Full wwPDB X-ray Structure Validation Report (i)

Feb 22, 2024 – 10:44 AM EST

PDB ID	:	4YSJ
Title	:	Calcium-Dependent Protein Kinase from Eimeria tenella in complex with ADP
Authors	:	Merritt, E.A.
Deposited on	:	2015-03-17
Resolution	:	2.70 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 (i) 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 (i)) were used in the production of this report:

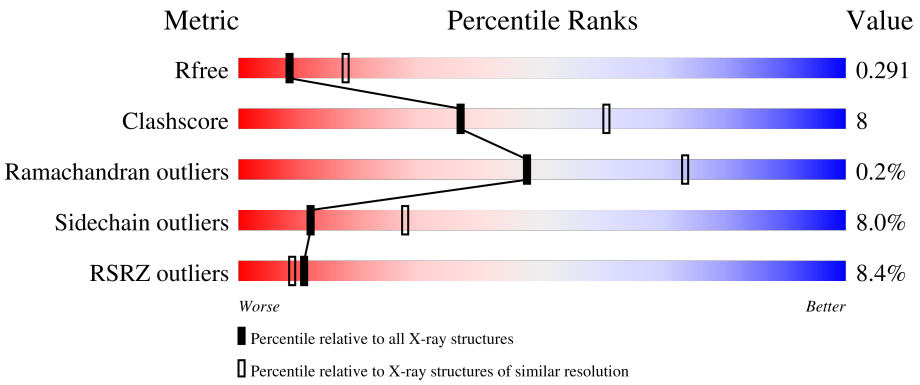
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 <=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	491	7% 73% 19% • 7%
1	B	491	9% 74% 19% • 6%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7409 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 Calmodulin-like domain protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	459	3661	2338	607	700	16	0	0	0
1	B	462	3682	2349	610	707	16	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q3HNM4
A	-2	PRO	-	expression tag	UNP Q3HNM4
A	-1	GLY	-	expression tag	UNP Q3HNM4
A	0	SER	-	expression tag	UNP Q3HNM4
A	392	ASP	ALA	See Remark 999	UNP Q3HNM4
B	-3	GLY	-	expression tag	UNP Q3HNM4
B	-2	PRO	-	expression tag	UNP Q3HNM4
B	-1	GLY	-	expression tag	UNP Q3HNM4
B	0	SER	-	expression tag	UNP Q3HNM4
B	392	ASP	ALA	See Remark 999	UNP Q3HNM4

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
2	A	4	4	4	0	0
2	B	4	4	4	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

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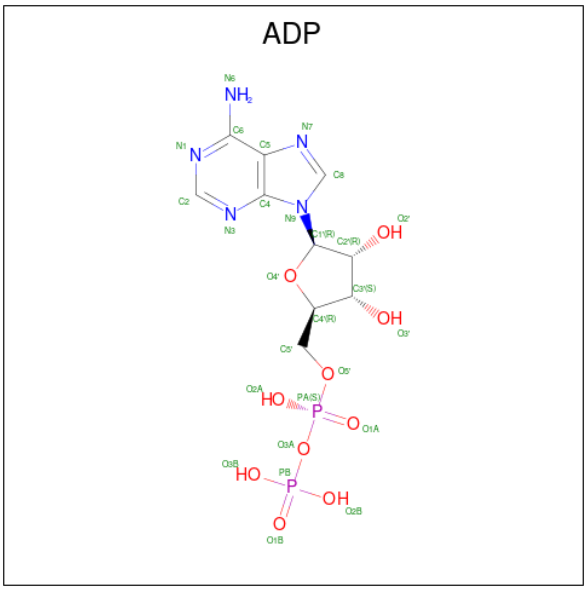
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	B	1	1	1	0	0

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

- Molecule 5 is water.

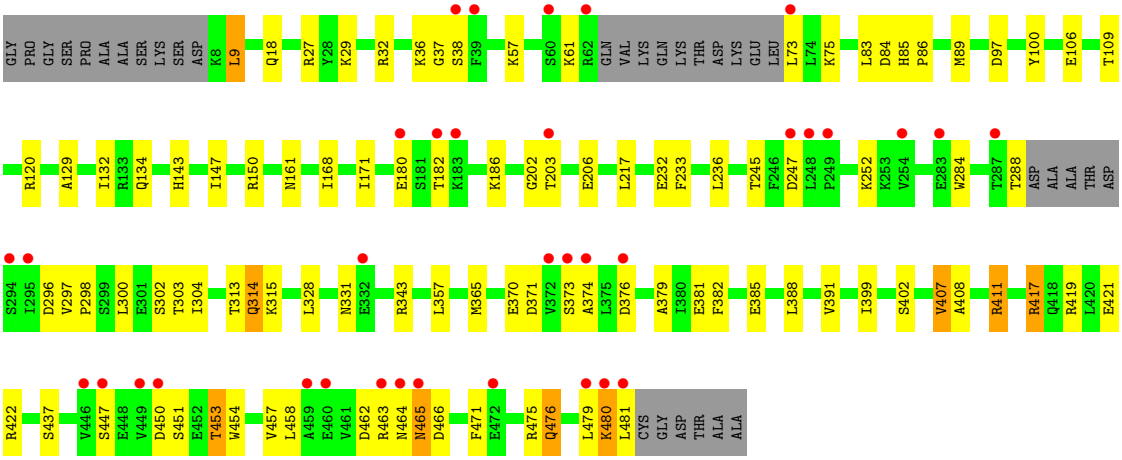
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	1	1	1	0	0
			Total	O		
5	B	1	1	1	0	0

