Full wwPDB X-ray Structure Validation Report (i)

Dec 7, 2023 – 04:35 am GMT

PDB ID	:	2V9J
Title	:	Crystal structure of the regulatory fragment of mammalian AMPK in complexes with Mg.ATP-AMP
Authors	:	Xiao, B.; Heath, R.; Saiu, P.; Leiper, F.C.; Leone, P.; Jing, C.; Walker, P.A.; Haire, L.; Eccleston, J.F.; Davis, C.T.; Martin, S.R.; Carling, D.; Gamblin, S.J.
Deposited on	:	2007-08-23
Resolution	:	2.53 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 (1)) were used in the production of this report:

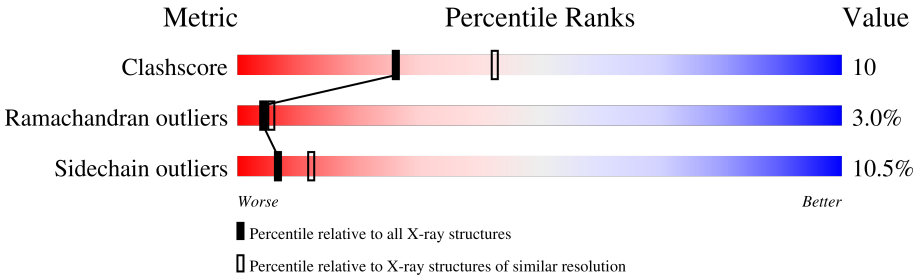
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 2.53 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	6463 (2.54-2.50)
Ramachandran outliers	138981	6335 (2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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%

Mol	Chain	Length	Quality of chain
1	A	157	41% 20% • • 35%
2	B	87	60% 17% 6% • 16%
3	E	330	69% 20% • • 8%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 4114 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	102	843	536	149	152	6	0	0	0

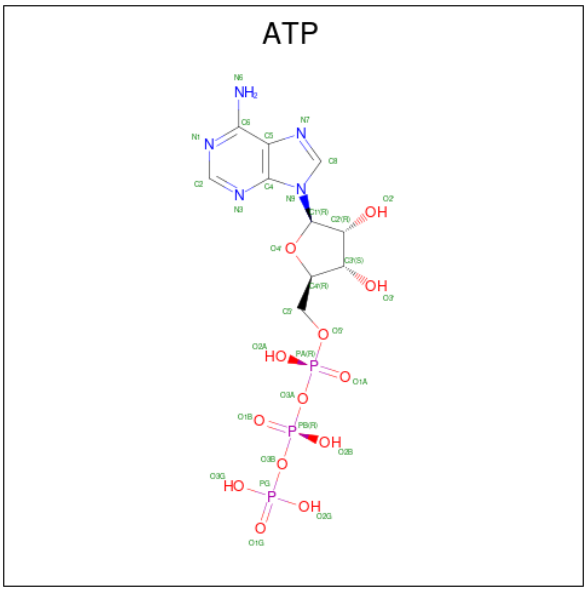
- Molecule 2 is a protein called 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT BETA-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	73	601	392	103	103	3	0	0	0

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

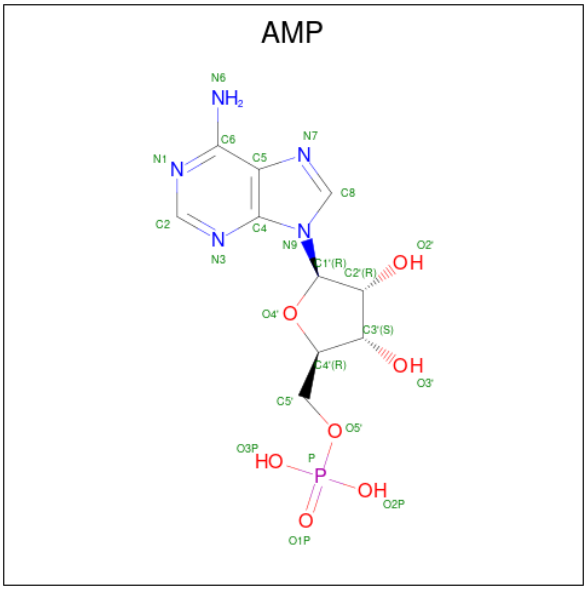
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	304	2441	1584	407	443	7	0	0	0

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
4	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	2	Total Mg 2 2	0	0

- Molecule 7 is water.

