



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 23, 2023 – 05:20 PM EDT

PDB ID : 5TSG  
Title : PilB from *Geobacter metallireducens* bound to ADP  
Authors : McCallum, M.; Tammam, S.; Khan, A.; Burrows, L.; Howell, P.L.  
Deposited on : 2016-10-28  
Resolution : 3.40 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

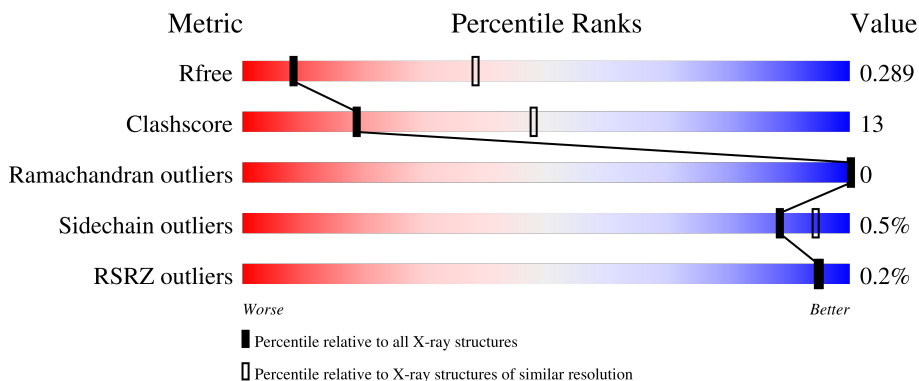
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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  $\geq 3$ , 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	B	588	 49% 16% 35%
1	C	588	 49% 15% 35%
1	D	588	 48% 17% 35%

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
5	FMT	D	602	-	X	-	-

## 2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 8356 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 Type IV pilus biogenesis ATPase PilB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	384	2749	1738	479	518	14	0	0	0
1	C	381	2802	1769	488	529	16	0	0	0
1	D	384	2742	1722	476	528	16	0	0	0

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	initiating methionine	UNP Q39VU7
B	-18	GLY	-	expression tag	UNP Q39VU7
B	-17	SER	-	expression tag	UNP Q39VU7
B	-16	SER	-	expression tag	UNP Q39VU7
B	-15	HIS	-	expression tag	UNP Q39VU7
B	-14	HIS	-	expression tag	UNP Q39VU7
B	-13	HIS	-	expression tag	UNP Q39VU7
B	-12	HIS	-	expression tag	UNP Q39VU7
B	-11	HIS	-	expression tag	UNP Q39VU7
B	-10	HIS	-	expression tag	UNP Q39VU7
B	-9	SER	-	expression tag	UNP Q39VU7
B	-8	SER	-	expression tag	UNP Q39VU7
B	-7	GLY	-	expression tag	UNP Q39VU7
B	-6	LEU	-	expression tag	UNP Q39VU7
B	-5	VAL	-	expression tag	UNP Q39VU7
B	-4	PRO	-	expression tag	UNP Q39VU7
B	-3	ARG	-	expression tag	UNP Q39VU7
B	-2	GLY	-	expression tag	UNP Q39VU7
B	-1	SER	-	expression tag	UNP Q39VU7
B	0	HIS	-	expression tag	UNP Q39VU7
B	482	GLY	ALA	conflict	UNP Q39VU7
C	-19	MET	-	initiating methionine	UNP Q39VU7
C	-18	GLY	-	expression tag	UNP Q39VU7