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.

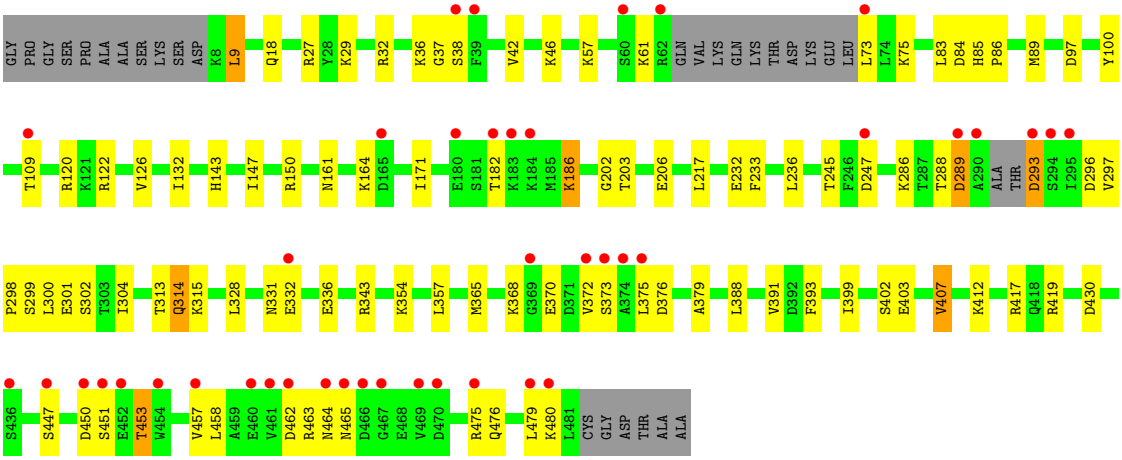
• Molecule 1: Calmodulin-like domain protein kinase

Chain A:



• Molecule 1: Calmodulin-like domain protein kinase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	93.54Å 108.42Å 109.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.57 – 2.70 38.57 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.3 (38.57-2.70) 98.3 (38.57-2.69)	Depositor EDS
R_{merge}	0.36	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.49 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.246 , 0.292 0.250 , 0.291	Depositor DCC
R_{free} test set	1523 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å^2)	49.8	Xtriage
Anisotropy	0.359	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 46.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7409	wwPDB-VP
Average B, all atoms (Å^2)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.79 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6257e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0.61	0/3723	0.77	2/5007 (0.0%)
1	B	0.61	0/3744	0.77	2/5036 (0.0%)
All	All	0.61	0/7467	0.77	4/10043 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	430	ASP	CB-CG-OD1	6.90	124.51	118.30
1	B	150	ARG	NE-CZ-NH2	-5.89	117.36	120.30
1	A	150	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	A	462	ASP	CB-CG-OD2	-5.29	113.54	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3661	0	3657	72	0
1	B	3682	0	3670	45	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
4	A	27	0	12	2	0
4	B	27	0	12	3	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
All	All	7409	0	7351	117	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 (117) 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:476:GLN:HG3	1:A:480:LYS:NZ	1.64	1.12
1:A:476:GLN:HG3	1:A:480:LYS:HZ3	1.15	1.00
1:A:454:TRP:O	1:A:458:LEU:HD12	1.61	0.99
1:A:476:GLN:CG	1:A:480:LYS:NZ	2.26	0.97
1:A:417:ARG:O	1:A:421:GLU:HG3	1.66	0.95
1:A:476:GLN:CG	1:A:480:LYS:HZ1	1.78	0.95
1:A:476:GLN:HG2	1:A:480:LYS:HZ1	1.37	0.88
1:B:296:ASP:OD2	1:B:299:SER:OG	1.97	0.81
1:B:462:ASP:O	1:B:465:ASN:ND2	2.17	0.78
1:A:376:ASP:OD2	1:A:379:ALA:HB2	1.84	0.77
1:A:106:GLU:CD	1:A:331:ASN:HD21	1.90	0.75
1:A:464:ASN:ND2	1:A:466:ASP:OD2	2.19	0.75
1:A:9:LEU:HD12	1:A:315:LYS:HE3	1.75	0.69
1:A:186:LYS:HA	1:A:202:GLY:O	1.91	0.69
1:B:186:LYS:HA	1:B:202:GLY:O	1.91	0.69
1:B:37:GLY:HA3	4:B:506:ADP:O2B	1.93	0.69
1:A:37:GLY:HA3	4:A:506:ADP:O2B	1.96	0.66
1:A:479:LEU:O	1:A:481:LEU:HD12	1.96	0.65
1:A:454:TRP:O	1:A:458:LEU:CD1	2.42	0.65
1:A:464:ASN:O	1:A:465:ASN:HB2	1.97	0.65
1:B:245:THR:OG1	1:B:247:ASP:HB2	1.97	0.64
1:B:372:VAL:O	1:B:375:LEU:HG	1.97	0.63
1:A:475:ARG:HG2	1:A:479:LEU:HD12	1.81	0.63
1:A:357:LEU:HD11	1:A:399:ILE:HD12	1.81	0.63
1:B:475:ARG:HG2	1:B:479:LEU:HD12	1.81	0.63
1:A:245:THR:OG1	1:A:247:ASP:HB2	1.98	0.62
1:A:458:LEU:HD12	1:A:458:LEU:H	1.63	0.62
1:B:42:VAL:HG21	4:B:506:ADP:C8	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:ASN:ND2	1:A:466:ASP:CG	2.54	0.61
1:B:336:GLU:N	1:B:336:GLU:OE1	2.34	0.61
1:A:9:LEU:HD12	1:A:315:LYS:CE	2.30	0.60
1:B:132:ILE:HG13	1:B:217:LEU:HD13	1.82	0.60
1:A:297:VAL:N	1:A:298:PRO:HD2	2.17	0.60
1:B:357:LEU:HD11	1:B:399:ILE:HD12	1.83	0.60
1:A:132:ILE:HG13	1:A:217:LEU:HD13	1.83	0.59
1:A:129:ALA:CB	1:A:288:THR:HG21	2.32	0.59
1:B:293:ASP:OD2	1:B:293:ASP:N	2.35	0.58
1:A:479:LEU:C	1:A:481:LEU:H	2.07	0.57
1:A:411:ARG:HB3	1:A:481:LEU:HD23	1.85	0.57
1:B:61:LYS:NZ	1:B:97:ASP:O	2.30	0.57
1:A:61:LYS:NZ	1:A:97:ASP:O	2.31	0.57
1:A:9:LEU:HD12	1:A:315:LYS:CD	2.35	0.56
1:A:303:THR:HG23	1:A:408:ALA:HB1	1.88	0.56
