



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 10:27 AM BST

PDB ID : 4EWV
Title : Crystal structure of GH3.12 in complex with AMPCPP
Authors : Zubieta, C.; Nanao, M.; Jez, J.
Deposited on : 2012-04-28
Resolution : 2.90 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 : 2.13.1
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) : 2.13.1

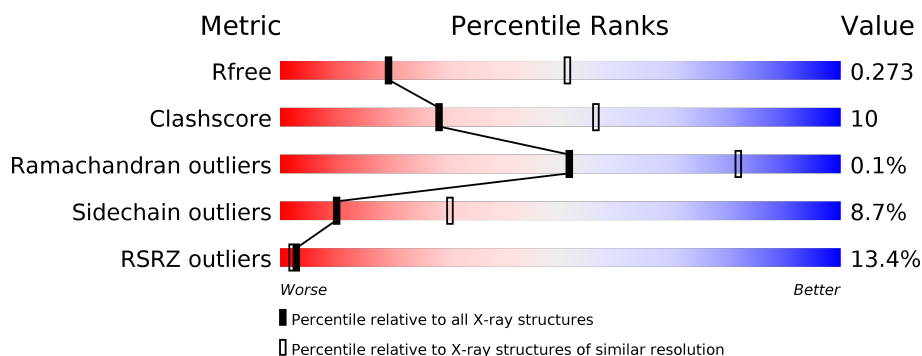
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 $\leq 5\%$. 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	581	<div> <div>12%</div> <div>64%</div> <div>16%</div> <div>•</div> <div>18%</div> </div>
1	B	581	<div> <div>10%</div> <div>63%</div> <div>20%</div> <div>•</div> <div>15%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	APC	A	601	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7167 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.

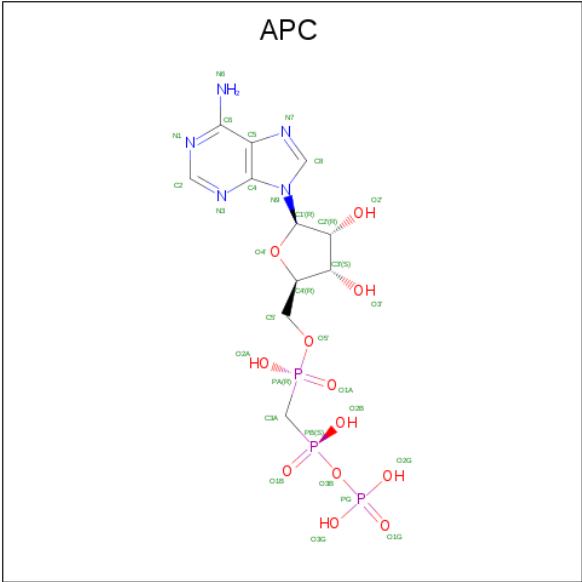
- Molecule 1 is a protein called 4-substituted benzoates-glutamate ligase GH3.12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	478	Total	C	N	O	S	0	1	0
			3531	2243	573	689	26			
1	B	492	Total	C	N	O	S	0	1	0
			3573	2266	590	693	24			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	EXPRESSION TAG	UNP Q9LYU4
A	-4	SER	-	EXPRESSION TAG	UNP Q9LYU4
A	-3	HIS	-	EXPRESSION TAG	UNP Q9LYU4
A	-2	MET	-	EXPRESSION TAG	UNP Q9LYU4
A	-1	ALA	-	EXPRESSION TAG	UNP Q9LYU4
A	0	SER	-	EXPRESSION TAG	UNP Q9LYU4
B	-5	GLY	-	EXPRESSION TAG	UNP Q9LYU4
B	-4	SER	-	EXPRESSION TAG	UNP Q9LYU4
B	-3	HIS	-	EXPRESSION TAG	UNP Q9LYU4
B	-2	MET	-	EXPRESSION TAG	UNP Q9LYU4
B	-1	ALA	-	EXPRESSION TAG	UNP Q9LYU4
B	0	SER	-	EXPRESSION TAG	UNP Q9LYU4

- Molecule 2 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (three-letter code: APC) (formula: C₁₁H₁₈N₅O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	11	5	12	3		
2	B	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

