



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 08:47 PM UTC

PDB ID : 1VRP / pdb_00001vrp
Title : The 2.1 Structure of T. californica Creatine Kinase Complexed with the Transition-State Analogue Complex, ADP-Mg 2+ /NO3-/Creatine
Authors : Lahiri, S.D.; Wang, P.F.; Babbitt, P.C.; McLeish, M.J.; Kenyon, G.L.; Allen, K.N.
Deposited on : 2005-04-25
Resolution : 2.10 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

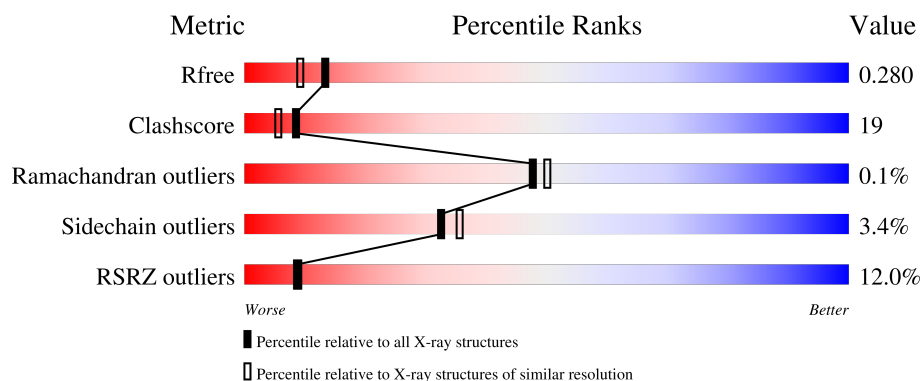
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	381	13% 65% 28% • •
1	B	381	10% 64% 30% • •

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6102 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.

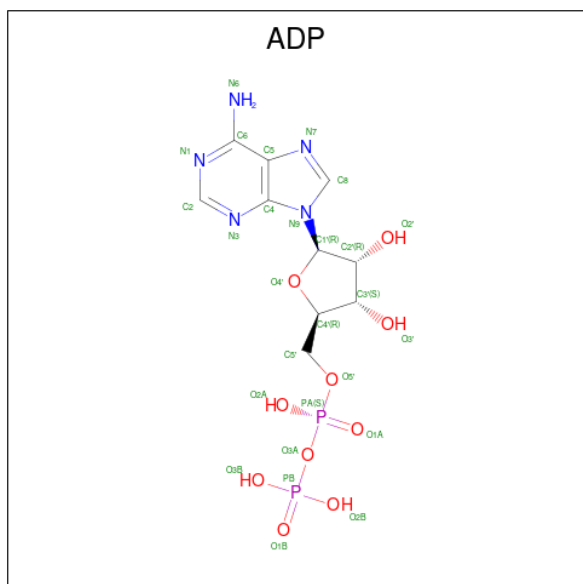
- Molecule 1 is a protein called Creatine Kinase, M chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	370	Total	C	N	O	S	0	0	0
			2921	1837	515	551	18			
1	B	374	Total	C	N	O	S	0	0	0
			2961	1864	523	556	18			

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

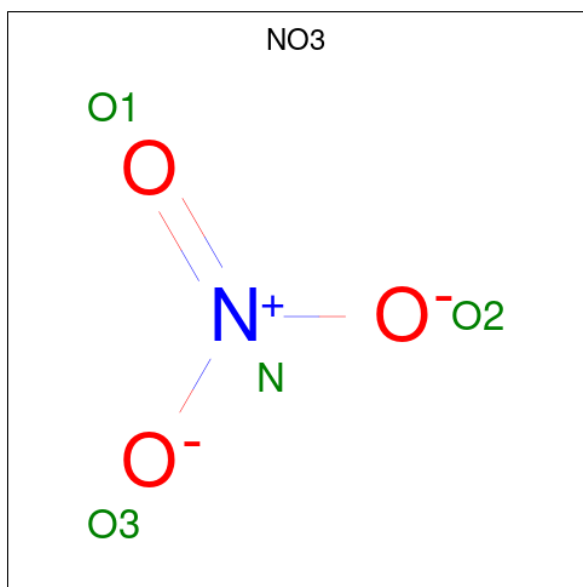
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

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



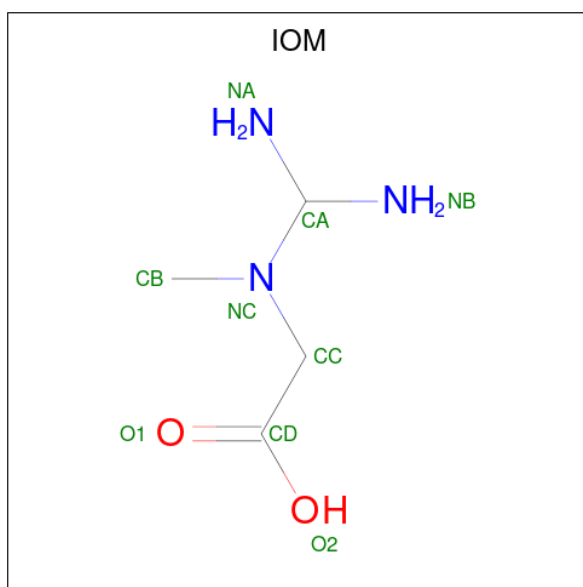
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is NITRATE ION (CCD ID: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	N	O	0	0
			4	1	3		

- Molecule 5 is (DIAMINOMETHYL-METHYL-AMINO)-ACETIC ACID (CCD ID: IOM) (formula: C₄H₁₁N₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			9	4	3	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	68	Total	O	0	0
			68	68		
6	B	83	Total	O	0	0
			83	83		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.63Å 87.19Å 127.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.42 – 2.10 50.42 – 2.10	Depositor EDS
% Data completeness (in resolution range)	91.3 (50.42-2.10) 91.3 (50.42-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.83 (at 2.10Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.242 , 0.278 0.242 , 0.280	Depositor DCC
R_{free} test set	4303 reflections (9.88%)	wwPDB-VP
Wilson B-factor (Å ²)	23.4	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6102	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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, NO3, ADP, IOM

