Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:29 pm BST

PDB ID	:	2Y8Q
Title	:	Structure of the regulatory fragment of mammalian AMPK in complex with one ADP
Authors	:	Xiao, B.; Sanders, M.J.; Underwood, E.; Heath, R.; Mayer, F.; Carmena, D.; Jing, C.; Walker, P.A.; Eccleston, J.F.; Haire, L.F.; Saiu, P.; Howell, S.A.; Aasland, R.; Martin, S.R.; Carling, D.; Gamblin, S.J.
Deposited on	:	2011-02-09
Resolution	:	2.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

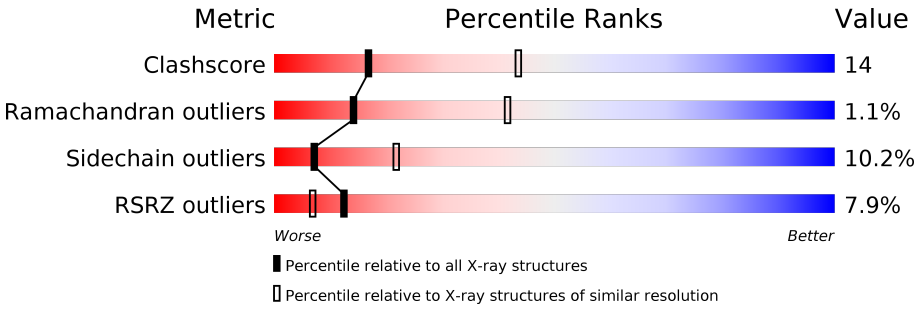
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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

Mol	Chain	Length	Quality of chain
1	A	173	2%, 44%, 13%, ·, 40%
2	B	87	11%, 64%, 14%, ··, 18%
3	E	330	7%, 66%, 21%, ··, 8%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3987 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 5'-AMP-ACTIVATED PROTEIN KINASE CATALYTIC SUBUNIT ALPHA-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	104	854	539	152	156	7	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	378	MET	-	expression tag	UNP P54645
A	379	SER	-	expression tag	UNP P54645
A	380	HIS	-	expression tag	UNP P54645
A	381	HIS	-	expression tag	UNP P54645
A	382	HIS	-	expression tag	UNP P54645
A	383	HIS	-	expression tag	UNP P54645
A	384	HIS	-	expression tag	UNP P54645
A	385	HIS	-	expression tag	UNP P54645
A	386	SER	-	expression tag	UNP P54645
A	387	GLY	-	expression tag	UNP P54645
A	388	LEU	-	expression tag	UNP P54645
A	389	VAL	-	expression tag	UNP P54645
A	390	PRO	-	expression tag	UNP P54645
A	391	ARG	-	expression tag	UNP P54645
A	392	GLY	-	expression tag	UNP P54645
A	393	SER	-	expression tag	UNP P54645
A	394	MET	-	expression tag	UNP P54645
A	395	ALA	-	expression tag	UNP P54645
A	545	ASN	-	expression tag	UNP P54645
A	546	SER	-	expression tag	UNP P54645
A	547	CYS	-	expression tag	UNP P54645
A	548	THR	-	expression tag	UNP P54645
A	549	VAL	-	expression tag	UNP P54645
A	550	ASN	-	expression tag	UNP P54645

- Molecule 2 is a protein called 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT BETA-

2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	71	Total	C	N	O	S	0	0	0
			586	384	100	99	3			

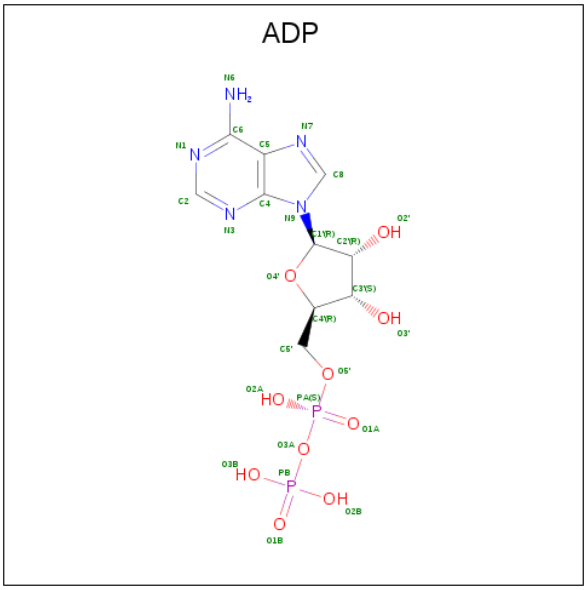
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	186	MET	-	expression tag	UNP O43741

- Molecule 3 is a protein called 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT GAMMA-1.