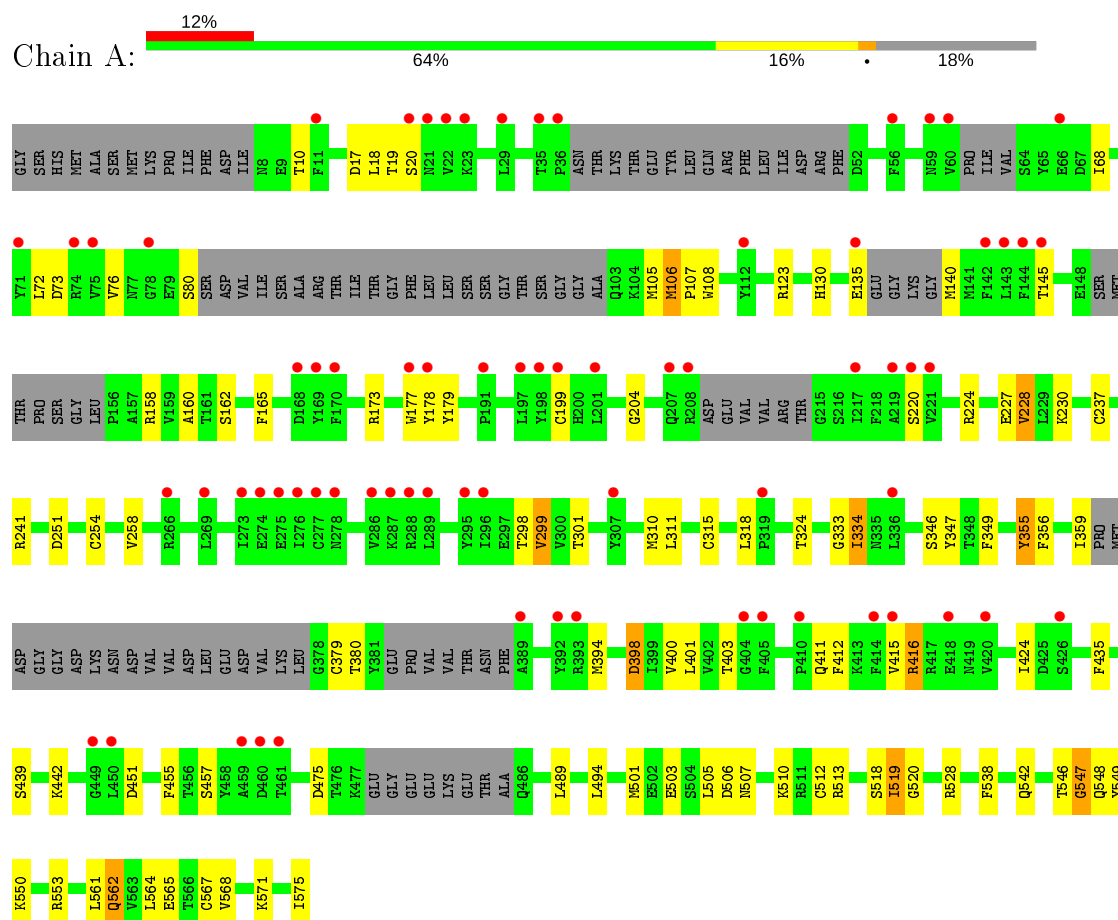
- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

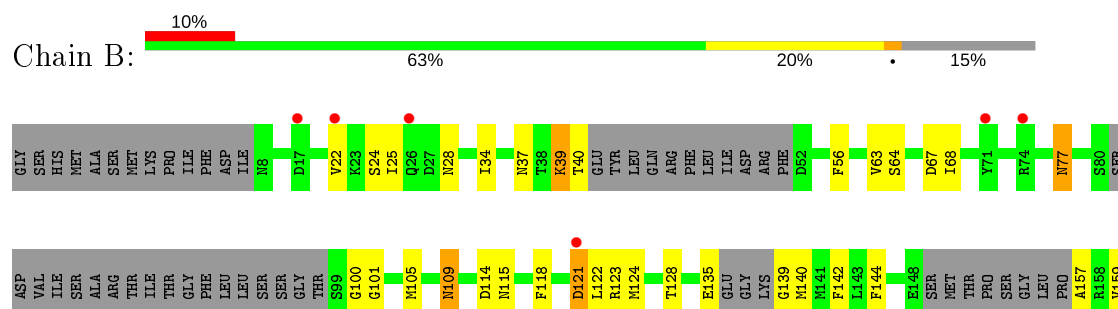
3 Residue-property plots

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: 4-substituted benzoates-glutamate ligase GH3.12



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4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	116.35Å 116.35Å 94.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.03 – 2.90 52.03 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.8 (52.03-2.90) 96.8 (52.03-2.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.243 , 0.286 0.243 , 0.273	Depositor DCC
R_{free} test set	1367 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	62.9	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 128.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.468 for h,-k,-l	Xtriage
Reported twinning fraction	0.502 for h,-k,-l	Depositor
Outliers	0 of 27318 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7167	wwPDB-VP
Average B, all atoms (Å ²)	123.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: APC, MN

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	0.24	0/3601	0.46	0/4899
1	B	0.23	0/3639	0.45	0/4955
All	All	0.23	0/7240	0.46	0/9854