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	0.78	6/2981 (0.2%)	1.18	23/4015 (0.6%)
1	B	0.61	1/3023 (0.0%)	1.06	14/4071 (0.3%)
All	All	0.70	7/6004 (0.1%)	1.12	37/8086 (0.5%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	325	VAL	C-O	-9.85	1.12	1.24
1	A	69	ILE	CA-C	-8.28	1.43	1.52
1	A	325	VAL	N-CA	-7.43	1.37	1.46
1	A	377	MET	C-O	-7.36	1.14	1.24
1	A	324	GLY	CA-C	-6.75	1.45	1.51
1	A	325	VAL	CA-CB	-5.41	1.47	1.54
1	B	122	ASP	CA-C	-5.12	1.46	1.52

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	323	GLY	CA-C-N	-11.61	113.75	121.65
1	A	323	GLY	C-N-CA	-11.61	113.75	121.65
1	B	122	ASP	CA-C-N	11.51	131.30	119.56
1	B	122	ASP	C-N-CA	11.51	131.30	119.56
1	A	377	MET	CA-C-N	-10.23	107.05	119.84
1	A	377	MET	C-N-CA	-10.23	107.05	119.84
1	B	232	GLU	N-CA-C	-9.23	102.15	113.41
1	A	291	LEU	N-CA-C	8.84	124.14	109.46
1	A	324	GLY	N-CA-C	-8.49	96.60	111.46
1	B	109	ASP	N-CA-C	-8.37	93.42	108.48
1	A	246	MET	N-CA-C	-7.72	102.78	112.90
1	A	324	GLY	CA-C-N	-7.72	108.07	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	324	GLY	C-N-CA	-7.72	108.07	121.97
1	A	329	ALA	N-CA-C	7.18	121.30	111.39
1	A	143	PRO	N-CA-C	6.95	119.17	110.70
1	A	213	ASP	N-CA-C	6.59	120.04	110.42
1	B	143	PRO	N-CA-C	6.58	118.72	110.70
1	A	328	ALA	CA-C-N	6.56	131.68	122.36
1	A	328	ALA	C-N-CA	6.56	131.68	122.36
1	A	211	TRP	C-N-CD	-6.50	106.31	120.60
1	B	27	ASN	N-CA-C	-6.47	97.87	108.41
1	A	289	THR	N-CA-C	-6.19	100.20	110.17
1	B	69	ILE	N-CA-C	5.83	116.57	108.23
1	A	242	LYS	N-CA-C	-5.82	102.30	110.50
1	A	321	GLY	N-CA-C	5.79	126.90	113.18
1	B	287	LEU	CB-CG-CD2	-5.76	93.42	110.70
1	A	42	LEU	N-CA-C	5.75	121.20	113.72
1	A	13	ASN	N-CA-C	-5.74	106.50	112.93
1	A	323	GLY	N-CA-C	5.73	126.77	113.18
1	B	120	ASP	N-CA-CB	-5.44	103.80	110.98
1	A	378	PRO	N-CA-C	5.38	123.54	112.47
1	B	361	VAL	N-CA-C	-5.31	105.14	110.30
1	B	170	GLN	N-CA-C	-5.15	102.76	110.23
1	A	296	HIS	N-CA-C	-5.08	99.51	108.20
1	B	287	LEU	CA-CB-CG	5.03	133.91	116.30
1	B	142	LEU	CA-C-N	5.03	125.56	120.38
1	B	142	LEU	C-N-CA	5.03	125.56	120.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2921	0	2890	107	0
1	B	2961	0	2932	117	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	27	0	12	1	0
3	B	27	0	12	0	0
4	B	4	0	0	0	0
5	B	9	0	9	1	0
6	A	68	0	0	8	0
6	B	83	0	0	10	0
All	All	6102	0	5855	224	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 19.