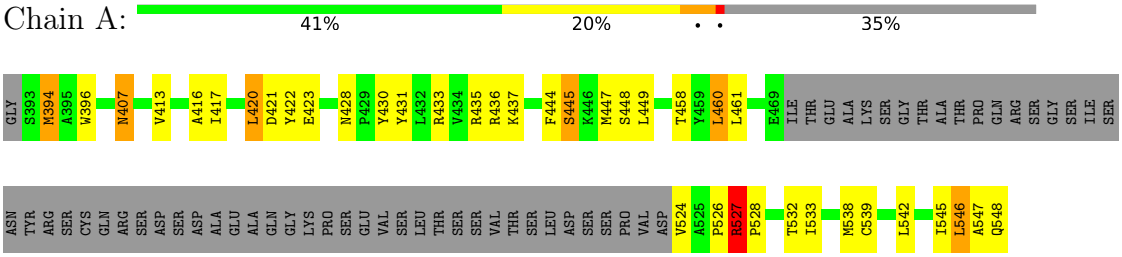
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	35	Total O 35 35	0	0
7	B	27	Total O 27 27	0	0
7	E	80	Total O 80 80	0	0

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. 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. 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.

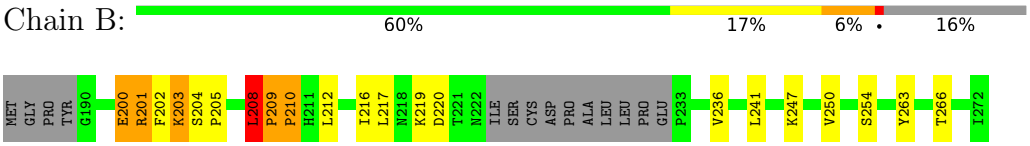
• Molecule 1: 5'-AMP-ACTIVATED PROTEIN KINASE CATALYTIC SUBUNIT ALPHA-1

Chain A:



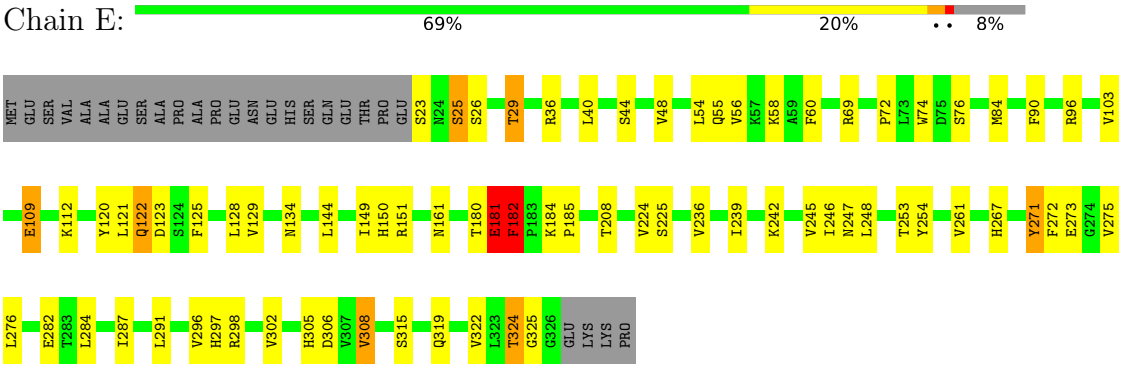
• Molecule 2: 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT BETA-2

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	48.79Å 120.69Å 127.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.53 19.98 – 2.53	Depositor EDS
% Data completeness (in resolution range)	96.2 (20.00-2.53) 96.3 (19.98-2.53)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.56 (at 2.53Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.225 , 0.266 0.273 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	50.5	Xtriage
Anisotropy	0.528	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 55.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	4114	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% 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: MG, AMP, ATP

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	0.52	0/861	0.69	1/1161 (0.1%)
2	B	0.51	0/616	0.70	0/832
3	E	0.50	0/2493	0.65	1/3384 (0.0%)
All	All	0.50	0/3970	0.67	2/5377 (0.0%)

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
2	B	0	1
3	E	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	460	LEU	CA-CB-CG	5.78	128.59	115.30
3	E	181	GLU	N-CA-C	-5.46	96.25	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	208	LEU	Peptide
3	E	182	PHE	Peptide

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	843	0	842	30	0
2	B	601	0	625	22	0
3	E	2441	0	2506	40	0
4	E	62	0	24	2	0
5	E	23	0	12	1	0
6	E	2	0	0	0	0
7	A	35	0	0	1	0
7	B	27	0	0	0	0
7	E	80	0	0	4	0
All	All	4114	0	4009	83	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 10.