1:A:463:ARG:O	1:A:465:ASN:ND2	2.39	0.55
1:A:233:PHE:HA	1:A:236:LEU:HD12	1.87	0.55
1:A:9:LEU:HD12	1:A:315:LYS:HD2	1.89	0.54
1:B:233:PHE:HA	1:B:236:LEU:HD12	1.88	0.54
1:B:297:VAL:N	1:B:298:PRO:HD2	2.24	0.53
1:A:471:PHE:CG	1:A:471:PHE:O	2.62	0.53
1:B:9:LEU:HD12	1:B:315:LYS:HE3	1.90	0.53
1:A:106:GLU:CD	1:A:331:ASN:ND2	2.61	0.52
1:A:464:ASN:HD21	1:A:466:ASP:CG	2.11	0.51
1:A:464:ASN:OD1	1:A:465:ASN:N	2.43	0.51
1:A:422:ARG:CG	1:A:422:ARG:HH21	2.24	0.51
1:A:313:THR:OG1	1:A:314:GLN:N	2.44	0.51
1:A:381:GLU:O	1:A:385:GLU:HG3	2.10	0.51
1:A:382:PHE:HA	1:A:385:GLU:HG3	1.93	0.50
1:B:89:MET:HB2	1:B:171:ILE:HG22	1.93	0.50
1:A:85:HIS:CG	1:A:86:PRO:HD2	2.46	0.50
1:A:203:THR:HG23	1:A:203:THR:O	2.11	0.50
1:B:126:VAL:HG21	1:B:289:ASP:OD2	2.11	0.50
1:B:109:THR:OG1	1:B:161:ASN:HA	2.12	0.50
1:B:313:THR:OG1	1:B:314:GLN:N	2.45	0.50
1:A:89:MET:HB2	1:A:171:ILE:HG22	1.94	0.49
1:A:84:ASP:OD2	1:A:402:SER:HB2	2.13	0.49
1:A:284:TRP:O	1:A:288:THR:HG22	2.13	0.49
1:A:471:PHE:O	1:A:471:PHE:CD1	2.65	0.49
1:A:97:ASP:HB3	1:A:100:TYR:H	1.78	0.48
1:B:57:LYS:NZ	4:B:506:ADP:O2A	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:THR:OG1	1:A:161:ASN:HA	2.14	0.48
1:A:479:LEU:HD23	1:A:479:LEU:HA	1.79	0.47
1:B:84:ASP:OD2	1:B:402:SER:HB2	2.15	0.47
1:B:97:ASP:HB3	1:B:100:TYR:H	1.80	0.47
1:A:391:VAL:HG13	1:A:407:VAL:HG21	1.95	0.47
1:A:57:LYS:NZ	4:A:506:ADP:O2A	2.43	0.46
1:B:354:LYS:HE3	1:B:354:LYS:HB2	1.86	0.46
1:B:314:GLN:HG3	1:B:457:VAL:HA	1.96	0.46
1:B:479:LEU:HD23	1:B:479:LEU:HA	1.83	0.46
1:A:300:LEU:O	1:A:304:ILE:HG12	2.15	0.46
1:A:453:THR:O	1:A:457:VAL:HG23	2.16	0.46
1:B:375:LEU:HD23	1:B:375:LEU:N	2.30	0.46
1:B:453:THR:O	1:B:457:VAL:HG23	2.16	0.45
1:A:297:VAL:N	1:A:298:PRO:CD	2.79	0.45
1:B:85:HIS:CG	1:B:86:PRO:HD2	2.51	0.45
1:B:143:HIS:ND1	1:B:206:GLU:HG3	2.32	0.45
1:B:232:GLU:HG2	1:B:236:LEU:HD11	1.99	0.45
1:A:143:HIS:ND1	1:A:206:GLU:HG3	2.32	0.45
1:B:300:LEU:O	1:B:304:ILE:HG12	2.16	0.45
1:B:328:LEU:HB3	1:B:419:ARG:HD2	1.99	0.45
1:A:232:GLU:HG2	1:A:236:LEU:HD11	1.99	0.44
1:B:391:VAL:HG13	1:B:407:VAL:HG21	1.98	0.44
1:A:314:GLN:HG3	1:A:457:VAL:HA	1.98	0.44
1:B:296:ASP:OD2	1:B:299:SER:CB	2.66	0.44
1:B:83:LEU:HD21	1:B:147:ILE:HD12	1.99	0.44
1:A:417:ARG:O	1:A:421:GLU:CG	2.51	0.43
1:A:9:LEU:H	1:A:9:LEU:HG	1.61	0.43
1:A:463:ARG:O	1:A:464:ASN:C	2.57	0.43
1:A:106:GLU:OE2	1:A:331:ASN:ND2	2.51	0.43
1:B:9:LEU:H	1:B:9:LEU:HG	1.58	0.43
1:A:9:LEU:CD1	1:A:315:LYS:HE3	2.47	0.42
1:A:381:GLU:O	1:A:385:GLU:CG	2.67	0.42
1:A:328:LEU:HB3	1:A:419:ARG:HD2	2.02	0.42
1:B:73:LEU:C	1:B:75:LYS:N	2.72	0.42
1:A:83:LEU:HD21	1:A:147:ILE:HD12	2.01	0.42
1:A:134:GLN:OE1	1:A:168:ILE:HB	2.20	0.41
1:A:437:SER:HB3	1:A:454:TRP:CE2	2.55	0.41
1:B:296:ASP:O	1:B:299:SER:OG	2.37	0.41
1:B:301:GLU:CD	1:B:368:LYS:HE2	2.40	0.41
1:A:371:ASP:HB3	1:A:374:ALA:HB3	2.03	0.41
1:B:376:ASP:HB3	1:B:379:ALA:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:LEU:C	1:A:75:LYS:N	2.73	0.41
1:A:479:LEU:C	1:A:481:LEU:N	2.74	0.40
1:B:464:ASN:OD1	1:B:465:ASN:N	2.53	0.40
1:A:376:ASP:HB3	1:A:379:ALA:HB3	2.03	0.40
1:B:463:ARG:C	1:B:465:ASN:HD22	2.24	0.40
1:B:464:ASN:O	1:B:465:ASN:HB2	2.20	0.40
1:B:393:PHE:HD1	1:B:403:GLU:HG2	1.87	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	453/491 (92%)	430 (95%)	21 (5%)	2 (0%)	34 60
1	B	456/491 (93%)	434 (95%)	22 (5%)	0	100 100
All	All	909/982 (93%)	864 (95%)	43 (5%)	2 (0%)	47 73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	465	ASN
1	A	480	LYS