All (224) 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:127:LEU:HD11	1:A:298:LYS:CE	1.77	1.12
1:A:127:LEU:HD11	1:A:298:LYS:HE3	1.05	1.01
1:B:191:HIS:HE1	6:B:472:HOH:O	1.45	0.99
1:B:119:ASP:OD1	1:B:120:ASP:OD1	1.81	0.99
1:B:238:ILE:HG21	1:B:240:MET:HE2	1.43	0.97
1:B:300:PRO:HD2	1:B:364:GLU:OE2	1.65	0.97
1:B:48:PRO:HD2	1:B:80:GLU:HG3	1.48	0.96
1:B:176:LEU:HA	1:B:179:MET:HE3	1.48	0.94
1:A:127:LEU:CD1	1:A:298:LYS:HE3	1.96	0.94
1:A:322:THR:HG21	6:A:428:HOH:O	1.67	0.93
1:A:228:TRP:HB2	1:A:236:ARG:HB2	1.53	0.90
1:A:322:THR:CG2	6:A:428:HOH:O	2.19	0.90
1:A:298:LYS:HG2	1:A:333:ILE:HG12	1.55	0.89
1:A:158:CYS:SG	1:A:235:LEU:HD21	2.12	0.89
1:A:69:ILE:HD13	1:A:69:ILE:H	1.35	0.88
1:B:238:ILE:CG2	1:B:240:MET:HE2	2.04	0.86
1:A:321:GLY:O	1:A:322:THR:HG23	1.75	0.86
1:A:298:LYS:HE2	1:A:333:ILE:HD11	1.59	0.85
1:B:199:SER:HA	1:B:326:ASP:OD1	1.78	0.82
1:B:310:GLU:O	1:B:314:ARG:HG3	1.79	0.81
1:A:323:GLY:O	1:A:333:ILE:HB	1.81	0.80
1:B:269:ARG:O	1:B:270:GLY:O	2.00	0.80
1:B:287:LEU:O	1:B:342:LEU:HG	1.81	0.80
1:B:226:LEU:HD13	1:B:240:MET:HE3	1.66	0.78
1:A:220:ASN:HD21	1:A:224:THR:H	1.31	0.78
1:A:320:ARG:HG2	1:A:335:ASP:HB3	1.64	0.78
1:A:179:MET:HE3	1:A:184:GLN:HG2	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:LEU:HB2	1:B:244:GLY:HA3	1.67	0.77
1:A:324:GLY:C	1:A:326:ASP:N	2.39	0.76
1:B:110:LEU:O	1:B:254:CYS:SG	2.43	0.76
1:A:97:HIS:HE1	1:A:284:PRO:O	1.69	0.76
1:B:357:VAL:O	1:B:361:VAL:HG23	1.88	0.74
1:A:241:GLN:NE2	1:A:252:ARG:HH22	1.87	0.73
1:A:49:SER:HB2	6:A:408:HOH:O	1.89	0.72
1:A:133:THR:HA	1:A:290:GLY:O	1.88	0.72
1:B:112:GLN:HG2	1:B:251:ARG:HA	1.69	0.72
1:A:321:GLY:O	1:A:322:THR:CG2	2.38	0.71
1:A:66:HIS:HB2	1:A:69:ILE:CD1	2.20	0.71
1:B:132:ARG:HG2	1:B:133:THR:N	2.04	0.71
1:A:66:HIS:HB2	1:A:69:ILE:HD11	1.72	0.70
1:B:215:ARG:HG3	1:B:230:ASN:O	1.90	0.70
1:A:201:LEU:HD22	6:A:435:HOH:O	1.92	0.70
1:A:324:GLY:C	1:A:326:ASP:H	2.00	0.69
1:A:264:PHE:HB3	1:A:269:ARG:O	1.94	0.68
1:A:125:TYR:CE1	1:A:365:LYS:HE2	2.29	0.68
1:B:80:GLU:CD	1:B:80:GLU:H	2.00	0.67
1:A:324:GLY:O	1:A:325:VAL:C	2.31	0.66
1:A:241:GLN:NE2	1:A:252:ARG:NH2	2.44	0.65
1:B:359:LEU:HD21	1:B:378:PRO:HD3	1.78	0.65
1:A:324:GLY:O	1:A:326:ASP:N	2.30	0.65
1:A:125:TYR:CE1	1:A:365:LYS:CE	2.79	0.65
1:B:364:GLU:O	1:B:368:GLU:HG3	1.97	0.64
1:A:109:ASP:O	1:A:346:GLU:HB2	1.98	0.64
1:B:300:PRO:CD	1:B:364:GLU:OE2	2.44	0.64
1:A:259:LYS:O	1:A:263:ILE:HG13	1.97	0.64
1:B:228:TRP:HB2	1:B:236:ARG:HB2	1.79	0.64
1:B:341:ARG:HA	1:B:349:GLN:NE2	2.12	0.63
1:A:69:ILE:H	1:A:69:ILE:CD1	2.11	0.63
1:B:274:ASN:HD21	1:B:277:LEU:N	1.97	0.63
1:B:307:LYS:HE3	1:B:374:ASP:OD1	1.99	0.62
1:B:191:HIS:CE1	6:B:472:HOH:O	2.32	0.62
1:B:274:ASN:HD21	1:B:277:LEU:CA	2.12	0.62
1:A:179:MET:HE3	1:A:184:GLN:CG	2.29	0.62
1:A:354:VAL:HG12	1:A:358:LYS:HE2	1.82	0.62
1:A:320:ARG:CG	1:A:335:ASP:HB3	2.30	0.61
1:B:314:ARG:O	1:B:381:LYS:HG2	2.00	0.61
1:A:97:HIS:CE1	1:A:284:PRO:O	2.54	0.60
1:A:66:HIS:O	1:A:69:ILE:O	2.18	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:PRO:HA	1:A:287:LEU:HD11	1.84	0.60
1:A:345:SER:O	1:A:348:GLU:N	2.35	0.60
1:B:359:LEU:O	1:B:363:MET:HG3	2.02	0.60
1:A:359:LEU:O	1:A:363:MET:HG3	2.01	0.59
1:B:274:ASN:HD21	1:B:277:LEU:HB2	1.67	0.59
1:B:316:ARG:HD2	1:B:381:LYS:O	2.03	0.59
1:B:307:LYS:O	1:B:311:VAL:HG23	2.01	0.59
1:B:112:GLN:NE2	1:B:112:GLN:H	2.00	0.59
1:A:356:GLY:O	1:A:360:MET:HG3	2.02	0.58
1:B:238:ILE:HG21	1:B:240:MET:CE	2.26	0.58
1:B:251:ARG:HD3	1:B:251:ARG:C	2.28	0.57
1:A:142:LEU:HB3	1:A:143:PRO:HD2	1.85	0.57
1:A:220:ASN:HD21	1:A:224:THR:N	2.02	0.57
1:A:28:ASN:OD1	1:A:31:ALA:CB	2.51	0.57
1:B:121:LEU:O	1:B:123:PRO:HD3	2.05	0.57
1:A:132:ARG:O	1:A:291:LEU:HA	2.05	0.57
1:B:126:VAL:HG22	1:B:297:VAL:CG1	2.34	0.57
1:A:245:ASN:O	1:A:249:VAL:HG23	2.05	0.56
1:B:101:LYS:HB2	1:B:104:ASP:OD2	2.05	0.56
1:B:286:ASN:O	1:B:290:GLY:HA2	2.06	0.56
1:B:78:ASP:OD1	1:B:80:GLU:HG2	2.06	0.56
1:B:274:ASN:HD21	1:B:277:LEU:H	1.55	0.55
1:A:42:LEU:HD11	1:A:87:ASP:HB2	1.87	0.55
1:B:261:GLU:HG2	1:B:271:PHE:HE2	1.72	0.55
1:A:180:SER:OG	1:A:183:GLU:HG3	2.06	0.55
1:A:100:TYR:CD2	1:A:342:LEU:HD21	2.42	0.54
1:B:354:VAL:O	1:B:358:LYS:HG3	2.07	0.54
1:A:238:ILE:HG21	1:A:240:MET:HE2	1.89	0.54
1:B:274:ASN:HD21	1:B:277:LEU:CB	2.21	0.54
1:B:69:ILE:HB	6:B:413:HOH:O	2.07	0.54
1:A:340:ASP:OD2	1:A:352:MET:HE1	2.08	0.54
1:A:119:ASP:HB2	1:A:245:ASN:ND2	2.23	0.53
1:A:28:ASN:OD1	1:A:31:ALA:N	2.36	0.53
1:B:12:LEU:HB3	6:B:461:HOH:O	2.08	0.53
1:B:251:ARG:HD3	1:B:252:ARG:N	2.24	0.53
1:B:226:LEU:N	1:B:226:LEU:HD12	2.24	0.53
1:A:125:TYR:CE1	1:A:365:LYS:HE3	2.44	0.53
1:B:8:ASN:N	6:B:448:HOH:O	2.41	0.52
1:B:126:VAL:HG22	1:B:297:VAL:HG12	1.91	0.52
1:B:274:ASN:ND2	1:B:277:LEU:HB2	2.24	0.52
1:A:320:ARG:HG2	1:A:335:ASP:CB	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:LEU:HB2	1:B:244:GLY:CA	2.38	0.52
1:A:322:THR:HG23	6:A:428:HOH:O	1.96	0.52
1:A:132:ARG:HG2	1:A:133:THR:N	2.24	0.52
1:B:197:PRO:HG3	1:B:211:TRP:CD2	2.45	0.51
1:B:120:ASP:OD1	1:B:120:ASP:N	2.43	0.51