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	547	GLY	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	3531	0	3189	54	0
1	B	3573	0	3192	74	0
2	A	31	0	14	9	0
2	B	31	0	14	8	0
3	A	1	0	0	0	0
All	All	7167	0	6409	133	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 (133) 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:550:LYS:NZ	2:A:601:APC:O1A	1.91	1.03
1:B:325:TYR:HD1	2:B:601:APC:N6	1.65	0.95
2:A:601:APC:H3A1	2:A:601:APC:H4'	1.51	0.91
1:A:398:ASP:CG	2:A:601:APC:O2'	2.11	0.87
1:A:398:ASP:OD2	2:A:601:APC:O2'	1.91	0.86
1:A:398:ASP:CG	2:A:601:APC:HO2'	1.78	0.85
2:A:601:APC:C3A	2:A:601:APC:H4'	2.04	0.83
1:B:245:LEU:HD21	1:B:255:GLN:HA	1.67	0.75
1:B:325:TYR:CD1	2:B:601:APC:N6	2.55	0.72
1:A:106:MET:N	1:A:106:MET:SD	2.62	0.72
1:A:439:SER:HA	1:A:442:LYS:HE2	1.71	0.72
1:B:196:SER:O	1:B:200:HIS:ND1	2.22	0.72
1:B:439:SER:HA	1:B:442:LYS:HE2	1.74	0.68
1:B:535:LEU:HD22	1:B:564:LEU:HD21	1.76	0.67
1:A:503:GLU:HA	1:A:510:LYS:HD3	1.74	0.67
1:A:512:CYS:HB3	1:A:518:SER:HB3	1.76	0.67
1:A:173:ARG:HE	1:A:179:TYR:HB3	1.59	0.66
1:B:124:MET:SD	1:B:176:ASN:ND2	2.65	0.65
1:B:24:SER:O	1:B:28:ASN:ND2	2.29	0.65
1:B:39:LYS:HE3	1:B:40:THR:HG23	1.79	0.64
1:B:453:LYS:HE2	1:B:475:ASP:HB2	1.81	0.63
1:A:398:ASP:OD1	2:A:601:APC:O2'	2.16	0.63
1:B:213:ARG:NH2	1:B:297:GLU:OE1	2.32	0.62
1:B:347:TYR:N	1:B:412:PHE:O	2.33	0.61
1:A:227:GLU:HA	1:A:230:LYS:HD3	1.82	0.60
1:A:379:CYS:SG	1:A:380:THR:N	2.75	0.59
1:A:347:TYR:N	1:A:412:PHE:O	2.26	0.59
1:B:109:ASN:ND2	1:B:157:ALA:O	2.36	0.59
1:B:497:CYS:HA	1:B:500:VAL:HG12	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:159:VAL:HG13	1:B:163:SER:HB3	1.85	0.58
1:B:507:ASN:OD1	1:B:507:ASN:N	2.37	0.57
1:B:424:ILE:HG21	1:B:466:GLY:HA3	1.86	0.57
1:B:333:GLY:HA3	1:B:349:PHE:HA	1.87	0.57
1:A:299:VAL:HG21	2:A:601:APC:N6	2.20	0.57
1:A:546:THR:HB	1:A:547:GLY:HA3	1.86	0.56
1:B:325:TYR:HD1	2:B:601:APC:C6	2.18	0.56
1:A:324:THR:HG23	1:A:334:ILE:HG22	1.88	0.56
1:B:25:ILE:HA	1:B:28:ASN:HB2	1.86	0.56
1:B:173:ARG:HE	1:B:179:TYR:HB3	1.71	0.55
1:B:282:TRP:HA	1:B:285:ILE:HD12	1.88	0.55
1:A:333:GLY:HA3	1:A:349:PHE:HA	1.88	0.54
1:B:173:ARG:NH2	1:B:179:TYR:O	2.33	0.53
1:B:176:ASN:ND2	1:B:177:TRP:H	2.09	0.51
1:A:123:ARG:NH1	1:A:324:THR:OG1	2.42	0.51
1:A:251:ASP:HB3	1:A:254:CYS:HB2	1.93	0.51
1:A:568:VAL:HG11	1:A:571:LYS:HE3	1.93	0.51
1:B:322:SER:HB2	1:B:345:VAL:HG11	1.92	0.51
2:A:601:APC:C4'	2:A:601:APC:H3A1	2.32	0.50
1:A:220:SER:OG	1:A:549:TYR:O	2.30	0.50
1:B:473:GLU:OE2	1:B:530:GLY:N	2.44	0.50
1:A:355:TYR:O	1:A:356:PHE:HB3	2.10	0.49
1:A:457:SER:OG	1:A:553:ARG:O	2.19	0.49
1:B:208:ARG:HA	1:B:290:TRP:NE1	2.26	0.49
1:B:63:VAL:O	1:B:395:ARG:N	2.44	0.48
1:B:64:SER:O	1:B:68:ILE:N	2.43	0.48
1:B:436:LYS:O	1:B:440:GLN:HG2	2.13	0.48
1:B:564:LEU:O	1:B:568:VAL:HG23	2.14	0.48
1:B:471:TYR:OH	1:B:565:GLU:OE2	2.31	0.48
1:A:199:CYS:SG	1:A:258:VAL:HG21	2.53	0.48
1:B:142:PHE:HA	1:B:200:HIS:HD2	1.78	0.48
1:A:355:TYR:HE1	1:A:394:MET:N	2.12	0.48
1:B:290:TRP:O	1:B:293:THR:OG1	2.30	0.47
1:A:173:ARG:HD2	1:A:179:TYR:HD1	1.79	0.47
1:B:289:LEU:H	1:B:289:LEU:HD23	1.80	0.47
1:A:237:CYS:O	1:A:241:ARG:HG2	2.15	0.47
