
1	A	104	ARG	3.0
1	B	236	ARG	3.0
1	A	4	VAL	3.0
1	A	388	ARG	3.0
1	B	260	HIS	3.0
1	A	260	HIS	2.9
1	A	304	HIS	2.9
1	A	103	ARG	2.9
1	B	179	ARG	2.9
1	A	178	THR	2.9
1	A	182	MET	2.8
1	A	236	ARG	2.8
1	A	177	SER	2.8
1	A	17	ARG	2.8
1	B	256	ASN	2.8
1	A	152	ASP	2.8
1	A	343	GLU	2.8
1	B	335	TRP	2.8
1	B	149	GLN	2.7
1	B	105	GLY	2.7
1	A	101	PHE	2.7
1	B	156	ALA	2.7
1	A	142	SER	2.7
1	B	108	ARG	2.7
1	A	374	THR	2.7
1	B	274	LEU	2.7
1	A	305	THR	2.6
1	B	350	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	150	GLU	2.6
1	B	113	ALA	2.6
1	B	139	ASP	2.5
1	B	88	ALA	2.5
1	B	229	GLN	2.5
1	A	146	ARG	2.5
1	B	175	ASP	2.5
1	B	153	LYS	2.5
1	B	84	ARG	2.5
1	A	379	ILE	2.5
1	B	28	LEU	2.4
1	B	343	GLU	2.4
1	B	39	PRO	2.4
1	A	256	ASN	2.3
1	A	268	LYS	2.3
1	A	330	VAL	2.3
1	A	322	GLU	2.3
1	B	176	PRO	2.3
1	B	181	ILE	2.3
1	A	180	GLY	2.3
1	A	153	LYS	2.2
1	B	184	LYS	2.2
1	B	190	SER	2.2
1	A	276	GLY	2.2
1	A	87	THR	2.2
1	B	41	HIS	2.2
1	B	103	ARG	2.2
1	B	234	THR	2.2
1	B	87	THR	2.1
1	B	81	PHE	2.1
1	B	151	ALA	2.1
1	B	85	ASN	2.1
1	B	385	GLU	2.1
1	A	225	ILE	2.1
1	B	378	VAL	2.1
1	A	278	SER	2.1
1	A	280	GLU	2.0
1	A	95	ARG	2.0
1	A	105	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

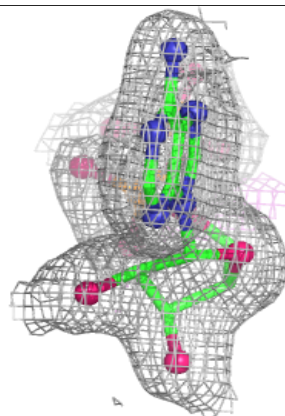
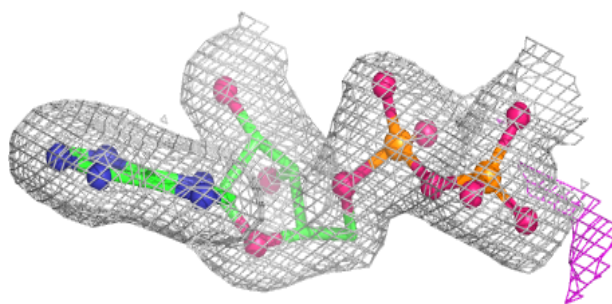
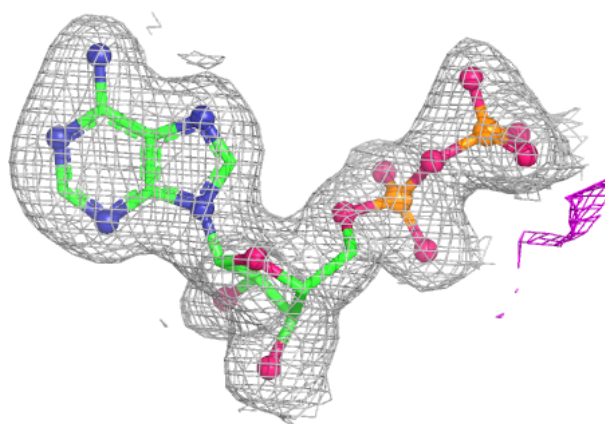
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