1:B:349:GLN:HA	1:B:352:MET:HE3	1.91	0.51
1:A:125:TYR:OH	1:A:365:LYS:HG2	2.12	0.51
1:B:153:LEU:O	1:B:157:LEU:HG	2.11	0.51
1:B:180:SER:OG	1:B:183:GLU:HG3	2.10	0.51
1:B:361:VAL:HG12	1:B:365:LYS:HE2	1.93	0.50
1:B:119:ASP:C	1:B:120:ASP:OD1	2.53	0.50
1:A:79:GLU:HB2	1:A:272:MET:SD	2.52	0.50
1:B:177:SER:HB2	6:B:470:HOH:O	2.11	0.50
1:B:175:PRO:HG2	1:B:178:SER:HB3	1.94	0.50
1:A:211:TRP:CD1	1:A:211:TRP:C	2.91	0.49
1:B:353:VAL:O	1:B:357:VAL:HG23	2.12	0.49
1:B:86:LYS:HE2	1:B:90:ASP:OD2	2.12	0.49
1:B:312:LEU:HD11	1:B:319:LYS:HD3	1.93	0.49
1:A:321:GLY:C	1:A:322:THR:HG23	2.38	0.49
1:B:66:HIS:HB3	1:B:69:ILE:O	2.13	0.49
1:B:181:ASP:HB2	6:B:445:HOH:O	2.12	0.49
1:B:86:LYS:HG2	6:B:464:HOH:O	2.12	0.49
1:B:192:PHE:CD2	1:B:223:LYS:HE3	2.48	0.49
1:A:251:ARG:HD3	1:A:251:ARG:C	2.38	0.48
1:B:311:VAL:HG22	1:B:377:MET:SD	2.52	0.48
1:B:289:THR:HB	1:B:346:GLU:HG3	1.94	0.48
1:A:250:PHE:O	1:A:253:PHE:HB3	2.12	0.48
1:A:341:ARG:O	1:A:349:GLN:NE2	2.46	0.48
1:B:112:GLN:H	1:B:112:GLN:HE21	1.60	0.48
1:A:30:MET:SD	1:A:30:MET:C	2.97	0.48
1:A:301:HIS:CE1	1:A:368:GLU:HG2	2.49	0.48
1:B:42:LEU:HB2	1:B:53:LEU:HD22	1.96	0.47
1:B:284:PRO:HA	1:B:287:LEU:HG	1.96	0.47
1:A:28:ASN:OD1	1:A:31:ALA:HB2	2.13	0.47
1:B:69:ILE:HD11	5:B:402:IOM:HCB1	1.96	0.47
1:B:192:PHE:CE2	1:B:223:LYS:HE3	2.50	0.47
1:A:227:VAL:CG1	1:A:235:LEU:HD22	2.44	0.47
1:B:79:GLU:OE1	1:B:272:MET:HG2	2.15	0.47
1:B:144:PRO:HG3	1:B:282:THR:HG23	1.97	0.47
1:B:273:TRP:CH2	1:B:275:GLU:OE2	2.68	0.47
1:A:23:LEU:HA	1:A:26:HIS:ND1	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:GLU:O	1:A:86:LYS:HE3	2.15	0.46
1:A:345:SER:O	1:A:345:SER:OG	2.31	0.46
1:A:364:GLU:O	1:A:368:GLU:HG3	2.15	0.46
1:B:42:LEU:HD11	1:B:87:ASP:HB2	1.96	0.46
1:B:274:ASN:ND2	1:B:277:LEU:H	2.12	0.46
1:B:261:GLU:HG2	1:B:271:PHE:CE2	2.49	0.46
1:B:126:VAL:HG13	1:B:295:VAL:HB	1.98	0.46
1:A:359:LEU:CD2	1:A:378:PRO:HG3	2.46	0.46
1:B:199:SER:CA	1:B:326:ASP:OD1	2.60	0.46
1:A:125:TYR:HE1	1:A:365:LYS:HE2	1.79	0.45
1:B:312:LEU:CD1	1:B:319:LYS:HD3	2.45	0.45
1:A:284:PRO:HA	1:A:287:LEU:CD1	2.44	0.45
1:A:291:LEU:HD23	1:A:291:LEU:C	2.41	0.45
1:B:341:ARG:HA	1:B:349:GLN:HE22	1.77	0.45
1:B:29:HIS:HD2	1:B:95:ASP:OD1	1.98	0.45
1:B:350:VAL:O	1:B:354:VAL:HG23	2.16	0.45
1:A:354:VAL:O	1:A:358:LYS:HE2	2.17	0.45
1:B:138:LYS:HE3	1:B:271:PHE:O	2.17	0.45
1:B:321:GLY:HA3	1:B:327:THR:O	2.18	0.44
1:A:125:TYR:CZ	1:A:365:LYS:HE2	2.52	0.44
1:B:226:LEU:CD1	1:B:240:MET:HE3	2.44	0.44
1:A:191:HIS:HB3	3:A:400:ADP:HI'	1.98	0.44
1:B:299:ILE:O	1:B:299:ILE:HG13	2.18	0.44
1:A:276:HIS:HE1	6:A:466:HOH:O	2.00	0.44
1:A:230:ASN:ND2	6:A:419:HOH:O	2.50	0.44
1:A:318:GLN:HG2	1:A:337:SER:O	2.18	0.44
1:B:381:LYS:HB2	1:B:381:LYS:NZ	2.32	0.44
1:A:66:HIS:HB2	1:A:69:ILE:HD13	1.98	0.44
1:A:153:LEU:HD21	1:A:269:ARG:CZ	2.48	0.44
1:B:121:LEU:HB3	1:B:126:VAL:HG21	2.00	0.44
1:B:241:GLN:OE1	1:B:252:ARG:NH2	2.39	0.44
1:A:145:HIS:HE1	6:A:405:HOH:O	2.00	0.43
1:B:132:ARG:HG3	6:B:460:HOH:O	2.18	0.43
1:B:299:ILE:HG13	1:B:303:CYS:HB3	1.99	0.43
1:B:121:LEU:O	1:B:123:PRO:CD	2.67	0.43
1:A:69:ILE:HD13	1:A:69:ILE:N	2.12	0.43
1:A:12:LEU:C	1:A:14:TYR:H	2.26	0.43
1:B:80:GLU:CD	1:B:80:GLU:N	2.74	0.43
1:A:72:VAL:HG11	1:A:284:PRO:HG2	1.99	0.43
1:A:171:GLY:C	1:A:172:LYS:HG3	2.44	0.43
1:B:11:LYS:NZ	1:B:54:ASP:OD2	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:376:LEU:O	1:B:378:PRO:HD3	2.18	0.43
1:A:220:ASN:HD22	1:A:220:ASN:C	2.26	0.43
1:A:122:ASP:OD1	1:A:124:ASN:HB2	2.19	0.42
1:B:289:THR:C	1:B:291:LEU:N	2.76	0.42
1:A:298:LYS:HG2	1:A:333:ILE:CG1	2.39	0.42
1:B:175:PRO:HG2	1:B:178:SER:CB	2.50	0.42
1:B:281:LEU:HD12	1:B:286:ASN:O	2.19	0.42
1:A:324:GLY:N	1:A:327:THR:O	2.52	0.42
1:A:102:PRO:HA	1:A:276:HIS:CE1	2.55	0.42
1:B:238:ILE:HG22	1:B:239:SER:N	2.34	0.42
1:B:106:HIS:HE1	1:B:289:THR:HG23	1.85	0.42
1:B:272:MET:HB3	1:B:280:VAL:HB	2.01	0.42
1:B:246:MET:HE1	1:B:294:GLY:O	2.20	0.41
1:B:238:ILE:HG22	1:B:240:MET:HE2	1.95	0.41
1:A:296:HIS:ND1	1:A:325:VAL:HG13	2.35	0.41
1:B:53:LEU:HD11	1:B:88:LEU:HD22	2.02	0.41
1:A:286:ASN:HD22	1:A:341:ARG:HE	1.69	0.41
1:A:69:ILE:CD1	1:A:69:ILE:N	2.76	0.41
1:B:120:ASP:O	1:B:121:LEU:C	2.62	0.41
1:A:42:LEU:HB2	1:A:53:LEU:HD22	2.03	0.41
1:A:285:SER:O	1:A:341:ARG:HG3	2.21	0.41
1:A:299:ILE:HB	1:A:302:LEU:HB3	2.03	0.41
1:A:51:PHE:CZ	1:A:55:ASP:HB3	2.56	0.41
1:A:62:ASP:O	1:A:64:PRO:HD3	2.20	0.41
1:A:208:ALA:O	1:A:211:TRP:HB2	2.21	0.40
1:A:176:LEU:HA	1:A:179:MET:HE2	2.02	0.40
1:A:281:LEU:HD12	1:A:286:ASN:O	2.21	0.40
1:B:110:LEU:HD23	1:B:110:LEU:HA	1.83	0.40
1:B:263:ILE:HD13	1:B:263:ILE:HG21	1.89	0.40
1:B:276:HIS:NE2	6:B:446:HOH:O	2.37	0.40
1:B:293:GLY:O	1:B:353:VAL:HG21	2.22	0.40
1:B:291:LEU:HD23	1:B:291:LEU:C	2.46	0.40
1:B:132:ARG:HB2	1:B:238:ILE:HG12	2.04	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	368/381 (97%)	356 (97%)	12 (3%)	0	100	100
1	B	372/381 (98%)	357 (96%)	14 (4%)	1 (0%)	36	36
All	All	740/762 (97%)	713 (96%)	26 (4%)	1 (0%)	48	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	270	GLY