All (83) 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:413:VAL:HA	1:A:546:LEU:HD12	1.17	1.16
2:B:203:LYS:HD3	2:B:204:SER:H	1.03	1.16
1:A:527:ARG:HG3	1:A:528:PRO:HD3	1.52	0.91
2:B:203:LYS:HD3	2:B:204:SER:N	1.84	0.91
1:A:532:THR:H	3:E:161:ASN:HD21	1.23	0.87
1:A:526:PRO:HG3	3:E:128:LEU:HD23	1.56	0.85
1:A:413:VAL:HA	1:A:546:LEU:CD1	2.04	0.84
2:B:203:LYS:CD	2:B:204:SER:H	1.88	0.83
1:A:542:LEU:O	1:A:546:LEU:HD22	1.82	0.79
2:B:208:LEU:O	2:B:210:PRO:HD3	1.82	0.79
3:E:282:GLU:HB2	3:E:287:ILE:HD11	1.64	0.78
3:E:225:SER:HB3	4:E:1328:ATP:O3G	1.89	0.73
1:A:447:MET:HE3	1:A:542:LEU:HD12	1.72	0.71
3:E:109:GLU:OE2	3:E:109:GLU:HA	1.90	0.71
3:E:150:HIS:HE1	7:E:2080:HOH:O	1.75	0.68
1:A:416:ALA:HB2	1:A:546:LEU:HB3	1.75	0.67
1:A:447:MET:CE	1:A:542:LEU:HD12	2.23	0.67
3:E:150:HIS:CE1	7:E:2080:HOH:O	2.48	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:208:LEU:HB3	2:B:209:PRO:HD3	1.77	0.65
1:A:527:ARG:CG	1:A:528:PRO:HD3	2.26	0.64
3:E:55:GLN:HB2	3:E:58:LYS:HD2	1.81	0.61
2:B:219:LYS:HG3	2:B:220:ASP:N	2.16	0.61
3:E:324:THR:HA	7:E:2071:HOH:O	2.01	0.60
3:E:253:THR:O	3:E:254:TYR:HB2	2.02	0.59
3:E:144:LEU:HA	3:E:149:ILE:HG22	1.84	0.59
1:A:449:LEU:HD23	1:A:461:LEU:HD11	1.84	0.58
1:A:447:MET:HE3	1:A:542:LEU:CD1	2.34	0.57
2:B:200:GLU:HB3	2:B:203:LYS:HG3	1.86	0.57
1:A:396:TRP:HB2	2:B:216:ILE:HB	1.86	0.57
2:B:247:LYS:O	2:B:250:VAL:HG12	2.06	0.56
3:E:282:GLU:HB2	3:E:287:ILE:CD1	2.35	0.56
1:A:417:ILE:HG23	1:A:422:TYR:HB2	1.89	0.55
2:B:200:GLU:O	2:B:202:PHE:N	2.33	0.55
1:A:532:THR:H	3:E:161:ASN:ND2	1.99	0.53
3:E:144:LEU:HD23	3:E:149:ILE:HG23	1.91	0.53
1:A:423:GLU:OE2	1:A:435:ARG:NH1	2.41	0.53
1:A:524:VAL:N	7:A:2028:HOH:O	2.41	0.53
3:E:273:GLU:O	3:E:273:GLU:HG3	2.10	0.52
3:E:56:VAL:HG13	3:E:60:PHE:CE1	2.45	0.51
1:A:546:LEU:HD23	1:A:547:ALA:N	2.25	0.51
3:E:271:TYR:HD2	3:E:272:PHE:H	1.59	0.51
2:B:203:LYS:H	2:B:203:LYS:HD2	1.76	0.50
2:B:208:LEU:O	2:B:210:PRO:CD	2.59	0.49
3:E:69:ARG:HB3	3:E:151:ARG:NH1	2.28	0.49
3:E:56:VAL:HG13	3:E:60:PHE:HE1	1.76	0.49
3:E:36:ARG:HD3	3:E:134:ASN:HA	1.95	0.48
2:B:200:GLU:C	2:B:202:PHE:N	2.66	0.48
2:B:200:GLU:HA	2:B:203:LYS:HB3	1.94	0.48
2:B:200:GLU:C	2:B:202:PHE:H	2.17	0.48
3:E:109:GLU:OE2	3:E:109:GLU:CA	2.60	0.48
3:E:181:GLU:O	3:E:181:GLU:HG2	2.14	0.47
3:E:319:GLN:NE2	7:E:2067:HOH:O	2.28	0.47
1:A:420:LEU:HD11	1:A:545:ILE:HG13	1.97	0.47
3:E:297:HIS:ND1	4:E:1327:ATP:O3G	2.37	0.46
3:E:120:TYR:C	3:E:122:GLN:H	2.18	0.46
1:A:437:LYS:HB2	1:A:444:PHE:CE2	2.51	0.46
3:E:180:THR:O	3:E:181:GLU:HB3	2.16	0.46
3:E:25:SER:O	3:E:29:THR:HB	2.16	0.45
3:E:225:SER:OG	5:E:1329:AMP:O2P	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:428:ASN:HB2	1:A:431:TYR:HB3	1.99	0.45
3:E:48:VAL:O	3:E:72:PRO:HD2	2.17	0.45
1:A:417:ILE:HG13	1:A:542:LEU:HD21	1.97	0.45
1:A:394:MET:HG2	2:B:219:LYS:HA	1.99	0.45
2:B:254:SER:HA	2:B:266:THR:O	2.17	0.44
1:A:539:CYS:SG	2:B:241:LEU:HD22	2.58	0.44
3:E:23:SER:HA	3:E:185:PRO:HB3	2.00	0.44
3:E:60:PHE:CE2	3:E:90:PHE:HB2	2.52	0.44
3:E:236:VAL:HB	3:E:308:VAL:HG12	2.00	0.44
1:A:420:LEU:O	1:A:421:ASP:HB2	2.18	0.43
1:A:430:TYR:CE2	2:B:205:PRO:HG3	2.54	0.42
3:E:273:GLU:O	3:E:273:GLU:CG	2.67	0.42
1:A:445:SER:HB3	1:A:538:MET:CE	2.50	0.42
1:A:545:ILE:O	1:A:545:ILE:HG22	2.20	0.42
3:E:182:PHE:HB2	3:E:184:LYS:HB2	2.01	0.42
2:B:263:TYR:O	3:E:44:SER:HA	2.19	0.41
1:A:533:ILE:HG21	3:E:74:TRP:CD2	2.54	0.41
3:E:242:LYS:O	3:E:245:VAL:HB	2.21	0.41
3:E:305:HIS:O	3:E:306:ASP:HB2	2.20	0.41
3:E:72:PRO:HA	3:E:84:MET:HE2	2.03	0.41
1:A:407:ASN:OD1	1:A:407:ASN:N	2.49	0.41
2:B:236:VAL:O	2:B:236:VAL:HG22	2.21	0.41
3:E:246:ILE:H	3:E:246:ILE:HG13	1.71	0.41
2:B:200:GLU:HG2	2:B:203:LYS:HB3	2.03	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	98/157 (62%)	93 (95%)	4 (4%)	1 (1%)	15 27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	69/87 (79%)	53 (77%)	11 (16%)	5 (7%)	1 1
3	E	302/330 (92%)	278 (92%)	16 (5%)	8 (3%)	5 7
All	All	469/574 (82%)	424 (90%)	31 (7%)	14 (3%)	4 5