*Continued on next page...*

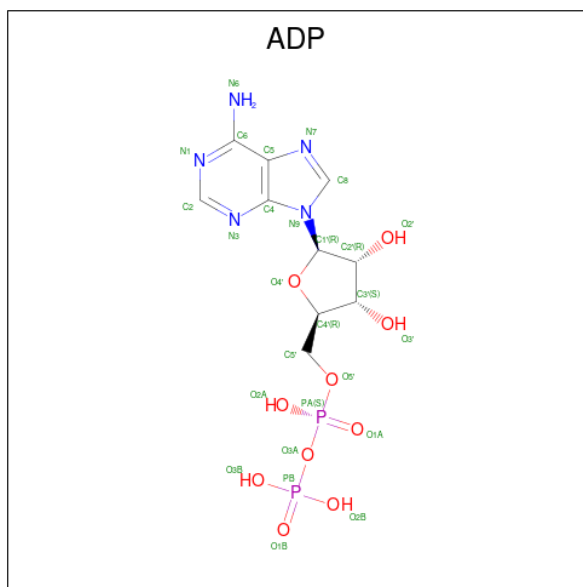
*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
C	-17	SER	-	expression tag	UNP Q39VU7
C	-16	SER	-	expression tag	UNP Q39VU7
C	-15	HIS	-	expression tag	UNP Q39VU7
C	-14	HIS	-	expression tag	UNP Q39VU7
C	-13	HIS	-	expression tag	UNP Q39VU7
C	-12	HIS	-	expression tag	UNP Q39VU7
C	-11	HIS	-	expression tag	UNP Q39VU7
C	-10	HIS	-	expression tag	UNP Q39VU7
C	-9	SER	-	expression tag	UNP Q39VU7
C	-8	SER	-	expression tag	UNP Q39VU7
C	-7	GLY	-	expression tag	UNP Q39VU7
C	-6	LEU	-	expression tag	UNP Q39VU7
C	-5	VAL	-	expression tag	UNP Q39VU7
C	-4	PRO	-	expression tag	UNP Q39VU7
C	-3	ARG	-	expression tag	UNP Q39VU7
C	-2	GLY	-	expression tag	UNP Q39VU7
C	-1	SER	-	expression tag	UNP Q39VU7
C	0	HIS	-	expression tag	UNP Q39VU7
C	482	GLY	ALA	conflict	UNP Q39VU7
D	-19	MET	-	initiating methionine	UNP Q39VU7
D	-18	GLY	-	expression tag	UNP Q39VU7
D	-17	SER	-	expression tag	UNP Q39VU7
D	-16	SER	-	expression tag	UNP Q39VU7
D	-15	HIS	-	expression tag	UNP Q39VU7
D	-14	HIS	-	expression tag	UNP Q39VU7
D	-13	HIS	-	expression tag	UNP Q39VU7
D	-12	HIS	-	expression tag	UNP Q39VU7
D	-11	HIS	-	expression tag	UNP Q39VU7
D	-10	HIS	-	expression tag	UNP Q39VU7
D	-9	SER	-	expression tag	UNP Q39VU7
D	-8	SER	-	expression tag	UNP Q39VU7
D	-7	GLY	-	expression tag	UNP Q39VU7
D	-6	LEU	-	expression tag	UNP Q39VU7
D	-5	VAL	-	expression tag	UNP Q39VU7
D	-4	PRO	-	expression tag	UNP Q39VU7
D	-3	ARG	-	expression tag	UNP Q39VU7
D	-2	GLY	-	expression tag	UNP Q39VU7
D	-1	SER	-	expression tag	UNP Q39VU7
D	0	HIS	-	expression tag	UNP Q39VU7
D	482	GLY	ALA	conflict	UNP Q39VU7

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



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

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula:  $CH_2O_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	1	Total C O 3 1 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	1	Total O 1 1	0	0







## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	112.12Å 112.12Å 299.18Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.55 – 3.40 48.55 – 3.31	Depositor EDS
% Data completeness (in resolution range)	76.7 (48.55-3.40) 71.1 (48.55-3.31)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.21	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.47 (at 3.33Å)	Xtrriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, $R_{free}$	0.273 , 0.290 0.273 , 0.289	Depositor DCC
$R_{free}$ test set	1162 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	84.0	Xtrriage
Anisotropy	0.099	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 69.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.085 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	8356	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	86.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.57% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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: ADP, ZN, FMT, MG

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	B	0.33	0/2791	0.68	2/3806 (0.1%)
1	C	0.32	0/2846	0.70	0/3873
1	D	0.29	0/2782	0.56	0/3793
All	All	0.31	0/8419	0.65	2/11472 (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
1	D	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	472	LEU	CA-CB-CG	8.47	134.78	115.30
1	B	342	LEU	CA-CB-CG	6.32	129.83	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	204	ILE	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	B	2749	0	2553	75	0
1	C	2802	0	2667	68	0
1	D	2742	0	2489	77	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	B	27	0	12	1	0
3	C	27	0	12	2	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	D	3	0	2	0	0
6	C	1	0	0	0	0
All	All	8356	0	7735	210	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 13.