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	320/330 (97%)	311 (97%)	9 (3%)	38	43
1	B	324/330 (98%)	311 (96%)	13 (4%)	28	29
All	All	644/660 (98%)	622 (97%)	22 (3%)	32	35

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	PRO
1	A	69	ILE
1	A	112	GLN
1	A	132	ARG
1	A	220	ASN

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Mol	Chain	Res	Type
1	A	241	GLN
1	A	286	ASN
1	A	299	ILE
1	A	342	LEU
1	B	48	PRO
1	B	80	GLU
1	B	87	ASP
1	B	112	GLN
1	B	120	ASP
1	B	132	ARG
1	B	143	PRO
1	B	185	GLN
1	B	187	LEU
1	B	226	LEU
1	B	274	ASN
1	B	306	GLU
1	B	381	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	HIS
1	A	97	HIS
1	A	112	GLN
1	A	114	ASN
1	A	145	HIS
1	A	191	HIS
1	A	220	ASN
1	A	230	ASN
1	A	241	GLN
1	A	276	HIS
1	A	286	ASN
1	A	318	GLN
1	B	8	ASN
1	B	29	HIS
1	B	112	GLN
1	B	114	ASN
1	B	184	GLN
1	B	185	GLN
1	B	191	HIS
1	B	274	ASN
1	B	349	GLN

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Mol	Chain	Res	Type
1	B	369	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 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	NO3	B	405	2	1,3,3	2.84	1 (100%)	0,3,3	-	-
3	ADP	A	400	2	28,29,29	3.09	4 (14%)	43,45,45	1.96	10 (23%)
3	ADP	B	401	2	28,29,29	3.12	4 (14%)	43,45,45	1.94	8 (18%)
5	IOM	B	402	-	5,8,8	4.60	1 (20%)	7,10,10	2.66	4 (57%)

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	400	2	-	0/16/32/32	0/3/3/3
3	ADP	B	401	2	-	0/16/32/32	0/3/3/3
5	IOM	B	402	-	-	0/4/8/8	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	400	ADP	PA-O3A	-14.94	1.43	1.59
3	B	401	ADP	PA-O3A	-14.69	1.43	1.59
5	B	402	IOM	CC-NC	10.00	1.57	1.46
3	B	401	ADP	PA-O5'	4.06	1.75	1.59
3	B	401	ADP	C5-N7	-3.26	1.33	1.39
3	A	400	ADP	C5-N7	-3.23	1.33	1.39
3	B	401	ADP	C4-N9	-2.90	1.31	1.37
4	B	405	NO3	O1-N	2.84	1.38	1.24
3	A	400	ADP	PA-O5'	-2.52	1.49	1.59
3	A	400	ADP	C4-N9	-2.37	1.32	1.37