1:B:39:LYS:HZ1	1:B:56:PHE:HZ	1.62	0.47
1:B:325:TYR:OH	1:B:398:ASP:OD2	2.33	0.47
1:B:245:LEU:HD23	1:B:258:VAL:HB	1.96	0.47
1:B:162:SER:HA	1:B:165:PHE:CD2	2.50	0.47
1:B:64:SER:H	1:B:67:ASP:HB3	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:ARG:NE	1:A:179:TYR:HB3	2.29	0.46
1:B:355:TYR:HH	1:B:389:ALA:N	2.12	0.46
1:B:216:SER:H	1:B:298:THR:HG23	1.80	0.46
1:B:122:LEU:HD12	1:B:123:ARG:N	2.30	0.46
1:A:107:PRO:HA	1:A:108:TRP:HA	1.60	0.46
1:B:114:ASP:OD2	1:B:115:ASN:N	2.48	0.46
1:B:380:THR:HG22	1:B:401:LEU:HB2	1.98	0.46
1:B:237:CYS:O	1:B:241:ARG:HG2	2.16	0.46
1:B:452:LEU:HD11	1:B:472:LEU:HD22	1.98	0.45
1:B:325:TYR:CD1	2:B:601:APC:C6	2.97	0.45
1:A:145:THR:HG23	1:A:162:SER:HB2	1.98	0.45
1:B:100:GLY:N	1:B:101:GLY:HA3	2.31	0.45
1:B:494:LEU:HD13	1:B:572:PHE:CG	2.52	0.45
1:A:162:SER:HA	1:A:165:PHE:CD2	2.52	0.45
1:A:455:PHE:O	1:A:553:ARG:NH1	2.49	0.45
1:B:77:ASN:OD1	1:B:77:ASN:N	2.48	0.45
1:A:519:ILE:HG13	1:A:520:GLY:N	2.31	0.45
1:A:19:THR:HA	1:A:20:SER:HA	1.72	0.45
1:A:73:ASP:O	1:A:76:VAL:HG22	2.16	0.45
1:B:216:SER:OG	1:B:218:PHE:O	2.34	0.45
2:B:601:APC:O2A	2:B:601:APC:O1B	2.35	0.45
1:A:160:ALA:HB1	1:A:548:GLN:NE2	2.32	0.44
1:B:177:TRP:CG	1:B:178:TYR:N	2.84	0.44
1:A:528:ARG:HG2	1:A:567:CYS:HB3	1.99	0.44
1:A:538:PHE:O	1:A:542:GLN:HG2	2.18	0.44
1:A:546:THR:O	1:A:549:TYR:HB2	2.17	0.44
1:A:562:GLN:HA	1:A:565:GLU:HB2	1.98	0.44
1:B:217:ILE:O	1:B:299:VAL:HG12	2.17	0.44
1:A:346:SER:OG	1:A:412:PHE:N	2.51	0.44
1:A:311:LEU:O	1:A:315:CYS:N	2.50	0.44
1:B:208:ARG:HA	1:B:290:TRP:HE1	1.83	0.44
1:A:224:ARG:O	1:A:228:VAL:HG12	2.18	0.43
1:B:144:PHE:HB3	1:B:193:ASN:ND2	2.34	0.43
1:B:308:VAL:HG13	1:B:320:LEU:HD12	2.00	0.43
1:B:124:MET:O	1:B:128:THR:OG1	2.32	0.43
1:A:177:TRP:CG	1:A:178:TYR:N	2.87	0.43
1:A:346:SER:HG	1:A:411:GLN:HB3	1.83	0.42
1:B:144:PHE:HZ	1:B:197:LEU:HD13	1.83	0.42
1:A:68:ILE:O	1:A:72:LEU:N	2.37	0.42
1:B:195:GLU:HA	1:B:248:TRP:CZ3	2.55	0.42
1:B:198:TYR:OH	1:B:239:ASN:OD1	2.25	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:MET:HE3	1:A:204:GLY:HA3	2.01	0.42
1:B:301:THR:HG22	1:B:302:GLY:H	1.84	0.42
1:A:346:SER:OG	1:A:411:GLN:HB3	2.20	0.42
1:B:39:LYS:NZ	1:B:39:LYS:HA	2.35	0.42
1:B:525:ARG:HD3	1:B:571:LYS:HG2	2.01	0.42
1:A:416:ARG:HB2	1:A:416:ARG:HH11	1.85	0.42
1:A:506:ASP:OD1	1:A:506:ASP:N	2.53	0.42
1:A:451:ASP:OD1	1:A:475:ASP:HB3	2.20	0.41
1:B:267:PRO:HA	1:B:270:ALA:HB3	2.02	0.41
1:B:123:ARG:NH1	1:B:324:THR:OG1	2.54	0.41
2:B:601:APC:O2A	2:B:601:APC:H4'	2.20	0.41
1:A:564:LEU:O	1:A:568:VAL:HG23	2.21	0.41
1:B:109:ASN:HA	1:B:109:ASN:HD22	1.68	0.41
1:B:139:GLY:O	1:B:181:TYR:HA	2.20	0.41
1:B:121:ASP:O	1:B:124:MET:HB3	2.21	0.41
1:B:535:LEU:HD11	1:B:560:ALA:HB1	2.02	0.41
1:A:227:GLU:O	1:A:230:LYS:HB2	2.21	0.41
1:B:34:ILE:HA	1:B:37:ASN:OD1	2.22	0.40
1:B:550:LYS:HE2	2:B:601:APC:O2B	2.20	0.40
1:B:140:MET:O	1:B:214:THR:HA	2.21	0.40
1:B:325:TYR:HA	2:B:601:APC:HN61	1.86	0.40
1:A:501:MET:O	1:A:505:LEU:HG	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	459/581 (79%)	434 (95%)	25 (5%)	0	100	100
1	B	473/581 (81%)	452 (96%)	20 (4%)	1 (0%)	47	78
All	All	932/1162 (80%)	886 (95%)	45 (5%)	1 (0%)	51	82