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	397/426 (93%)	370 (93%)	27 (7%)	16 36
1	B	399/426 (94%)	362 (91%)	37 (9%)	9 21
All	All	796/852 (93%)	732 (92%)	64 (8%)	12 27

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	18	GLN
1	A	27	ARG
1	A	29	LYS
1	A	32	ARG
1	A	36	LYS
1	A	38	SER
1	A	120	ARG
1	A	180	GLU
1	A	182	THR
1	A	252	LYS
1	A	296	ASP
1	A	302	SER
1	A	314	GLN
1	A	343	ARG
1	A	365	MET
1	A	370	GLU
1	A	373	SER
1	A	388	LEU
1	A	407	VAL
1	A	411	ARG
1	A	417	ARG
1	A	447	SER
1	A	450	ASP
1	A	451	SER
1	A	453	THR
1	A	476	GLN
1	B	9	LEU
1	B	18	GLN
1	B	27	ARG
1	B	29	LYS
1	B	32	ARG
1	B	36	LYS
1	B	38	SER
1	B	46	LYS

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Mol	Chain	Res	Type
1	B	120	ARG
1	B	122	ARG
1	B	164	LYS
1	B	182	THR
1	B	186	LYS
1	B	203	THR
1	B	286	LYS
1	B	288	THR
1	B	289	ASP
1	B	293	ASP
1	B	302	SER
1	B	314	GLN
1	B	331	ASN
1	B	332	GLU
1	B	343	ARG
1	B	365	MET
1	B	370	GLU
1	B	373	SER
1	B	388	LEU
1	B	407	VAL
1	B	412	LYS
1	B	417	ARG
1	B	447	SER
1	B	450	ASP
1	B	451	SER
1	B	453	THR
1	B	458	LEU
1	B	476	GLN
1	B	480	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	314	GLN
1	A	331	ASN
1	B	18	GLN
1	B	314	GLN
1	B	377	GLN
1	B	465	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 10 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	$\#\|Z\| > 2$
4	ADP	B	506	3	24,29,29	1.21	2 (8%)	29,45,45	1.72	9 (31%)
4	ADP	A	506	3	24,29,29	1.23	2 (8%)	29,45,45	1.49	7 (24%)

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	B	506	3	-	2/12/32/32	0/3/3/3
4	ADP	A	506	3	-	2/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	506	ADP	C2'-C1'	-3.59	1.48	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	506	ADP	C2'-C1'	-3.56	1.48	1.53
4	B	506	ADP	C5-C4	2.20	1.46	1.40
4	A	506	ADP	C5-C4	2.07	1.46	1.40

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	506	ADP	N3-C2-N1	-4.17	122.17	128.68
4	A	506	ADP	N3-C2-N1	-3.90	122.58	128.68
4	B	506	ADP	O2A-PA-O1A	3.88	131.43	112.24
4	A	506	ADP	O3B-PB-O1B	2.61	120.89	110.68
4	A	506	ADP	C2-N1-C6	2.59	123.18	118.75
4	B	506	ADP	C1'-N9-C4	-2.38	122.46	126.64
4	B	506	ADP	C2-N1-C6	2.35	122.78	118.75
4	A	506	ADP	O2B-PB-O1B	2.34	119.84	110.68
4	A	506	ADP	O2A-PA-O1A	2.31	123.68	112.24
4	B	506	ADP	C3'-C2'-C1'	2.27	104.39	100.98
4	A	506	ADP	C1'-N9-C4	-2.19	122.78	126.64
4	B	506	ADP	PA-O3A-PB	-2.18	125.33	132.83
4	B	506	ADP	N6-C6-N1	2.18	123.10	118.57
4	A	506	ADP	N6-C6-N1	2.13	123.00	118.57
4	B	506	ADP	O4'-C1'-C2'	-2.12	103.83	106.93
4	B	506	ADP	O2B-PB-O1B	2.03	118.65	110.68

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	506	ADP	PA-O3A-PB-O2B
4	A	506	ADP	PB-O3A-PA-O1A
4	B	506	ADP	PB-O3A-PA-O1A
4	A	506	ADP	PB-O3A-PA-O2A

There are no ring outliers.