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	400	ADP	C5-C4-N3	-6.05	118.38	126.72
3	B	401	ADP	C5-C4-N3	-5.77	118.77	126.72
3	A	400	ADP	N3-C4-N9	5.23	136.06	127.17
3	B	401	ADP	N3-C4-N9	5.13	135.90	127.17
5	B	402	IOM	CB-NC-CC	4.72	117.32	110.45
3	B	401	ADP	N3-C2-N1	-3.84	122.77	128.58
3	A	400	ADP	N3-C2-N1	-3.80	122.83	128.58
3	A	400	ADP	C6-C5-C4	3.78	122.34	117.18
3	B	401	ADP	C6-C5-C4	3.71	122.24	117.18
3	B	401	ADP	O2A-PA-O5'	3.67	124.18	107.57
5	B	402	IOM	CD-CC-NC	3.38	121.09	112.48
3	A	400	ADP	C2-N3-C4	3.15	119.53	111.83
3	B	401	ADP	C6-C5-N7	-3.10	126.11	132.09
3	A	400	ADP	C6-C5-N7	-3.02	126.28	132.09
3	B	401	ADP	C2-N3-C4	2.95	119.03	111.83
5	B	402	IOM	CC-NC-CA	2.76	120.76	114.41
5	B	402	IOM	CB-NC-CA	2.55	121.91	115.07
3	A	400	ADP	O5'-PA-O1A	2.53	118.98	108.94
3	A	400	ADP	O3A-PA-O1A	-2.37	103.59	110.70
3	A	400	ADP	O2B-PB-O3A	2.37	112.57	104.64
3	B	401	ADP	C4-N9-C8	2.19	108.04	105.74
3	A	400	ADP	C4-N9-C8	2.02	107.86	105.74

There are no chirality outliers.

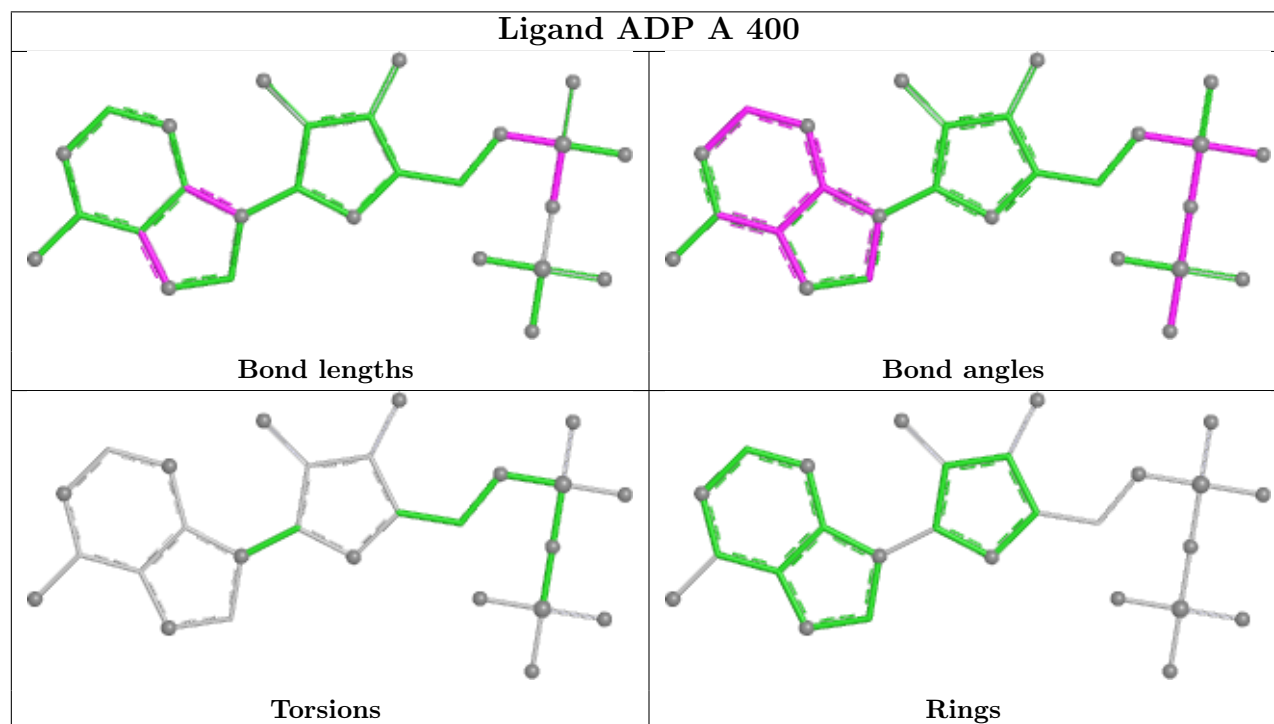
There are no torsion outliers.