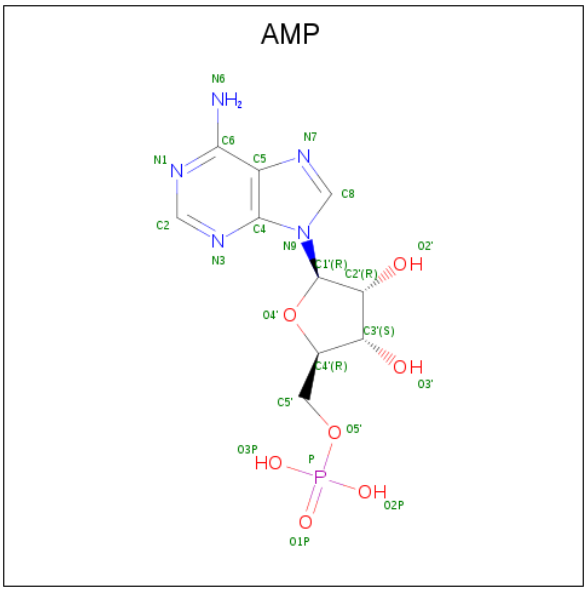
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	304	Total	C	N	O	S	0	0	0
			2441	1584	407	443	7			

- 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
4	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 5 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	E	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 6 is water.

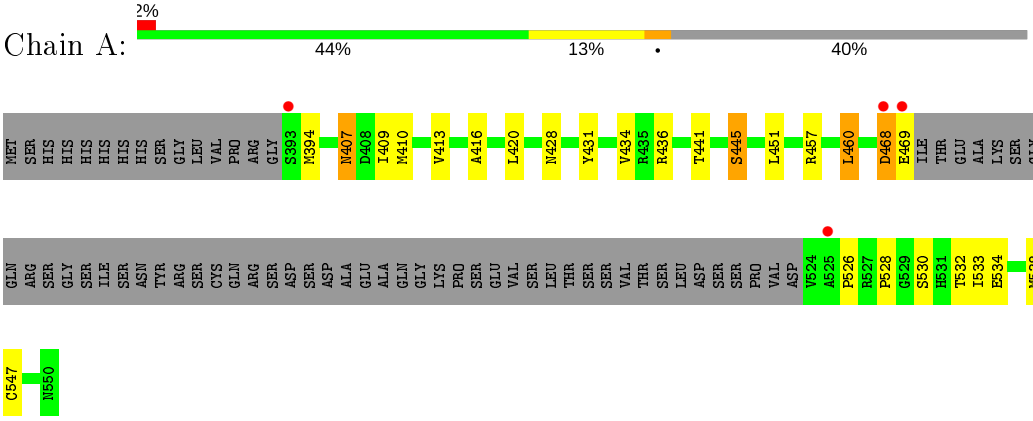
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	6	Total	O	0	0
			6	6		
6	B	11	Total	O	0	0
			11	11		
6	E	39	Total	O	0	0
			39	39		

3 Residue-property plots (i)

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

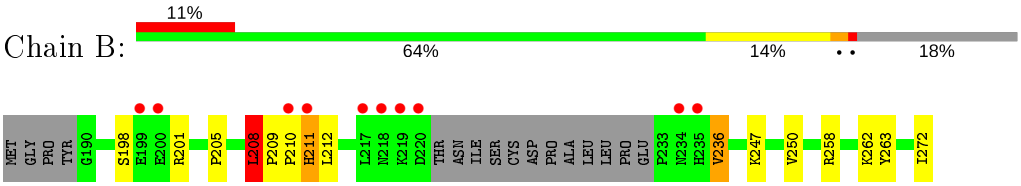
• Molecule 1: 5'-AMP-ACTIVATED PROTEIN KINASE CATALYTIC SUBUNIT ALPHA-1

Chain A:



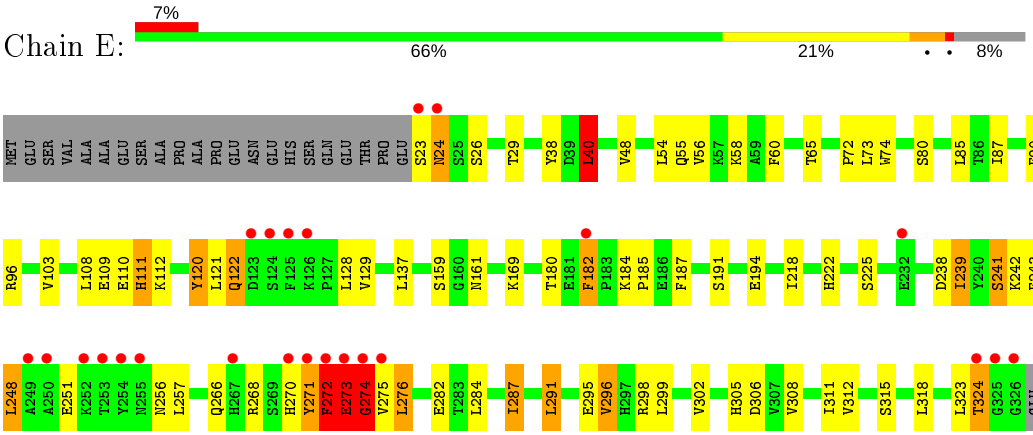
• Molecule 2: 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT BETA-2