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	122	GLN
3	E	181	GLU
2	B	201	ARG
2	B	208	LEU
3	E	208	THR
3	E	325	GLY
2	B	209	PRO
3	E	25	SER
3	E	26	SER
3	E	121	LEU
3	E	324	THR
1	A	527	ARG
2	B	200	GLU
2	B	210	PRO

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	94/141 (67%)	82 (87%)	12 (13%)	4 7
2	B	69/81 (85%)	65 (94%)	4 (6%)	20 36
3	E	277/299 (93%)	247 (89%)	30 (11%)	6 11
All	All	440/521 (84%)	394 (90%)	46 (10%)	7 12

All (46) 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	433	ARG
1	A	436	ARG
1	A	445	SER
1	A	448	SER
1	A	458	THR
1	A	460	LEU
1	A	527	ARG
1	A	546	LEU
1	A	548	GLN
2	B	201	ARG
2	B	203	LYS
2	B	212	LEU
2	B	217	LEU
3	E	29	THR
3	E	40	LEU
3	E	54	LEU
3	E	76	SER
3	E	96	ARG
3	E	103	VAL
3	E	109	GLU
3	E	112	LYS
3	E	123	ASP
3	E	125	PHE
3	E	129	VAL
3	E	181	GLU
3	E	182	PHE
3	E	224	VAL
3	E	239	ILE
3	E	247	ASN
3	E	248	LEU
3	E	261	VAL
3	E	267	HIS
3	E	271	TYR
3	E	275	VAL
3	E	276	LEU
3	E	284	LEU
3	E	291	LEU
3	E	296	VAL
3	E	298	ARG
3	E	302	VAL

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Mol	Chain	Res	Type
3	E	308	VAL
3	E	315	SER
3	E	322	VAL

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

Mol	Chain	Res	Type
2	B	214	GLN
2	B	234	ASN
3	E	147	ASN
3	E	161	ASN
3	E	168	HIS
3	E	202	ASN
3	E	266	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	ATP	E	1327	6	26,33,33	1.29	3 (11%)	31,52,52	1.69	7 (22%)
4	ATP	E	1328	6	26,33,33	1.32	3 (11%)	31,52,52	1.67	6 (19%)
5	AMP	E	1329	-	22,25,25	1.04	1 (4%)	25,38,38	1.53	5 (20%)

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	ATP	E	1327	6	-	3/18/38/38	0/3/3/3
4	ATP	E	1328	6	-	3/18/38/38	0/3/3/3
5	AMP	E	1329	-	-	2/6/26/26	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1327	ATP	PG-O1G	3.74	1.62	1.50
4	E	1328	ATP	PG-O1G	3.64	1.62	1.50
5	E	1329	AMP	C5-C4	2.61	1.47	1.40
4	E	1327	ATP	C5-C4	2.60	1.47	1.40
4	E	1327	ATP	PB-O1B	2.48	1.59	1.50
4	E	1328	ATP	PB-O1B	2.37	1.59	1.50
4	E	1328	ATP	C5-C4	2.35	1.47	1.40