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	22	VAL

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	359/527 (68%)	325 (90%)	34 (10%)	8	26
1	B	351/527 (67%)	323 (92%)	28 (8%)	12	33
All	All	710/1054 (67%)	648 (91%)	62 (9%)	10	30

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	THR
1	A	17	ASP
1	A	18	LEU
1	A	80	SER
1	A	105	MET
1	A	106	MET
1	A	130	HIS
1	A	135	GLU
1	A	158	ARG
1	A	228	VAL
1	A	298	THR
1	A	299	VAL
1	A	301	THR
1	A	310	MET
1	A	318	LEU
1	A	334	ILE
1	A	355	TYR
1	A	359	ILE
1	A	398	ASP
1	A	400	VAL
1	A	401	LEU
1	A	403	THR

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Mol	Chain	Res	Type
1	A	415	VAL
1	A	416	ARG
1	A	424	ILE
1	A	435	PHE
1	A	489	LEU
1	A	494	LEU
1	A	507	ASN
1	A	513	ARG
1	A	519	ILE
1	A	561	LEU
1	A	562	GLN
1	A	575	ILE
1	B	39	LYS
1	B	77	ASN
1	B	105	MET
1	B	109	ASN
1	B	118	PHE
1	B	121	ASP
1	B	135	GLU
1	B	173	ARG
1	B	245	LEU
1	B	251	ASP
1	B	285	ILE
1	B	298	THR
1	B	356	PHE
1	B	357	GLU
1	B	381	TYR
1	B	384	VAL
1	B	401	LEU
1	B	403	THR
1	B	415	VAL
1	B	416	ARG
1	B	424	ILE
1	B	435	PHE
1	B	489	LEU
1	B	494	LEU
1	B	507	ASN
1	B	513	ARG
1	B	569	VAL
1	B	575	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	312	ASN
1	A	548	GLN
1	B	109	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 3 ligands modelled in this entry, 1 is 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	$\# Z > 2$
2	APC	A	601	3	27,33,33	1.35	5 (18%)	31,52,52	1.43	4 (12%)
2	APC	B	601	-	27,33,33	1.35	5 (18%)	31,52,52	1.43	4 (12%)

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
2	APC	A	601	3	-	4/15/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	APC	B	601	-	-	11/15/38/38	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	APC	PA-O5'	2.80	1.61	1.57
2	B	601	APC	PB-O3B	2.78	1.61	1.58
2	A	601	APC	PB-O3B	2.78	1.61	1.58
2	B	601	APC	PA-O5'	2.78	1.61	1.57
2	A	601	APC	C5-C4	2.51	1.47	1.40
2	B	601	APC	C5-C4	2.51	1.47	1.40
2	A	601	APC	PA-O2A	2.17	1.61	1.56
2	B	601	APC	PB-O2B	2.16	1.61	1.56
2	A	601	APC	PB-O2B	2.15	1.61	1.56
2	B	601	APC	PA-O2A	2.14	1.61	1.56

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	APC	C3'-C2'-C1'	3.53	106.29	100.98
2	B	601	APC	C3'-C2'-C1'	3.51	106.27	100.98
2	A	601	APC	PG-O3B-PB	-3.44	120.51	132.62
2	B	601	APC	PG-O3B-PB	-3.43	120.52	132.62
2	B	601	APC	N3-C2-N1	-3.20	123.68	128.68
2	A	601	APC	N3-C2-N1	-3.15	123.75	128.68
2	A	601	APC	C4-C5-N7	-2.70	106.58	109.40
2	B	601	APC	C4-C5-N7	-2.69	106.59	109.40

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	APC	C4'-C5'-O5'-PA
2	A	601	APC	C3'-C4'-C5'-O5'
2	B	601	APC	PA-C3A-PB-O1B
2	B	601	APC	PA-C3A-PB-O2B
2	B	601	APC	PA-C3A-PB-O3B
2	B	601	APC	PB-C3A-PA-O1A
2	B	601	APC	PB-C3A-PA-O5'
2	B	601	APC	C5'-O5'-PA-O1A
2	B	601	APC	C4'-C5'-O5'-PA