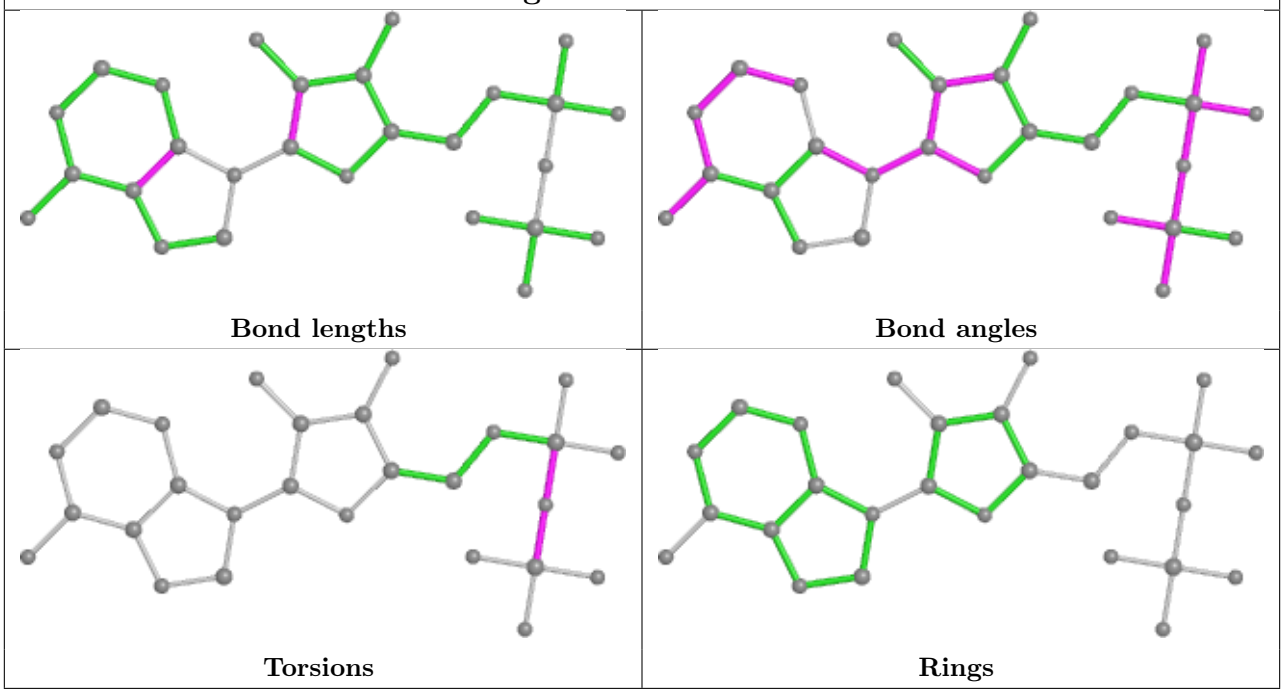
2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	506	ADP	3	0
4	A	506	ADP	2	0

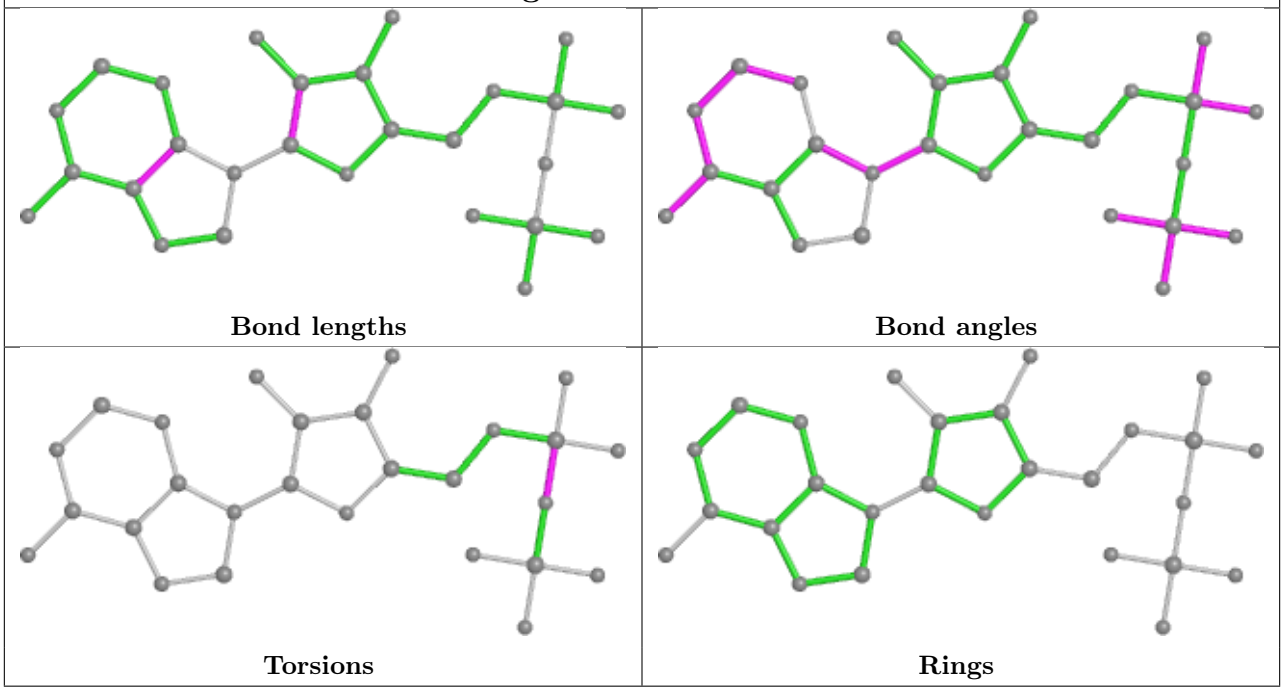
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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