All (210) 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:D:543:ARG:O	1:D:547:LEU:HD13	1.51	1.10
1:D:475:ALA:O	1:D:477:VAL:N	1.88	1.05
1:D:477:VAL:HG22	1:D:547:LEU:HD23	1.46	0.97
1:C:543:ARG:HH12	1:C:566:ALA:HA	1.30	0.94
1:D:214:ARG:HD3	1:D:221:LEU:HD21	1.55	0.89
1:B:197:ARG:NH1	1:B:497:ASN:OD1	2.10	0.83
1:B:249:GLU:HG2	1:B:252:LEU:HD12	1.60	0.83
1:B:213:VAL:HB	1:B:225:MET:HB2	1.60	0.80
1:D:336:TYR:HE2	1:D:358:PHE:HB2	1.47	0.78
1:B:320:MET:HB3	1:B:415:VAL:HG23	1.64	0.78
1:C:324:THR:HG21	1:C:427:THR:HG21	1.66	0.77
1:D:475:ALA:O	1:D:477:VAL:HG23	1.85	0.76
1:C:213:VAL:HB	1:C:225:MET:HB2	1.66	0.76
1:C:543:ARG:NH1	1:C:566:ALA:HA	2.00	0.76
1:D:421:THR:HG22	1:D:430:ARG:HH11	1.49	0.76