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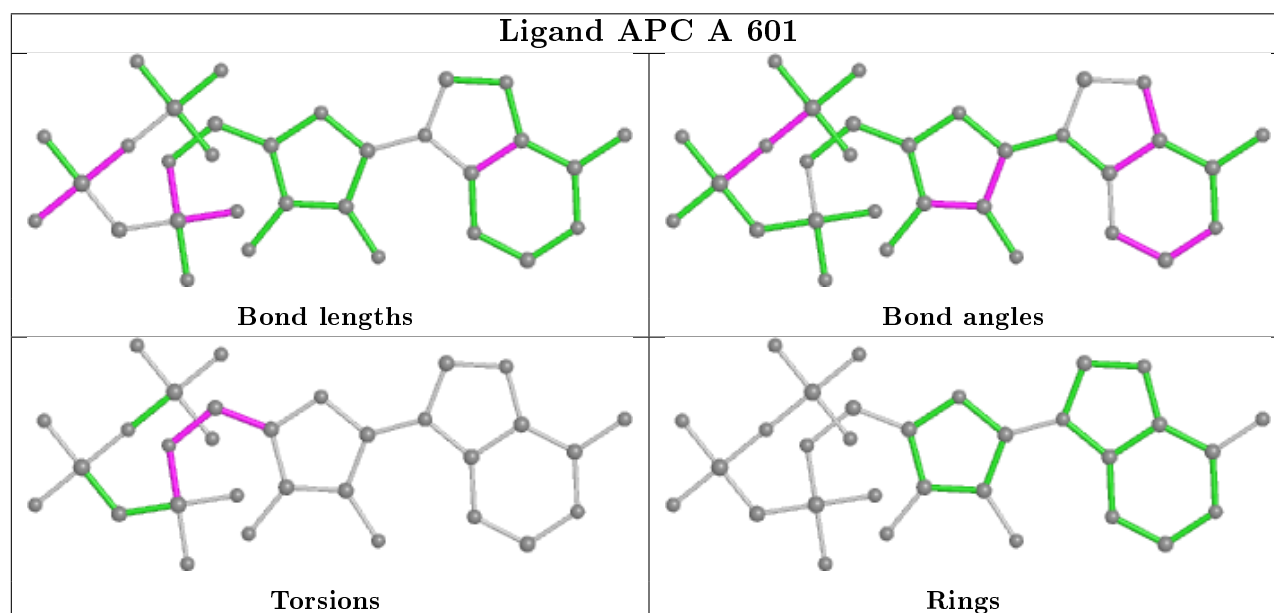
Mol	Chain	Res	Type	Atoms
2	B	601	APC	C3'-C4'-C5'-O5'
2	A	601	APC	O4'-C4'-C5'-O5'
2	B	601	APC	O4'-C4'-C5'-O5'
2	B	601	APC	PB-C3A-PA-O2A
2	B	601	APC	C5'-O5'-PA-O2A
2	A	601	APC	C5'-O5'-PA-C3A

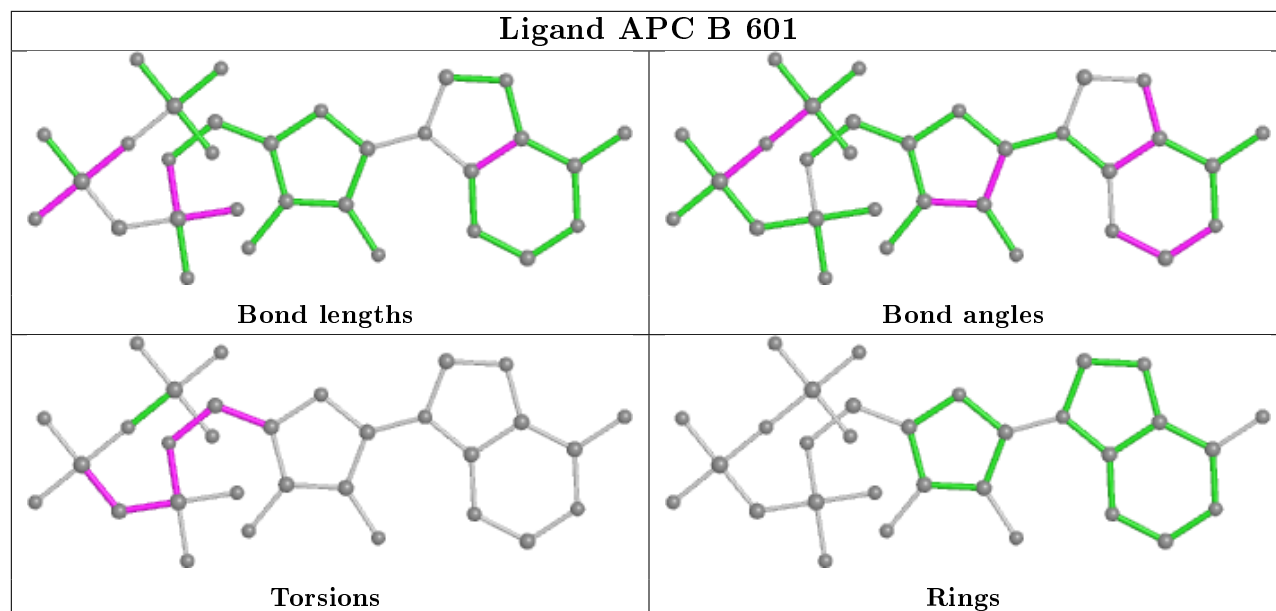
There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	APC	9	0
2	B	601	APC	8	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	478/581 (82%)	0.64	71 (14%)	2 1	14, 119, 236, 334	0
1	B	492/581 (84%)	0.57	59 (11%)	4 3	28, 118, 217, 318	0
All	All	970/1162 (83%)	0.60	130 (13%)	3 2	14, 119, 230, 334	0

All (130) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	396	VAL	21.0
1	A	220	SER	13.7
1	A	393	ARG	12.3
1	B	455	PHE	10.1
1	A	36	PRO	9.7
1	A	414	PHE	9.4
1	A	21	ASN	9.4
1	A	307	TYR	9.3
1	B	263	GLY	9.2
1	A	198	TYR	8.7
1	A	143	LEU	8.3
1	B	397	GLY	8.1
1	A	461	THR	7.9
1	A	144	PHE	7.7
1	B	394	MET	7.7
1	A	405	PHE	7.4
1	A	392	TYR	7.2
1	B	546	THR	6.9
1	A	278	ASN	6.8
1	B	121	ASP	6.8
1	A	56	PHE	6.8
1	A	169	TYR	6.4
1	B	194	THR	6.3
1	A	295	TYR	6.3