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	1328	ATP	PA-O3A-PB	-4.85	116.17	132.83
4	E	1327	ATP	N3-C2-N1	-4.27	122.00	128.68
4	E	1327	ATP	PA-O3A-PB	-3.66	120.27	132.83
5	E	1329	AMP	N3-C2-N1	-3.43	123.31	128.68
4	E	1328	ATP	N3-C2-N1	-3.35	123.44	128.68
4	E	1328	ATP	O3G-PG-O2G	3.26	120.09	107.64
4	E	1327	ATP	PB-O3B-PG	-3.21	121.80	132.83
5	E	1329	AMP	C4-C5-N7	-3.01	106.26	109.40
4	E	1327	ATP	O3G-PG-O2G	2.88	118.64	107.64
4	E	1328	ATP	C4-C5-N7	-2.69	106.59	109.40
4	E	1327	ATP	C2-N1-C6	2.67	123.32	118.75
5	E	1329	AMP	O3P-P-O1P	2.51	120.53	110.68
4	E	1328	ATP	PB-O3B-PG	-2.48	124.30	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	1327	ATP	C3'-C2'-C1'	2.38	104.56	100.98
4	E	1328	ATP	C3'-C2'-C1'	2.24	104.35	100.98
4	E	1327	ATP	C4-C5-N7	-2.21	107.10	109.40
5	E	1329	AMP	O3P-P-O5'	-2.09	101.17	106.73
5	E	1329	AMP	C1'-N9-C4	-2.07	123.01	126.64

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	1327	ATP	C5'-O5'-PA-O3A
4	E	1328	ATP	O4'-C4'-C5'-O5'
5	E	1329	AMP	C5'-O5'-P-O1P
5	E	1329	AMP	C5'-O5'-P-O2P
4	E	1328	ATP	C3'-C4'-C5'-O5'
4	E	1327	ATP	C5'-O5'-PA-O1A
4	E	1327	ATP	C5'-O5'-PA-O2A
4	E	1328	ATP	C5'-O5'-PA-O1A

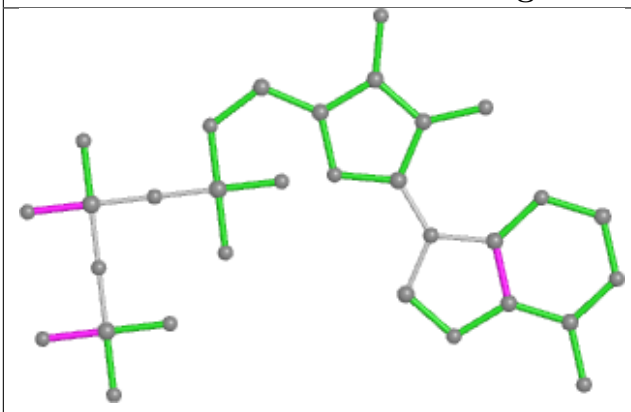
There are no ring outliers.

3 monomers are involved in 3 short contacts:

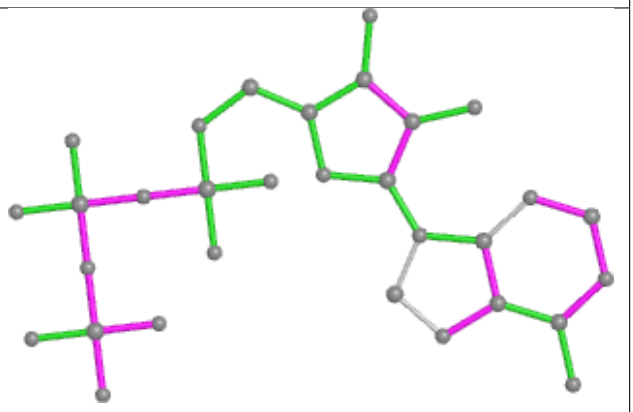
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1327	ATP	1	0
4	E	1328	ATP	1	0
5	E	1329	AMP	1	0

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 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.