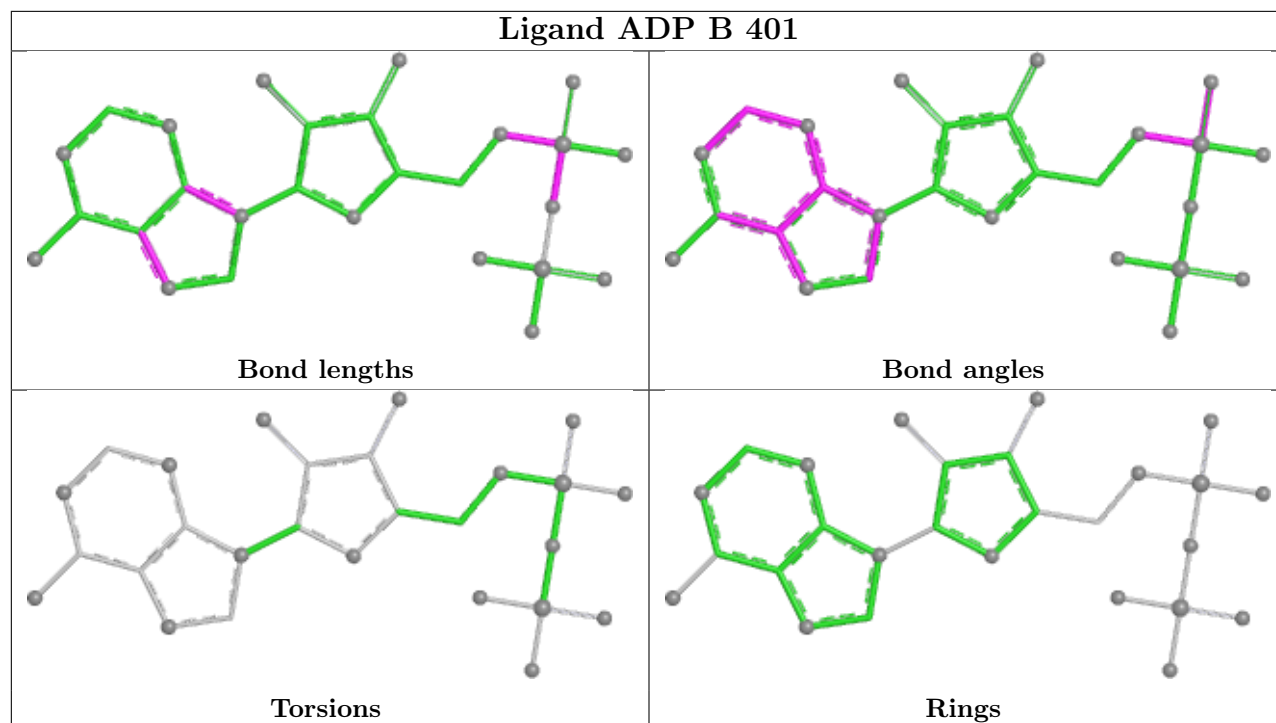
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	400	ADP	1	0
5	B	402	IOM	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 [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	370/381 (97%)	0.88	49 (13%)	7 7	12, 26, 43, 55	0
1	B	374/381 (98%)	0.70	40 (10%)	11 11	11, 27, 48, 81	0
All	All	744/762 (97%)	0.79	89 (11%)	9 9	11, 26, 45, 81	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	323	GLY	10.0
1	A	324	GLY	9.1
1	B	120	ASP	7.0
1	A	326	ASP	6.9
1	A	331	GLY	6.6
1	A	330	VAL	6.6
1	A	69	ILE	5.8
1	A	328	ALA	5.6
1	A	321	GLY	5.5
1	A	329	ALA	5.3
1	A	327	THR	5.0
1	A	325	VAL	4.6
1	A	241	GLN	4.4
1	A	322	THR	4.3
1	A	68	PHE	4.2
1	A	345	SER	4.1
1	A	12	LEU	4.1
1	B	98	GLY	3.9
1	A	125	TYR	3.9
1	A	221	ASN	3.9
1	A	28	ASN	3.8
1	A	245	ASN	3.6
1	B	110	LEU	3.6
1	A	269	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	9	LYS	3.4
1	B	178	SER	3.4
1	A	375	ASP	3.4
1	B	121	LEU	3.4
1	B	313	LYS	3.3
1	A	332	SER	3.3
1	A	167	GLY	3.2
1	A	70	MET	3.2
1	B	267	ALA	3.1
1	B	265	VAL	3.1
1	B	380	GLN	3.0
1	A	290	GLY	3.0
1	A	66	HIS	2.9
1	A	232	GLU	2.9
1	B	100	TYR	2.9
1	A	27	ASN	2.8
1	B	232	GLU	2.7
1	B	166	THR	2.7
1	B	221	ASN	2.7
1	B	119	ASP	2.7
1	A	298	LYS	2.7
1	B	245	ASN	2.6
1	B	116	LYS	2.6
1	A	128	SER	2.6
1	B	332	SER	2.6
1	A	304	LYS	2.5
1	B	381	LYS	2.5
1	B	109	ASP	2.5
1	A	210	ASP	2.5
1	A	67	PRO	2.5
1	B	12	LEU	2.5
1	A	98	GLY	2.5
1	A	309	SER	2.5
1	B	117	GLY	2.4
1	B	263	ILE	2.4
1	A	172	LYS	2.4
1	B	69	ILE	2.4
1	B	177	SER	2.4
1	B	168	GLU	2.3
1	B	27	ASN	2.3
1	A	166	THR	2.3
1	A	289	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	13	ASN	2.3
1	B	212	PRO	2.3
1	B	287	LEU	2.3
1	B	372	SER	2.2
1	B	274	ASN	2.2
1	B	371	LYS	2.2
1	B	111	ASN	2.2
1	A	87	ASP	2.2
1	B	118	GLY	2.2
1	A	333	ILE	2.2
1	A	341	ARG	2.2
1	A	369	ASN	2.2
1	A	95	ASP	2.2
1	A	361	VAL	2.1
1	B	125	TYR	2.1
1	A	120	ASP	2.1
1	B	99	GLY	2.1
1	B	297	VAL	2.1
1	B	273	TRP	2.1
1	A	320	ARG	2.0
1	B	123	PRO	2.0
1	B	309	SER	2.0
1	A	65	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](#)