Ligand ADP B 506



Ligand ADP A 506



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	459/491 (93%)	0.57	35 (7%) 13 12	55, 75, 114, 133	0
1	B	462/491 (94%)	0.66	42 (9%) 9 7	51, 76, 115, 137	0
All	All	921/982 (93%)	0.61	77 (8%) 11 9	51, 76, 115, 137	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	461	VAL	5.9
1	B	460	GLU	5.5
1	A	450	ASP	5.4
1	A	73	LEU	5.4
1	B	73	LEU	5.2
1	B	479	LEU	5.0
1	B	369	GLY	5.0
1	B	293	ASP	4.7
1	A	182	THR	4.4
1	B	182	THR	4.3
1	B	467	GLY	3.8
1	B	60	SER	3.8
1	A	463	ARG	3.7
1	B	294	SER	3.7
1	B	39	PHE	3.6
1	B	374	ALA	3.6
1	A	62	ARG	3.4
1	A	481	LEU	3.4
1	A	39	PHE	3.3
1	A	283	GLU	3.3
1	A	248	LEU	3.3
1	A	247	ASP	3.3
1	A	464	ASN	3.3
1	B	290	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	465	ASN	3.2
1	A	60	SER	3.1
1	B	447	SER	3.0
1	A	480	LYS	3.0
1	A	295	ILE	2.9
1	B	295	ILE	2.9
1	B	465	ASN	2.9
1	A	479	LEU	2.8
1	B	450	ASP	2.8
1	A	203	THR	2.8
1	B	184	LYS	2.7
1	B	457	VAL	2.7
1	B	109	THR	2.7
1	B	332	GLU	2.7
1	A	254	VAL	2.7
1	B	480	LYS	2.6
1	B	462	ASP	2.6
1	A	447	SER	2.6
1	B	180	GLU	2.6
1	A	287	THR	2.5
1	B	372	VAL	2.5
1	B	464	ASN	2.5
1	A	374	ALA	2.5
1	A	459	ALA	2.5
1	B	451	SER	2.5
1	B	470	ASP	2.5
1	B	247	ASP	2.5
1	B	289	ASP	2.5
1	A	294	SER	2.5
1	A	372	VAL	2.4
1	A	180	GLU	2.4
1	A	376	ASP	2.4
1	B	38	SER	2.3
1	A	446	VAL	2.3
1	B	454	TRP	2.3
1	A	460	GLU	2.2
1	B	183	LYS	2.2
1	B	373	SER	2.2
1	B	375	LEU	2.2
1	A	249	PRO	2.2
1	A	373	SER	2.2
1	A	38	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	436	SER	2.2
1	B	62	ARG	2.1
1	B	475	ARG	2.1
1	A	183	LYS	2.1
1	A	332	GLU	2.1
1	B	469	VAL	2.1
1	B	466	ASP	2.1
1	B	452	GLU	2.1
1	A	449	VAL	2.1
1	B	165	ASP	2.1
1	A	472	GLU	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)

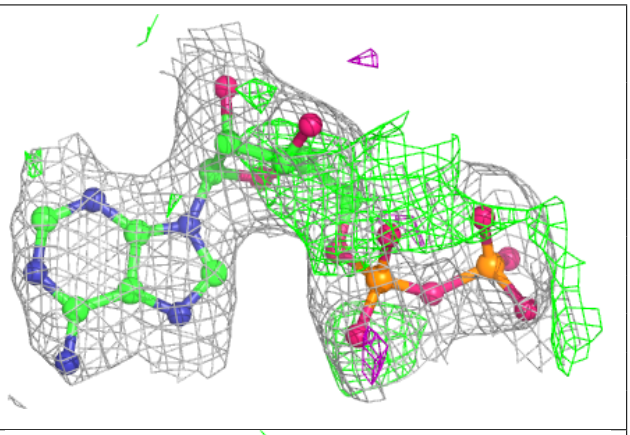
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