Chain B:



• Molecule 3: 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT GAMMA-1

Chain E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	49.03Å 119.92Å 130.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 19.93 – 2.80	Depositor EDS
% Data completeness (in resolution range)	93.8 (20.00-2.80) 93.9 (19.93-2.80)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.02 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.5	Depositor
R, R_{free}	0.232 , 0.275 0.229 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	66.7	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 36.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3987	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AMP, 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	0.46	0/872	0.63	1/1178 (0.1%)
2	B	0.46	0/601	0.75	0/811
3	E	0.62	3/2493 (0.1%)	0.84	10/3384 (0.3%)
All	All	0.57	3/3966 (0.1%)	0.78	11/5373 (0.2%)

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	1
2	B	0	1
3	E	0	4
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	273	GLU	C-N	16.53	1.62	1.33
3	E	274	GLY	N-CA	8.19	1.58	1.46
3	E	274	GLY	CA-C	7.27	1.63	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	274	GLY	O-C-N	17.53	150.74	122.70
3	E	273	GLU	C-N-CA	-12.14	96.80	122.30
3	E	272	PHE	C-N-CA	-10.90	94.45	121.70
3	E	272	PHE	CA-C-N	-10.78	93.48	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	274	GLY	CA-C-N	-8.89	97.65	117.20
3	E	274	GLY	CA-C-O	-8.47	105.36	120.60
3	E	272	PHE	O-C-N	8.36	136.08	122.70
1	A	460	LEU	CA-CB-CG	7.68	132.97	115.30
3	E	274	GLY	N-CA-C	-6.17	97.68	113.10
3	E	276	LEU	CA-CB-CG	-6.00	101.51	115.30
3	E	40	LEU	CA-CB-CG	5.06	126.95	115.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	546	SER	Peptide
2	B	208	LEU	Peptide
3	E	182	PHE	Peptide
3	E	272	PHE	Mainchain
3	E	273	GLU	Mainchain
3	E	274	GLY	Mainchain

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	854	0	845	17	0
2	B	586	0	612	13	0
3	E	2441	0	2506	89	0
4	E	27	0	12	0	0
5	E	23	0	12	0	0
6	A	6	0	0	0	0
6	B	11	0	0	0	0
6	E	39	0	0	15	0
All	All	3987	0	3987	112	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 14.