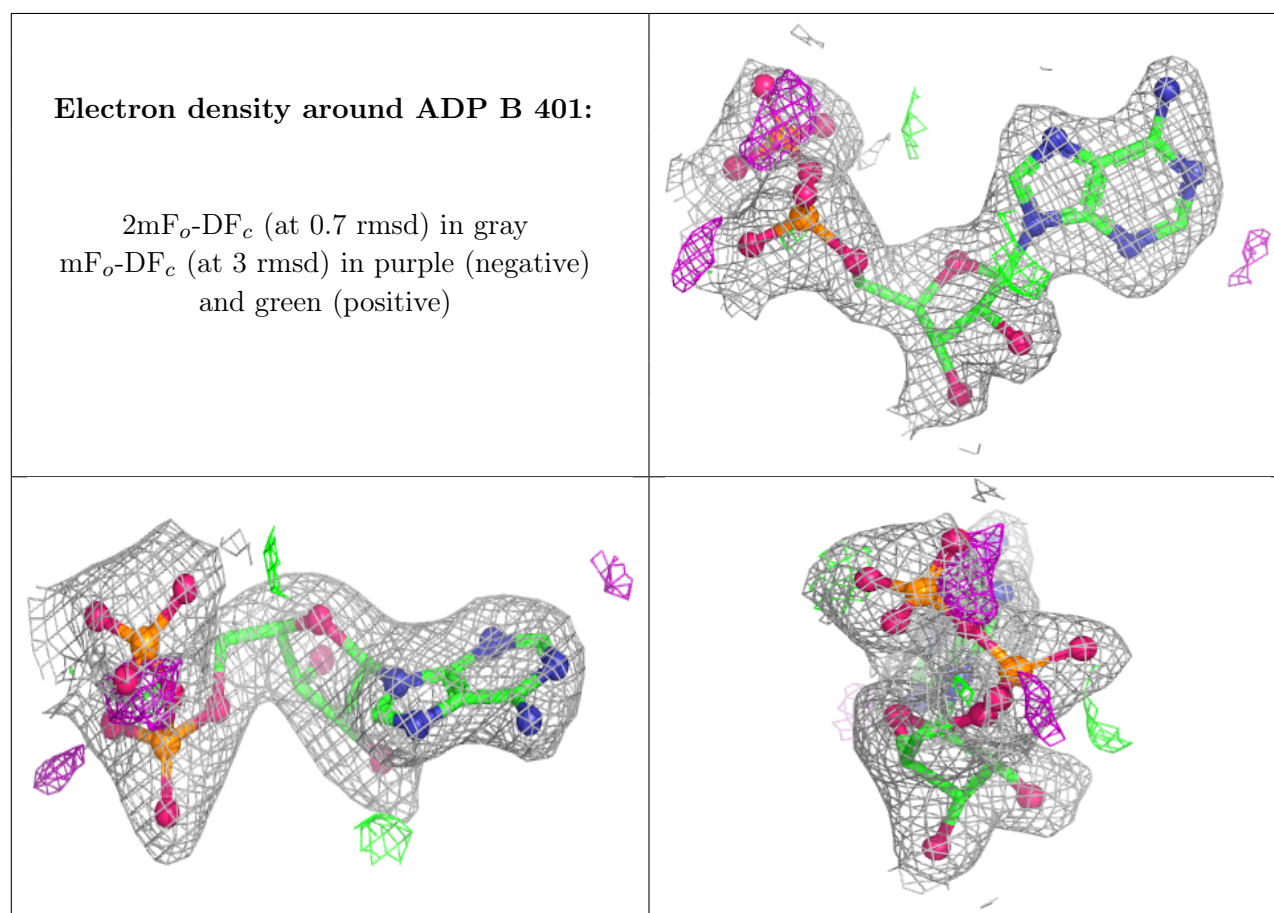
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

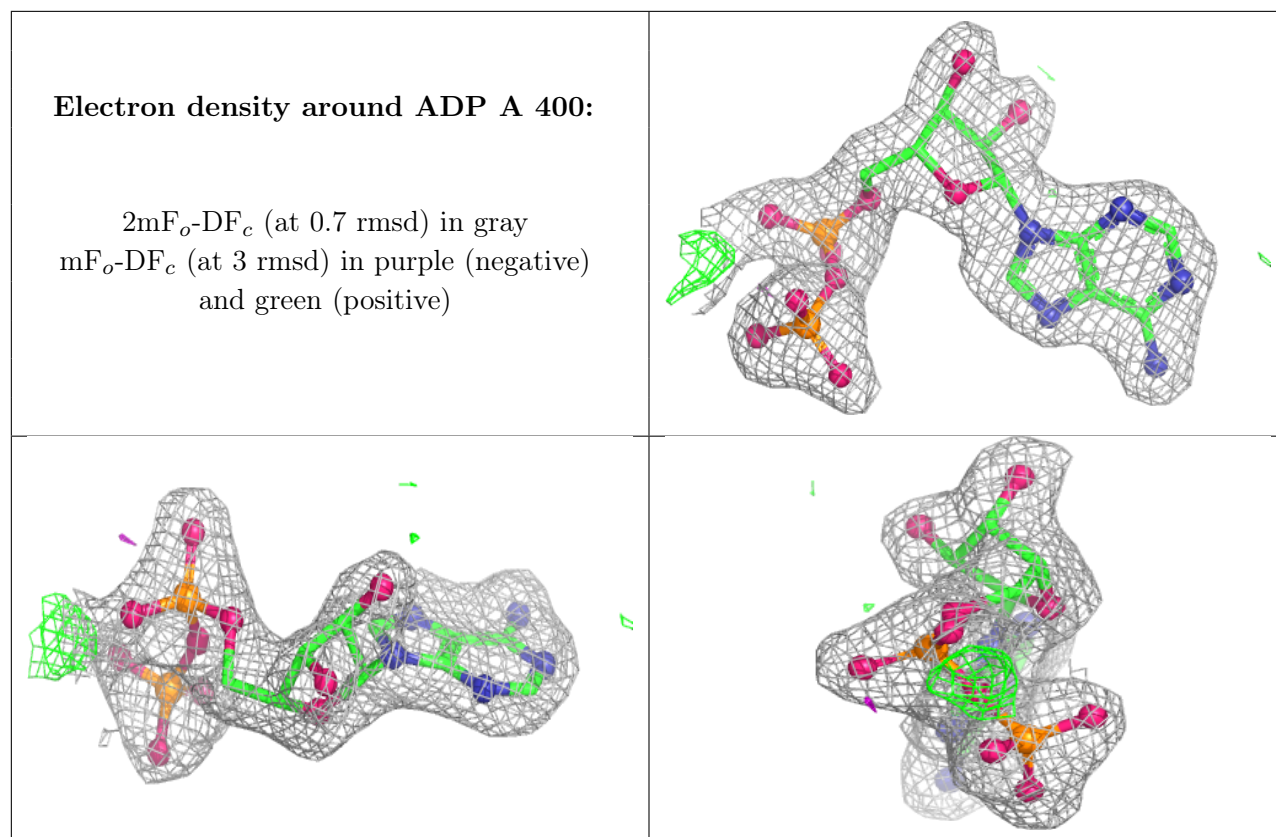
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NO3	B	405	4/4	0.73	0.26	31,33,36,37	0
2	MG	A	404	1/1	0.77	0.15	43,43,43,43	0
3	ADP	B	401	27/27	0.94	0.10	22,27,34,35	0
2	MG	B	403	1/1	0.94	0.09	26,26,26,26	0
5	IOM	B	402	9/9	0.94	0.08	17,20,23,25	0
3	ADP	A	400	27/27	0.96	0.08	22,25,27,28	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.