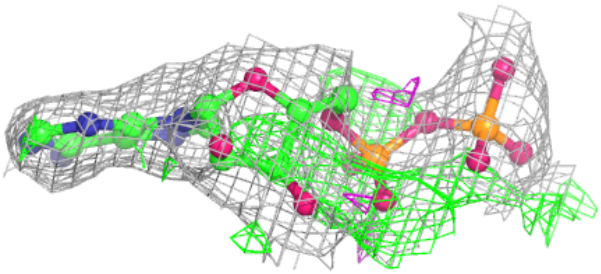
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CA	B	503	1/1	0.62	0.10	101,101,101,101	0
3	MG	A	505	1/1	0.62	0.30	42,42,42,42	1
3	MG	B	505	1/1	0.80	0.31	40,40,40,40	1
2	CA	A	501	1/1	0.87	0.11	67,67,67,67	0
4	ADP	B	506	27/27	0.92	0.26	28,40,46,51	27
4	ADP	A	506	27/27	0.93	0.30	31,43,47,49	27
2	CA	A	503	1/1	0.94	0.06	91,91,91,91	0
2	CA	B	501	1/1	0.95	0.12	74,74,74,74	0
2	CA	A	502	1/1	0.95	0.05	63,63,63,63	0
2	CA	A	504	1/1	0.95	0.08	106,106,106,106	0
2	CA	B	502	1/1	0.97	0.10	70,70,70,70	0
2	CA	B	504	1/1	0.97	0.06	108,108,108,108	0

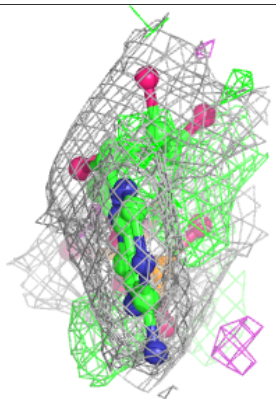
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADP B 506:

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

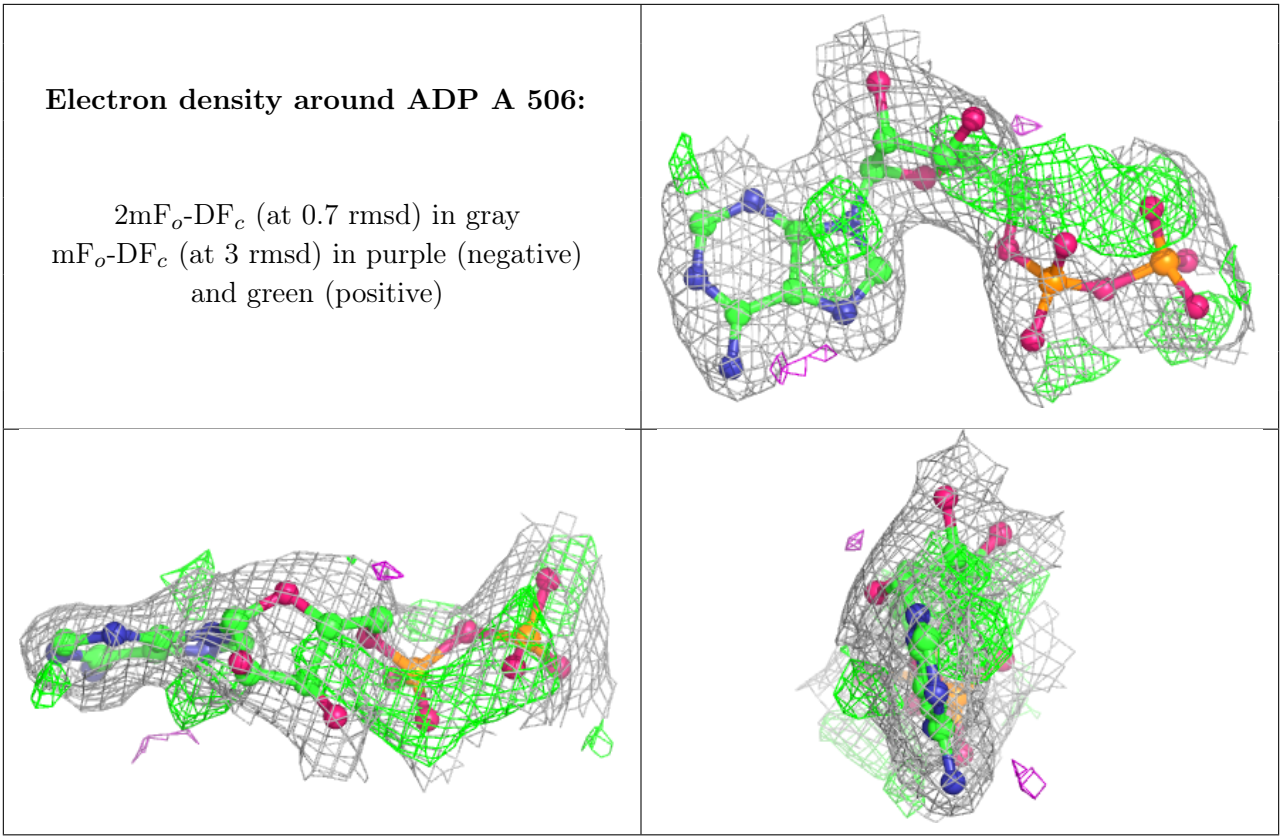






Electron density around ADP A 506:

$2mF_o$-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.