All (112) 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)
3:E:271:TYR:O	3:E:272:PHE:HB3	1.46	1.07
3:E:271:TYR:HE2	3:E:273:GLU:HB2	1.31	0.95
3:E:251:GLU:HG2	6:E:2024:HOH:O	1.68	0.94
3:E:271:TYR:CD2	3:E:272:PHE:N	2.35	0.92
3:E:271:TYR:CE2	3:E:273:GLU:HB2	2.09	0.88
3:E:271:TYR:O	3:E:272:PHE:CB	2.23	0.83
3:E:271:TYR:HD2	3:E:272:PHE:H	1.20	0.82
2:B:208:LEU:O	2:B:210:PRO:CD	2.28	0.81
2:B:198:SER:HB2	2:B:201:ARG:HG3	1.62	0.81
3:E:121:LEU:C	3:E:122:GLN:HG3	2.01	0.80
2:B:208:LEU:O	2:B:210:PRO:HD3	1.83	0.78
1:A:526:PRO:HG2	3:E:128:LEU:HD23	1.67	0.77
3:E:276:LEU:HD22	3:E:276:LEU:N	2.04	0.73
3:E:323:LEU:O	3:E:324:THR:HG23	1.89	0.73
3:E:108:LEU:O	3:E:111:HIS:HB2	1.91	0.70
3:E:60:PHE:CE1	3:E:90:PHE:HB2	2.27	0.69
1:A:532:THR:H	3:E:161:ASN:HD21	1.39	0.68
3:E:248:LEU:O	6:E:2024:HOH:O	2.13	0.67
3:E:270:HIS:CD2	3:E:271:TYR:H	2.12	0.67
3:E:271:TYR:CG	3:E:272:PHE:N	2.60	0.67
3:E:242:LYS:O	3:E:245:VAL:HB	1.96	0.66
2:B:208:LEU:O	2:B:210:PRO:HD2	1.95	0.65
3:E:121:LEU:O	3:E:122:GLN:HG3	1.97	0.65
1:A:543:ILE:O	1:A:547:CYS:HB3	1.98	0.64
3:E:112:LYS:HA	6:E:2009:HOH:O	1.96	0.64
3:E:251:GLU:CG	6:E:2024:HOH:O	2.37	0.63
3:E:91:ILE:HD13	3:E:242:LYS:HG2	1.81	0.62
3:E:274:GLY:H	3:E:276:LEU:H	1.48	0.62
3:E:273:GLU:HG3	3:E:296:VAL:HG22	1.83	0.61
3:E:270:HIS:CG	3:E:271:TYR:H	2.20	0.60
2:B:236:VAL:HG13	2:B:236:VAL:O	2.01	0.59
3:E:276:LEU:N	3:E:276:LEU:CD2	2.66	0.58
3:E:248:LEU:HD12	6:E:2023:HOH:O	2.03	0.58
3:E:239:ILE:HG21	3:E:273:GLU:HB3	1.84	0.58
3:E:291:LEU:HD13	3:E:299:LEU:HG	1.85	0.58
3:E:24:ASN:ND2	6:E:2001:HOH:O	2.36	0.58
3:E:272:PHE:O	3:E:272:PHE:CG	2.56	0.58
2:B:210:PRO:HG2	2:B:212:LEU:HD12	1.86	0.57
3:E:272:PHE:CE2	3:E:276:LEU:HD21	2.40	0.57
3:E:282:GLU:HB2	3:E:287:ILE:CD1	2.35	0.56
3:E:273:GLU:HG3	3:E:296:VAL:CG2	2.35	0.56
3:E:275:VAL:C	3:E:276:LEU:HD22	2.25	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:323:LEU:C	3:E:324:THR:CG2	2.75	0.55
3:E:194:GLU:HB2	6:E:2019:HOH:O	2.07	0.55
3:E:271:TYR:O	3:E:272:PHE:CD1	2.63	0.52
3:E:282:GLU:HB2	3:E:287:ILE:HD11	1.92	0.52
3:E:26:SER:HB3	3:E:29:THR:H	1.75	0.52
3:E:225:SER:HA	3:E:242:LYS:HD2	1.92	0.51
3:E:323:LEU:O	3:E:324:THR:CG2	2.58	0.51
3:E:56:VAL:HG23	6:E:2009:HOH:O	2.09	0.51
3:E:48:VAL:O	3:E:72:PRO:HD2	2.10	0.51
3:E:274:GLY:N	3:E:276:LEU:H	2.09	0.50
3:E:257:LEU:HB2	6:E:2027:HOH:O	2.10	0.50
3:E:245:VAL:HA	6:E:2022:HOH:O	2.12	0.49
2:B:209:PRO:C	2:B:211:HIS:H	2.16	0.48
3:E:218:ILE:HG23	3:E:222:HIS:HD2	1.79	0.48
3:E:91:ILE:HG13	3:E:245:VAL:HG11	1.95	0.48
1:A:528:PRO:HA	3:E:80:SER:CB	2.44	0.48
1:A:407:ASN:OD1	1:A:407:ASN:N	2.40	0.47
3:E:169:LYS:NZ	3:E:295:GLU:HB3	2.29	0.47
2:B:262:LYS:HE3	3:E:38:TYR:CZ	2.49	0.47
3:E:112:LYS:CA	6:E:2009:HOH:O	2.59	0.47
3:E:270:HIS:CG	3:E:271:TYR:N	2.83	0.47
2:B:209:PRO:C	2:B:211:HIS:N	2.67	0.47
1:A:468:ASP:O	1:A:469:GLU:HB2	2.14	0.47
1:A:445:SER:HB3	1:A:538:MET:CE	2.45	0.46
3:E:266:GLN:C	3:E:268:ARG:H	2.18	0.46
3:E:111:HIS:O	6:E:2009:HOH:O	2.21	0.46
3:E:276:LEU:HD13	3:E:276:LEU:HA	1.57	0.46
3:E:40:LEU:HD21	3:E:137:LEU:HD22	1.97	0.46
3:E:270:HIS:O	3:E:271:TYR:CB	2.63	0.46
3:E:121:LEU:N	6:E:2010:HOH:O	2.49	0.45
1:A:528:PRO:HA	3:E:80:SER:HB2	1.97	0.45
3:E:87:ILE:HG23	3:E:246:ILE:HG23	1.98	0.45
3:E:56:VAL:N	6:E:2009:HOH:O	2.35	0.45
3:E:271:TYR:HE2	3:E:273:GLU:CB	2.16	0.45
1:A:416:ALA:CB	1:A:546:SER:HB3	2.47	0.45
1:A:410:MET:HE3	1:A:451:LEU:HD22	1.99	0.44
3:E:305:HIS:O	3:E:306:ASP:HB2	2.16	0.44
3:E:191:SER:OG	3:E:194:GLU:HG2	2.16	0.44
3:E:241:SER:O	3:E:244:ASP:HB2	2.18	0.44
3:E:60:PHE:CD1	3:E:90:PHE:HB2	2.52	0.44
1:A:445:SER:HB3	1:A:538:MET:HE1	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:258:ARG:HG3	2:B:263:TYR:CE1	2.52	0.44
3:E:273:GLU:C	3:E:275:VAL:H	2.20	0.44
1:A:428:ASN:HD22	1:A:431:TYR:HB3	1.83	0.43
2:B:198:SER:CB	2:B:201:ARG:HG3	2.43	0.43
1:A:409:ILE:O	1:A:413:VAL:HG13	2.18	0.43
3:E:87:ILE:HD12	3:E:246:ILE:HG12	2.00	0.43
3:E:271:TYR:O	3:E:272:PHE:HD1	2.00	0.43
3:E:275:VAL:O	3:E:275:VAL:HG12	2.19	0.43
3:E:120:TYR:O	3:E:122:GLN:HG3	2.19	0.43
3:E:299:LEU:HB2	3:E:312:VAL:HG13	2.00	0.42
3:E:243:PHE:CE1	3:E:246:ILE:HD11	2.54	0.42
1:A:533:ILE:HG21	3:E:74:TRP:CD2	2.54	0.42
1:A:416:ALA:HB2	1:A:546:SER:HB3	2.01	0.42
3:E:120:TYR:O	3:E:122:GLN:CG	2.68	0.42
1:A:530:SER:O	1:A:534:GLU:HG3	2.20	0.41
1:A:451:LEU:HD23	2:B:205:PRO:HG3	2.02	0.41
3:E:184:LYS:HA	3:E:185:PRO:HD3	1.92	0.41
3:E:243:PHE:C	3:E:245:VAL:H	2.24	0.41
3:E:273:GLU:HG2	3:E:276:LEU:HB2	2.01	0.41
3:E:73:LEU:HD21	3:E:85:LEU:HB2	2.02	0.41
3:E:270:HIS:CD2	3:E:271:TYR:N	2.83	0.41
3:E:291:LEU:CD1	3:E:299:LEU:HG	2.50	0.41
3:E:23:SER:HB3	3:E:187:PHE:HD2	1.85	0.41
3:E:248:LEU:C	6:E:2024:HOH:O	2.56	0.41
3:E:120:TYR:HD1	3:E:120:TYR:O	2.04	0.40
3:E:242:LYS:O	3:E:245:VAL:CB	2.68	0.40
3:E:55:GLN:HB2	3:E:58:LYS:HD2	2.02	0.40
3:E:120:TYR:C	3:E:120:TYR:CD1	2.94	0.40
2:B:247:LYS:O	2:B:250:VAL:HG12	2.22	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	100/173 (58%)	99 (99%)	1 (1%)	0	100 100
2	B	67/87 (77%)	58 (87%)	8 (12%)	1 (2%)	10 33
3	E	302/330 (92%)	276 (91%)	22 (7%)	4 (1%)	12 36
All	All	469/590 (80%)	433 (92%)	31 (7%)	5 (1%)	14 41