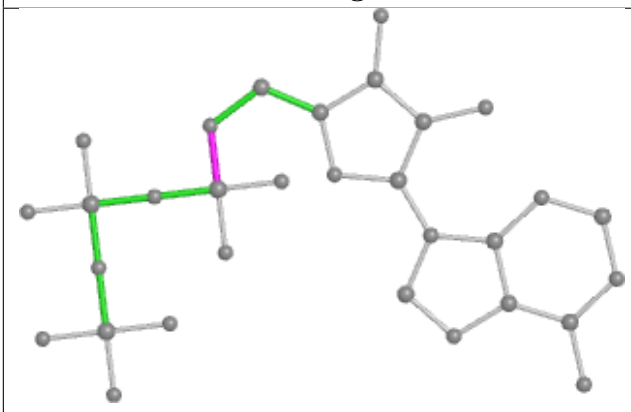
Ligand ATP E 1327



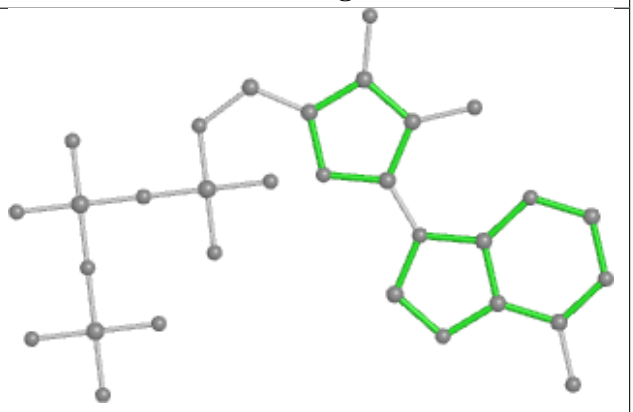
Bond lengths



Bond angles

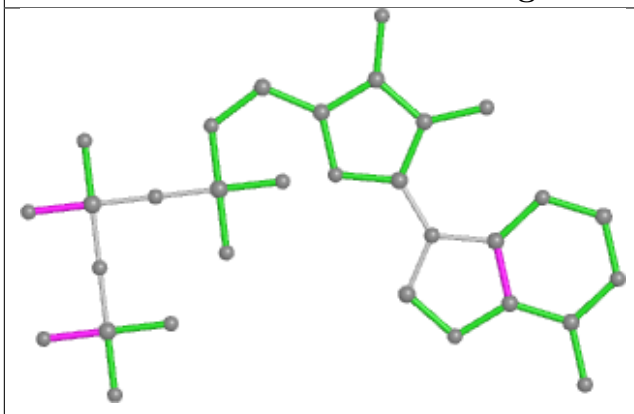


Torsions

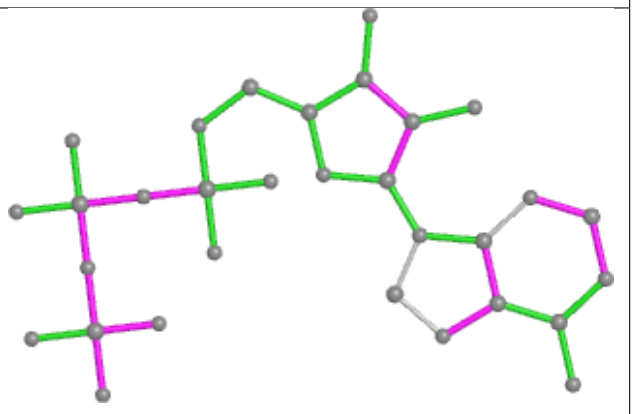


Rings

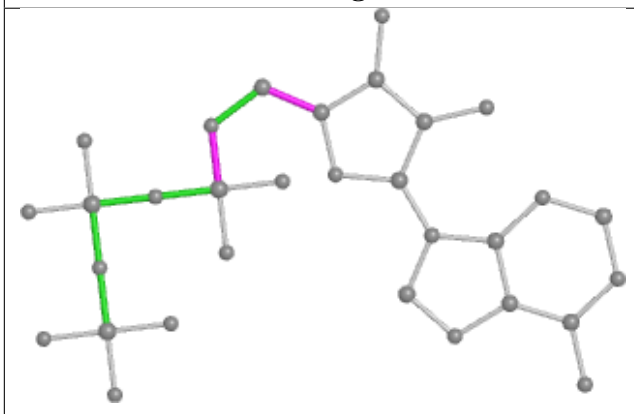
Ligand ATP E 1328



Bond lengths



Bond angles



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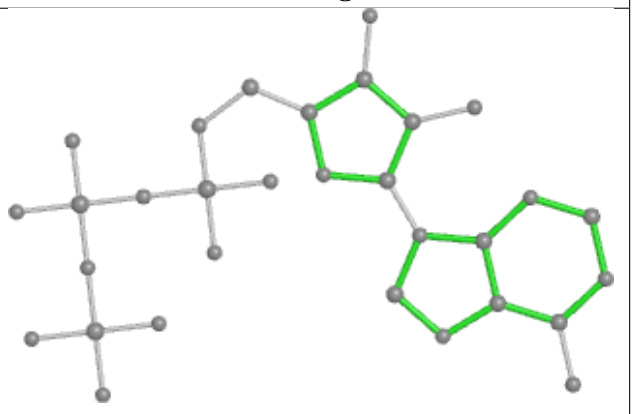
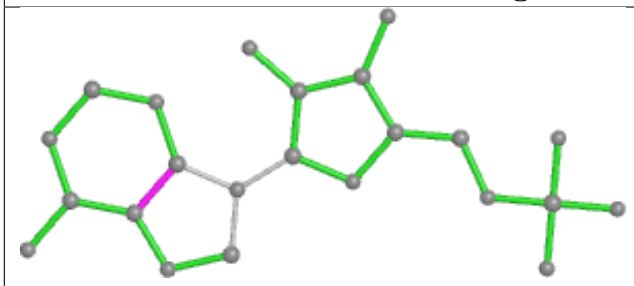
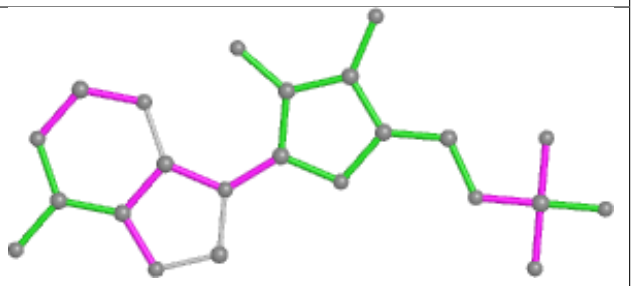