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Mol	Chain	Res	Type	RSRZ
1	A	404	GLY	6.2
1	B	332	PHE	5.9
1	B	520	GLY	5.6
1	B	454	ASP	5.6
1	A	288	ARG	5.6
1	B	395	ARG	5.5
1	B	456	THR	5.3
1	B	289	LEU	5.0
1	A	60	VAL	4.9
1	A	191	PRO	4.8
1	B	518	SER	4.7
1	B	557	SER	4.7
1	B	349	PHE	4.6
1	A	170	PHE	4.3
1	B	288	ARG	4.2
1	A	112	TYR	4.1
1	B	258	VAL	4.1
1	A	219	ALA	4.1
1	B	17	ASP	4.1
1	A	201	LEU	3.9
1	A	199	CYS	3.8
1	A	178	TYR	3.7
1	B	466	GLY	3.7
1	A	459	ALA	3.7
1	B	356	PHE	3.7
1	B	284	GLY	3.6
1	B	398	ASP	3.6
1	B	354	SER	3.6
1	A	275	GLU	3.6
1	A	221	VAL	3.6
1	B	74	ARG	3.4
1	A	273	ILE	3.4
1	B	292	ASN	3.4
1	A	277	CYS	3.4
1	B	330	THR	3.4
1	A	319	PRO	3.3
1	B	324	THR	3.3
1	B	516[A]	ASP	3.3
1	B	539	PHE	3.3
1	A	59	ASN	3.3
1	A	142	PHE	3.3
1	B	285	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	323	THR	3.2
1	B	226	ILE	3.1
1	A	22	VAL	3.1
1	A	217	ILE	3.1
1	A	286	VAL	3.0
1	A	74	ARG	3.0
1	B	541	SER	3.0
1	B	452	LEU	3.0
1	A	145	THR	3.0
1	A	287	LYS	2.9
1	B	290	TRP	2.9
1	A	135	GLU	2.9
1	B	545	SER	2.9
1	B	22	VAL	2.9
1	A	274	GLU	2.8
1	A	450	LEU	2.8
1	A	296	ILE	2.8
1	B	550	LYS	2.8
1	B	254	CYS	2.8
1	A	460	ASP	2.8
1	A	266	ARG	2.7
1	B	187	VAL	2.7
1	B	71	TYR	2.7
1	A	71	TYR	2.7
1	A	78	GLY	2.7
1	A	410	PRO	2.7
1	B	26	GLN	2.7
1	A	208	ARG	2.6
1	A	426	SER	2.6
1	B	543	GLY	2.6
1	A	29	LEU	2.6
1	A	66	GLU	2.6
1	B	453	LYS	2.6
1	B	311	LEU	2.6
1	B	313	TYR	2.6
1	B	318	LEU	2.5
1	A	420	VAL	2.5
1	A	168	ASP	2.5
1	A	23	LYS	2.5
1	A	415	VAL	2.5
1	A	177	TRP	2.4
1	A	289	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	246	SER	2.4
1	B	538	PHE	2.3
1	B	521	PRO	2.3
1	A	276	ILE	2.3
1	B	393	ARG	2.3
1	B	331	THR	2.3
1	B	334	ILE	2.3
1	B	193	ASN	2.2
1	A	11	PHE	2.2
1	A	20	SER	2.2
1	B	531	THR	2.2
1	A	389	ALA	2.2
1	A	269	LEU	2.1
1	A	35	THR	2.1
1	A	336	LEU	2.1
1	B	476	THR	2.1
1	A	197	LEU	2.1
1	A	418	GLU	2.1
1	A	449	GLY	2.1
1	A	75	VAL	2.1
1	A	207	GLN	2.0
1	B	434	LEU	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.

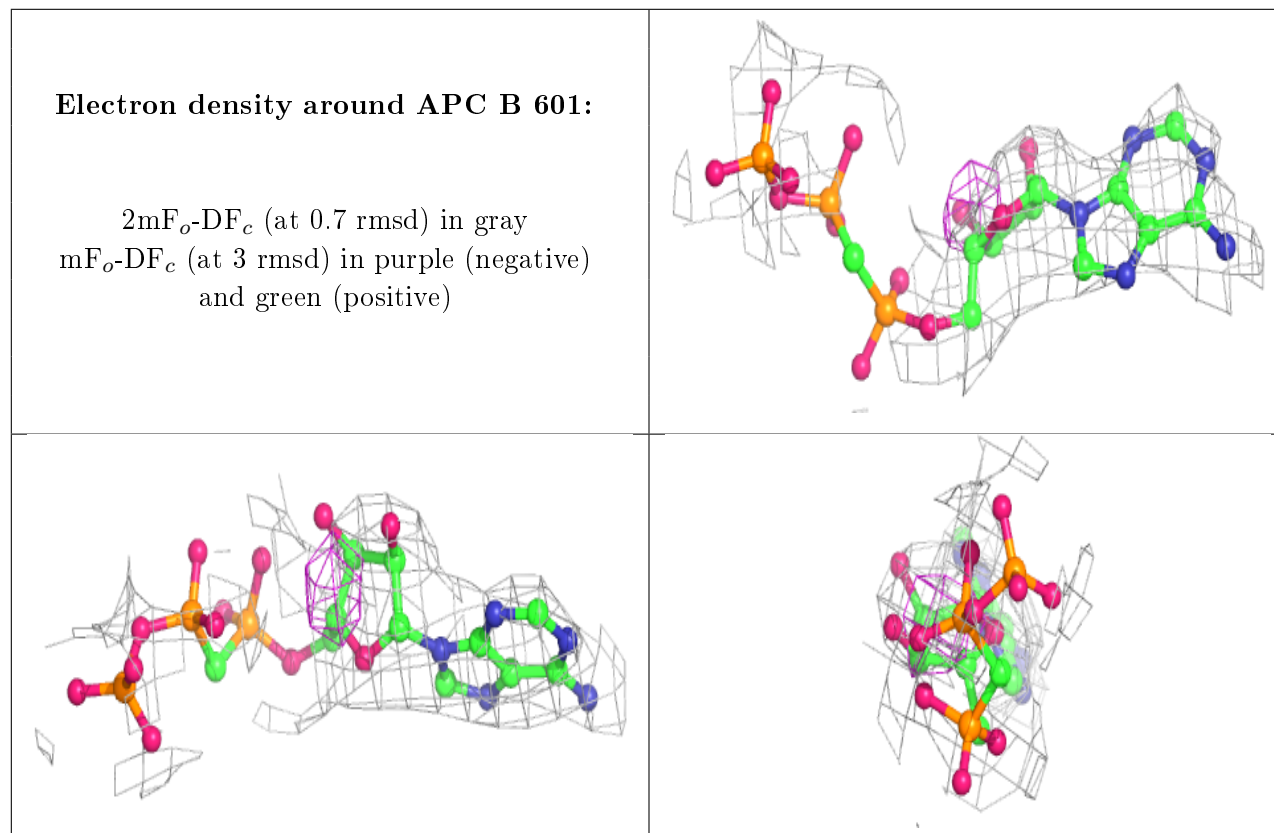
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	APC	B	601	31/31	0.84	0.23	48,122,172,262	0