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	271	TYR
3	E	272	PHE
3	E	256	ASN
2	B	208	LEU
3	E	182	PHE

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	97/157 (62%)	87 (90%)	10 (10%)	7 21
2	B	67/81 (83%)	64 (96%)	3 (4%)	27 60
3	E	277/299 (93%)	245 (88%)	32 (12%)	5 17
All	All	441/537 (82%)	396 (90%)	45 (10%)	7 22

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	394	MET
1	A	407	ASN
1	A	420	LEU
1	A	434	VAL
1	A	436	ARG
1	A	441	THR
1	A	445	SER
1	A	457	ARG

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Mol	Chain	Res	Type
1	A	460	LEU
1	A	468	ASP
2	B	211	HIS
2	B	236	VAL
2	B	272	ILE
3	E	24	ASN
3	E	40	LEU
3	E	54	LEU
3	E	65	THR
3	E	94	LEU
3	E	96	ARG
3	E	103	VAL
3	E	109	GLU
3	E	110	GLU
3	E	111	HIS
3	E	120	TYR
3	E	122	GLN
3	E	129	VAL
3	E	159	SER
3	E	180	THR
3	E	238	ASP
3	E	239	ILE
3	E	241	SER
3	E	248	LEU
3	E	272	PHE
3	E	273	GLU
3	E	284	LEU
3	E	287	ILE
3	E	291	LEU
3	E	296	VAL
3	E	298	ARG
3	E	302	VAL
3	E	308	VAL
3	E	311	ILE
3	E	315	SER
3	E	318	LEU
3	E	324	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	428	ASN

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Mol	Chain	Res	Type
3	E	161	ASN
3	E	222	HIS
3	E	247	ASN
3	E	255	ASN
3	E	267	HIS
3	E	270	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	ADP	E	1327	-	24,29,29	1.08	3 (12%)	29,45,45	1.32	4 (13%)
5	AMP	E	1328	-	22,25,25	1.02	1 (4%)	25,38,38	1.54	4 (16%)

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	E	1327	-	-	3/12/32/32	0/3/3/3
5	AMP	E	1328	-	-	3/6/26/26	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1327	ADP	C5-C4	2.52	1.47	1.40
4	E	1327	ADP	O4'-C1'	2.51	1.44	1.41
5	E	1328	AMP	C5-C4	2.50	1.47	1.40
4	E	1327	ADP	C2-N3	2.14	1.35	1.32