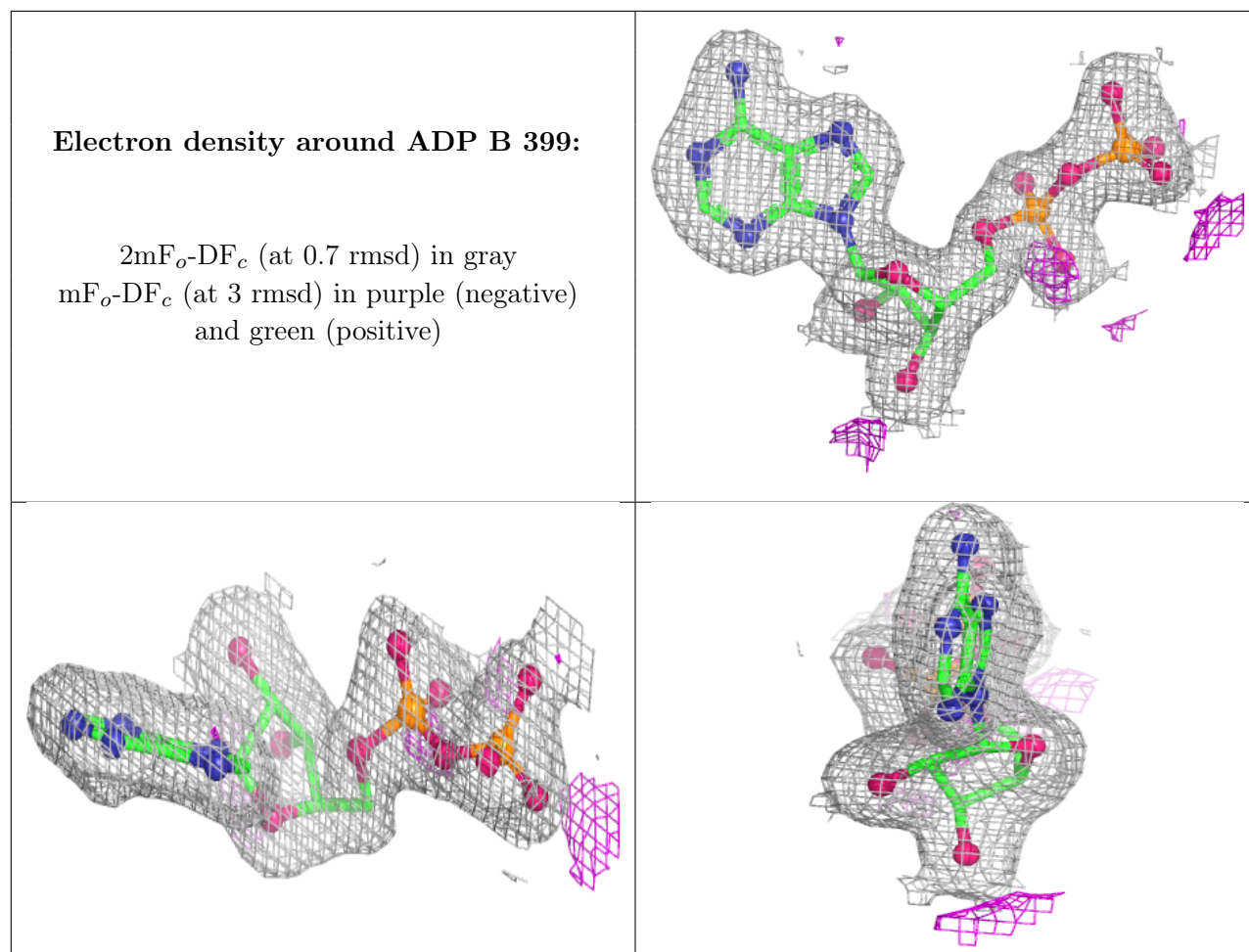
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	A	390	1/1	0.98	0.03	40,40,40,40	0
2	MG	B	391	1/1	0.98	0.04	35,35,35,35	0
3	ADP	A	398	27/27	0.98	0.06	29,35,37,39	0
3	ADP	B	399	27/27	0.98	0.05	24,30,35,37	0

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 ADP A 398:

$2mF_o - DF_c$ (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.