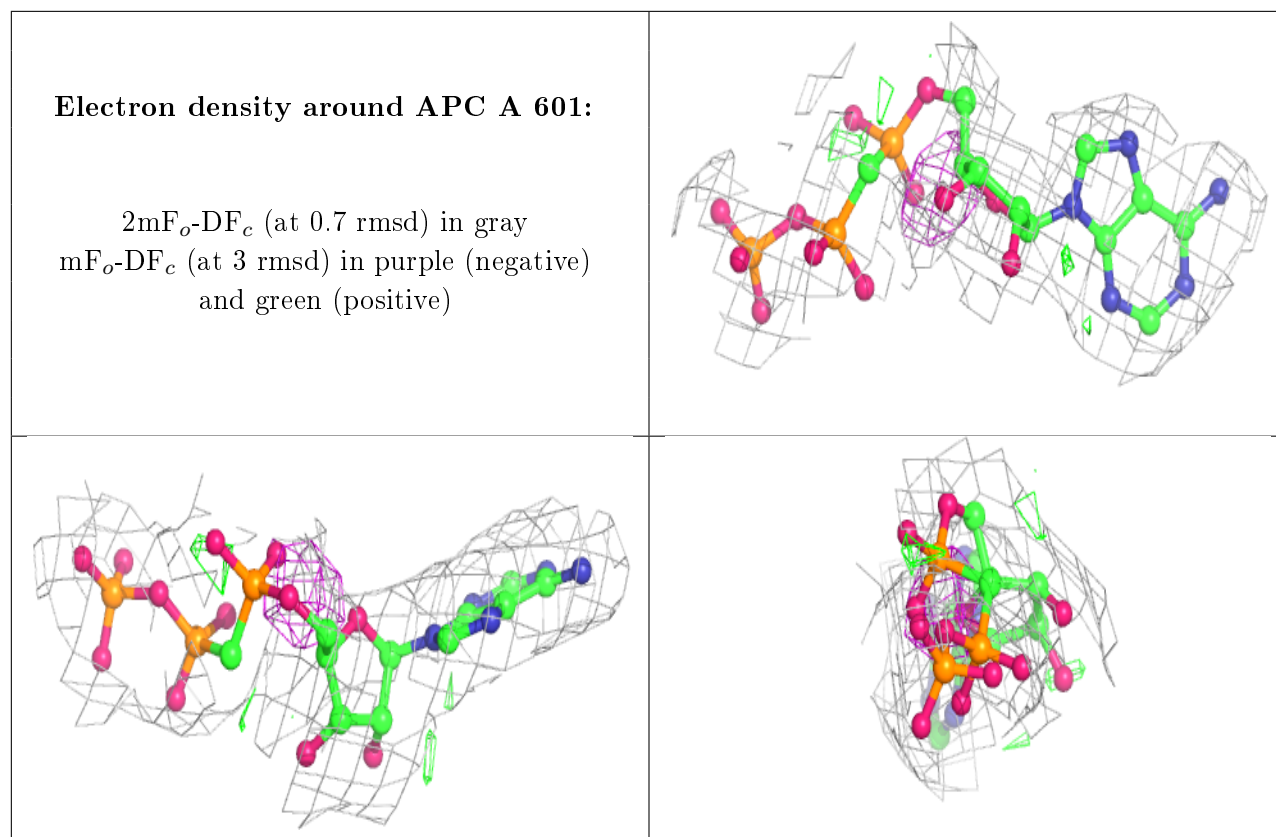
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	APC	A	601	31/31	0.90	0.17	39,78,181,223	0
3	MN	A	602	1/1	0.94	0.13	118,118,118,118	0

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.