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	E	1328	AMP	N3-C2-N1	-4.15	122.19	128.68
4	E	1327	ADP	N3-C2-N1	-2.90	124.14	128.68
4	E	1327	ADP	C4-C5-N7	-2.88	106.40	109.40
5	E	1328	AMP	C4-C5-N7	-2.82	106.46	109.40
5	E	1328	AMP	C2-N1-C6	2.62	123.23	118.75
4	E	1327	ADP	PA-O3A-PB	-2.56	124.05	132.83
5	E	1328	AMP	P-O5'-C5'	2.26	124.53	118.30
4	E	1327	ADP	O3B-PB-O2B	2.23	116.16	107.64

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	1327	ADP	C5'-O5'-PA-O1A
5	E	1328	AMP	C5'-O5'-P-O3P
4	E	1327	ADP	O4'-C4'-C5'-O5'
5	E	1328	AMP	C5'-O5'-P-O1P
4	E	1327	ADP	C3'-C4'-C5'-O5'
5	E	1328	AMP	C5'-O5'-P-O2P

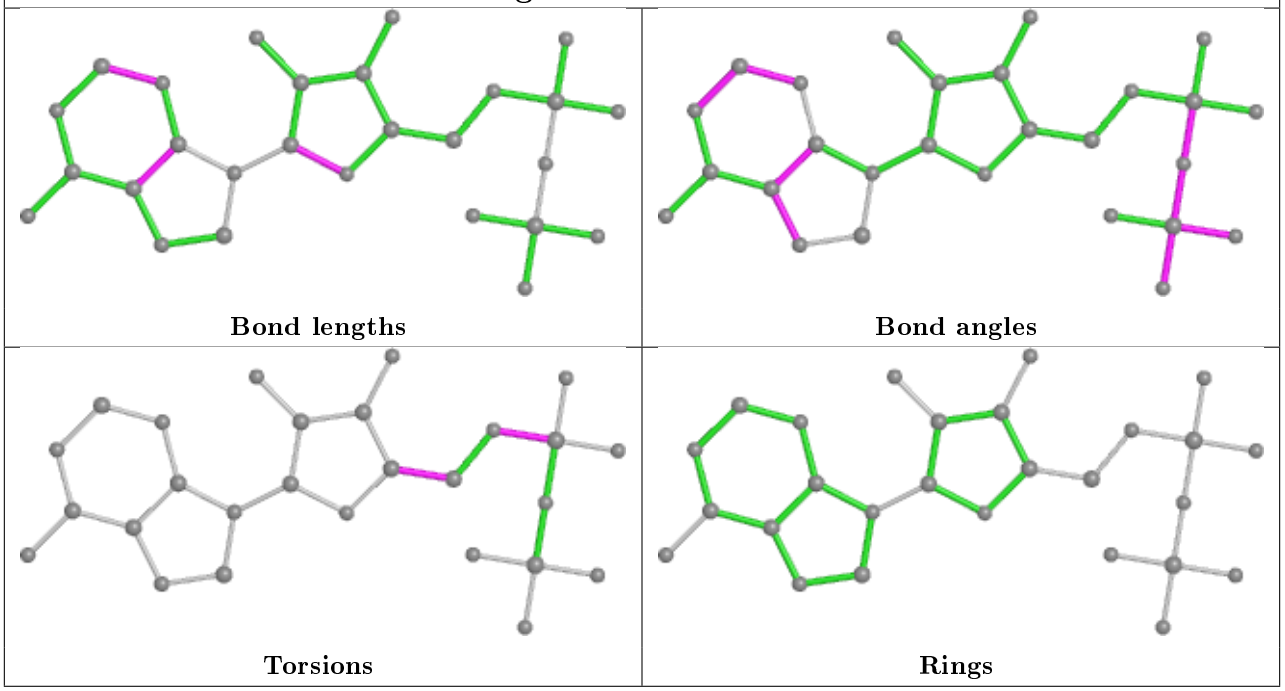
There are no ring outliers.

No monomer is involved in short contacts.