Rings

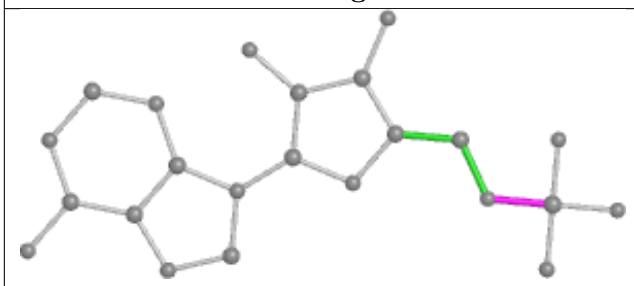
Ligand AMP E 1329



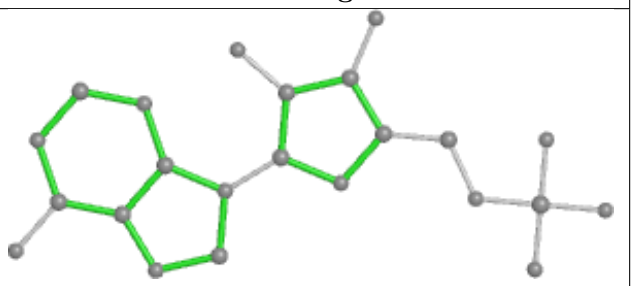
Bond lengths



Bond angles



Torsions



Rings

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

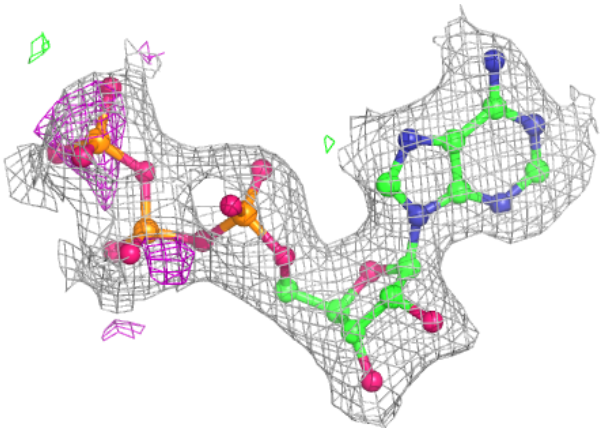
6.4 Ligands

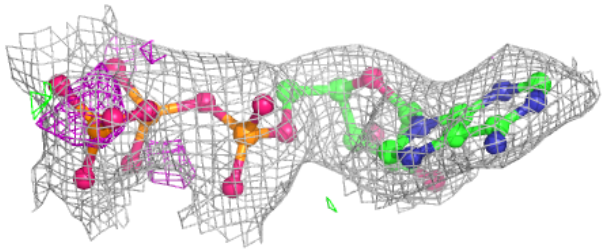
Unable to reproduce the depositors R factor - this section is therefore empty.

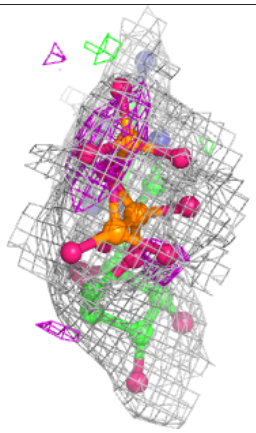
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP 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)