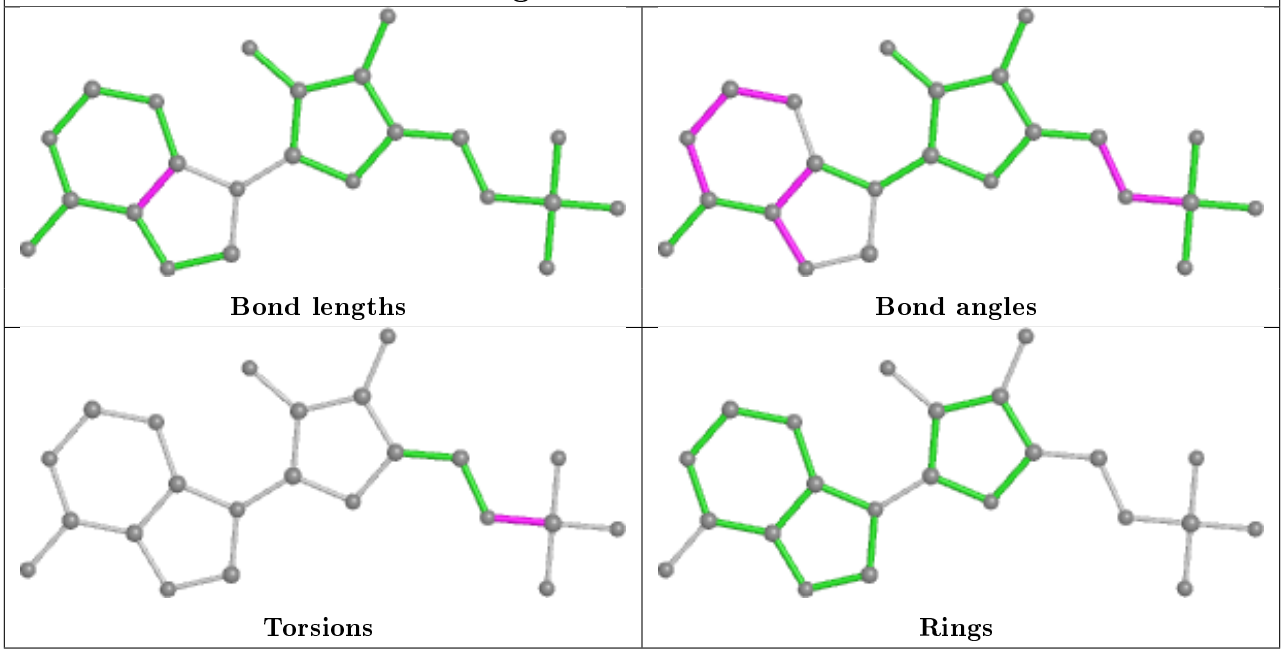
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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 E 1327



Ligand AMP E 1328



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	E	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	273:GLU	C	274:GLY	N	1.62

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	104/173 (60%)	-0.15	4 (3%) 40 30	42, 64, 98, 116	0
2	B	71/87 (81%)	0.44	10 (14%) 2 1	43, 88, 117, 137	0
3	E	304/330 (92%)	-0.02	24 (7%) 12 7	36, 60, 107, 128	6 (1%)
All	All	479/590 (81%)	0.02	38 (7%) 12 7	36, 63, 110, 137	6 (1%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	326	GLY	7.4
3	E	125	PHE	6.1
3	E	250	ALA	5.7
3	E	23	SER	5.2
3	E	274	GLY	5.2
2	B	220	ASP	5.0
3	E	24	ASN	4.3
3	E	249	ALA	4.0
3	E	271	TYR	3.8
2	B	219	LYS	3.6
2	B	235	HIS	3.6
3	E	267	HIS	3.6
3	E	253	THR	3.5
3	E	325	GLY	3.4
3	E	272	PHE	3.3
3	E	252	LYS	3.3
2	B	210	PRO	3.2
3	E	275	VAL	3.2
2	B	200	GLU	3.2
3	E	123	ASP	3.1
3	E	232	GLU	3.1
3	E	124	SER	3.0
2	B	218	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
2	B	217	LEU	2.9
2	B	199	GLU	2.9
1	A	525	ALA	2.9
3	E	255	ASN	2.6
1	A	393	SER	2.6
3	E	273	GLU	2.5
3	E	182	PHE	2.3
3	E	270	HIS	2.2
3	E	254	TYR	2.2
1	A	469	GLU	2.2
2	B	211	HIS	2.2
2	B	234	ASN	2.1
3	E	324	THR	2.1
1	A	468	ASP	2.1
3	E	126	LYS	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 carbohydrates in this entry.

6.4 Ligands (i)

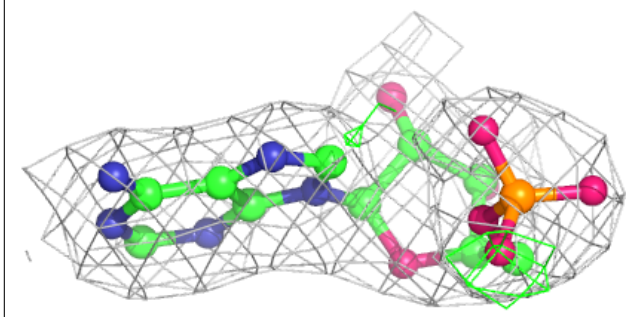
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

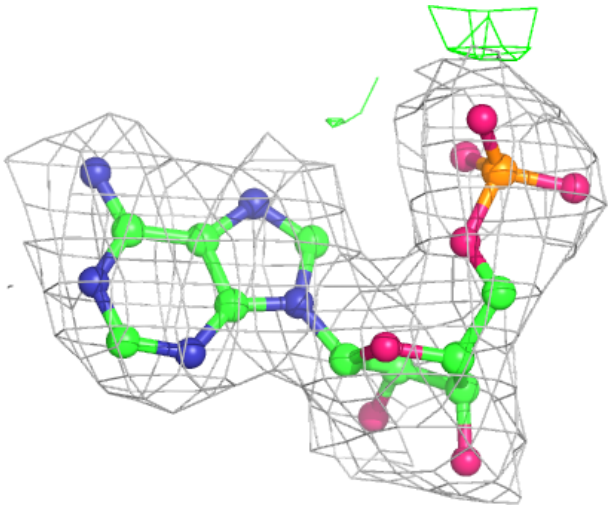
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	AMP	E	1328	23/23	0.97	0.10	37,39,45,46	0
4	ADP	E	1327	27/27	0.98	0.09	44,48,51,53	0

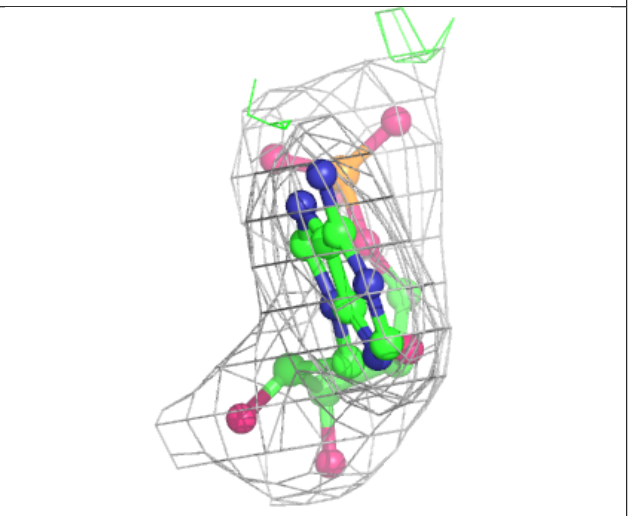
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around AMP E 1328:

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

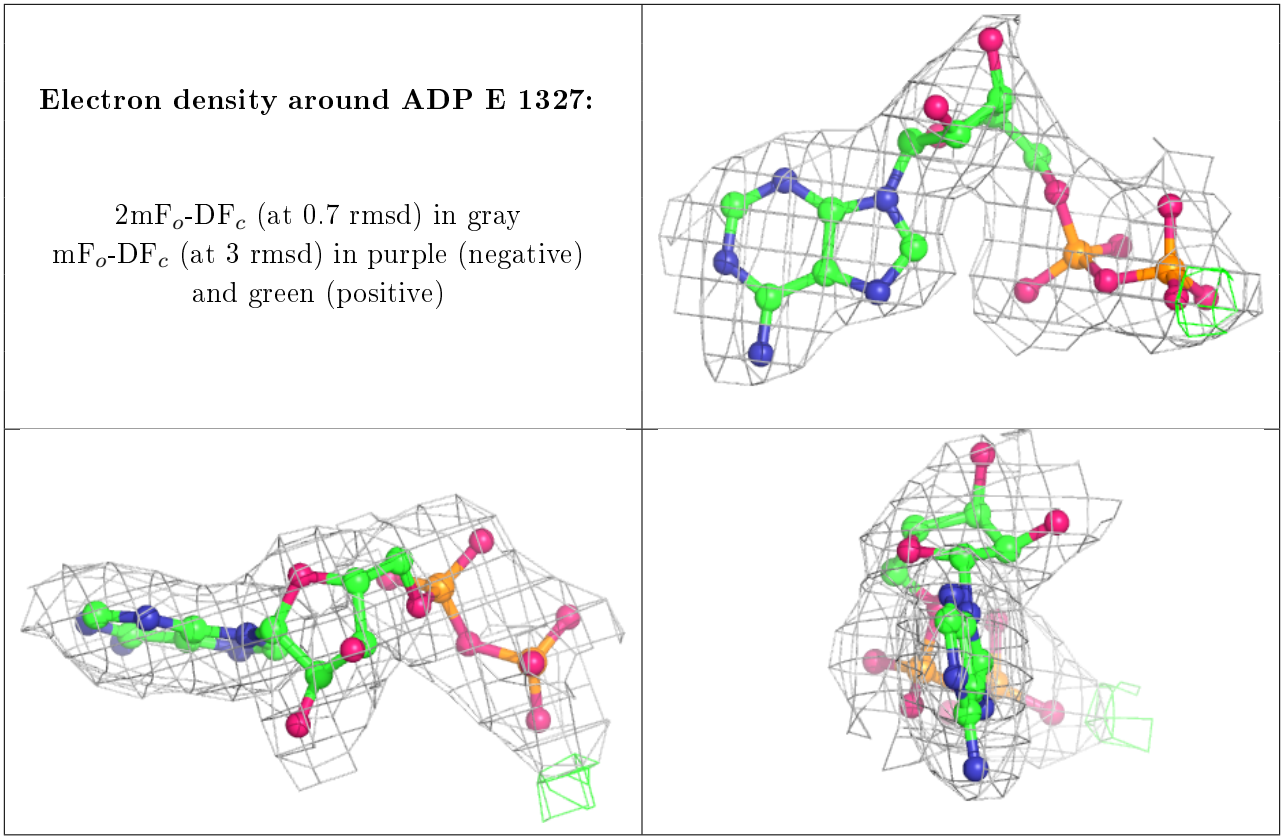






Electron density around ADP E 1327:

$2mF_o$-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

There are no such residues in this entry.