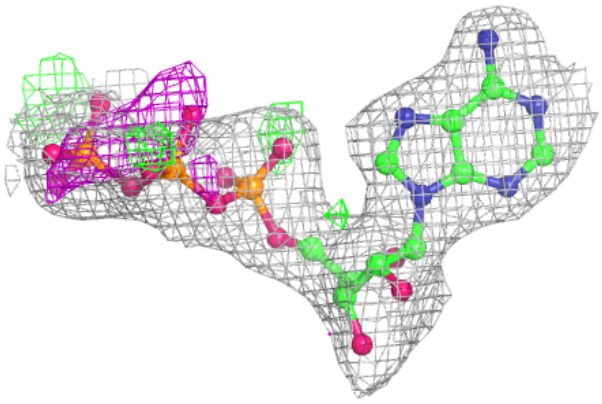


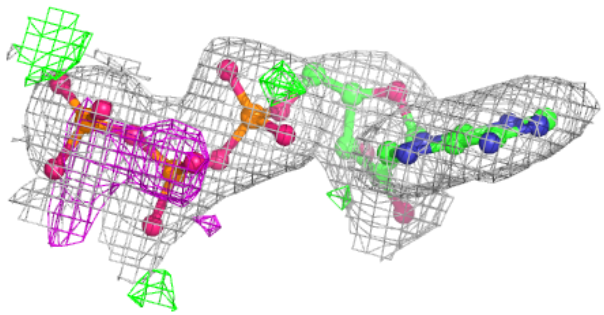


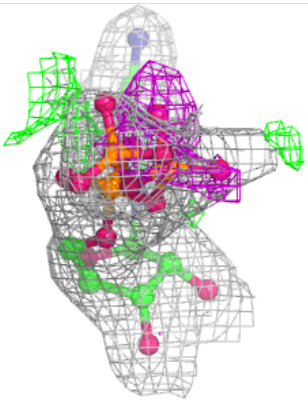


Electron density around ATP E 1328:

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

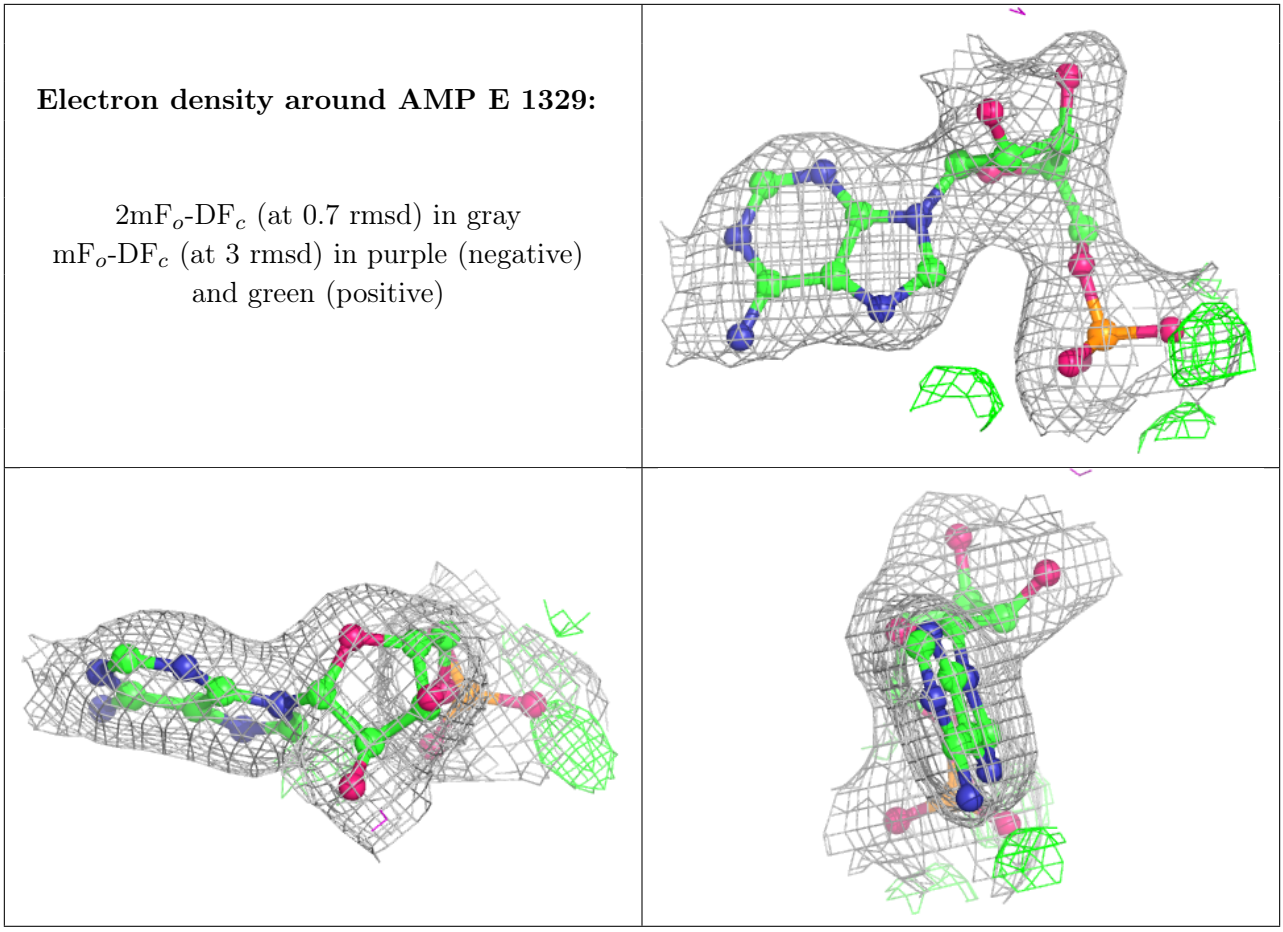






Electron density around AMP E 1329:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.