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:346:THR:HG23	1:D:347:GLU:HG3	1.68	0.75
1:B:455:ARG:NE	1:B:559:GLU:OE2	2.14	0.74
1:D:421:THR:HG22	1:D:430:ARG:NH1	2.01	0.74
1:D:477:VAL:CG2	1:D:547:LEU:HD23	2.18	0.74
1:C:375:ASN:OD1	1:C:376:PHE:N	2.23	0.72
1:C:348:ASN:HD22	1:C:388:PRO:HA	1.55	0.71
1:D:423:ASP:HB3	1:D:425:PRO:HD2	1.72	0.71
1:C:351:THR:HG23	1:C:365:GLN:HA	1.73	0.71
1:D:514:LEU:HD22	1:D:537:LEU:HD13	1.72	0.70
1:B:277:THR:OG1	1:B:280:GLY:O	2.10	0.67
1:D:213:VAL:HB	1:D:225:MET:HB2	1.76	0.67
1:D:543:ARG:O	1:D:547:LEU:CD1	2.37	0.67
1:D:270:TYR:HE1	1:D:287:LEU:HD22	1.61	0.66
1:D:274:VAL:HG22	1:D:283:VAL:HG22	1.80	0.63
1:B:249:GLU:OE2	1:B:251:ARG:HB2	1.99	0.63
1:B:275:LEU:HD21	1:C:366:VAL:HG22	1.81	0.63
1:D:375:ASN:OD1	1:D:376:PHE:N	2.32	0.62
1:B:251:ARG:HH12	1:C:372:ILE:HG21	1.64	0.62
1:C:541:THR:HG22	1:C:542:MET:H	1.63	0.62
1:D:336:TYR:CE2	1:D:358:PHE:HB2	2.32	0.62
1:C:408:ALA:O	1:C:411:THR:HG22	2.00	0.61
1:C:319:GLY:HA3	1:C:446:ASN:OD1	1.99	0.61
1:D:541:THR:OG1	1:D:567:ASP:OD2	2.09	0.61
1:B:377:ALA:O	1:B:381:ARG:HG3	2.00	0.61
1:C:455:ARG:NE	1:C:559:GLU:OE2	2.25	0.61
1:D:563:VAL:HG23	1:D:564:THR:HG23	1.81	0.60
1:B:452:ARG:NH1	1:B:542:MET:SD	2.75	0.60
1:C:310:PHE:O	1:C:314:ILE:HG13	2.01	0.60
1:D:316:LYS:HE3	1:D:446:ASN:ND2	2.17	0.59
1:C:310:PHE:CE2	1:C:314:ILE:HD11	2.38	0.59
1:B:526:ASN:O	1:B:530:ILE:HD12	2.01	0.59
1:C:560:VAL:O	1:C:564:THR:HG22	2.03	0.58
1:B:391:ILE:HB	1:B:415:VAL:HG12	1.85	0.58
1:B:541:THR:HG22	1:B:542:MET:H	1.67	0.58
1:C:329:SER:OG	1:C:451:GLN:O	2.22	0.58
1:B:424:ALA:HB3	1:B:509:GLN:HE21	1.68	0.58
1:C:201:ASP:OD2	1:D:387:ASP:OD2	2.22	0.58
1:B:396:ILE:HG13	1:B:419:LEU:HD21	1.86	0.57
1:C:534:SER:HB2	1:C:539:ILE:HD11	1.85	0.57
1:B:563:VAL:HG23	1:B:564:THR:H	1.69	0.56
1:B:270:TYR:HB3	1:B:287:LEU:HA	1.87	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:517:ILE:O	1:D:521:ILE:HD12	2.05	0.56
1:B:477:VAL:HG12	1:B:478:SER:O	2.06	0.56
1:D:216:ARG:HA	1:D:221:LEU:HA	1.88	0.55
1:B:275:LEU:HD21	1:C:366:VAL:CG2	2.36	0.55
1:B:331:LYS:HA	1:B:451:GLN:NE2	2.21	0.55
1:D:470:GLN:NE2	1:D:474:ASP:OD1	2.39	0.55
1:D:399:PHE:HD1	1:D:434:MET:O	1.89	0.55
1:C:296:ASP:O	1:C:300:LEU:HD13	2.07	0.55
1:D:321:VAL:HB	1:D:416:LEU:HD23	1.89	0.55
1:D:212:ARG:HH21	1:D:214:ARG:HH21	1.54	0.55
1:D:201:ASP:HB2	1:D:216:ARG:HB3	1.90	0.54
1:C:423:ASP:OD1	1:C:424:ALA:N	2.37	0.54
1:D:215:TYR:CD2	1:D:224:VAL:HG21	2.43	0.54
1:B:320:MET:CG	1:B:445:VAL:HG12	2.37	0.53
1:D:270:TYR:CE1	1:D:287:LEU:HD22	2.43	0.53
1:D:469:ILE:O	1:D:473:ILE:N	2.33	0.53
1:D:399:PHE:CE2	1:D:403:GLU:HB2	2.43	0.53
1:D:559:GLU:OE2	1:D:562:ARG:NH2	2.30	0.53
1:D:208:GLU:HB2	1:D:279:PHE:CD1	2.44	0.53
1:D:303:GLU:HG3	1:D:304:PRO:HD2	1.91	0.53
1:C:293:LEU:HG	1:C:295:LEU:HD13	1.89	0.52
1:D:411:THR:HB	1:D:413:HIS:HD2	1.74	0.52
1:C:250:ARG:HA	1:C:281:GLU:OE2	2.09	0.52
1:C:303:GLU:HG2	1:C:304:PRO:HD2	1.91	0.52
1:D:406:ILE:HG21	1:D:440:LEU:HG	1.91	0.52
1:D:477:VAL:HG12	1:D:478:SER:N	2.23	0.52
1:D:541:THR:OG1	1:D:544:GLN:OE1	2.26	0.51
1:D:461:CYS:SG	1:D:493:CYS:HB3	2.51	0.51
1:B:329:SER:OG	1:B:452:ARG:HA	2.10	0.51
1:B:559:GLU:O	1:B:563:VAL:HG22	2.10	0.50
1:B:251:ARG:NH1	1:C:372:ILE:HG21	2.25	0.50
1:B:250:ARG:HA	1:B:281:GLU:OE2	2.12	0.50
1:D:547:LEU:N	1:D:547:LEU:HD12	2.27	0.50
1:B:218:ASP:HA	1:B:504:ARG:NH2	2.27	0.50
1:D:543:ARG:HH22	1:D:561:LEU:HD23	1.75	0.50
1:C:320:MET:HB3	1:C:445:VAL:HA	1.94	0.49
1:C:540:LYS:HE2	1:C:548:THR:HG21	1.94	0.49
1:D:321:VAL:HG13	1:D:447:LEU:HD23	1.94	0.49
1:B:278:LEU:HD11	1:C:356:VAL:HG21	1.94	0.49
1:C:380:LEU:HG	1:C:404:ILE:HG22	1.95	0.49
1:B:245:LEU:HD21	1:B:255:ASP:O	2.12	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:306:ALA:HA	1:C:510:VAL:HG21	1.95	0.49
1:B:296:ASP:HB3	1:B:299:LYS:HE2	1.95	0.49
1:B:541:THR:HG22	1:B:542:MET:N	2.28	0.49
1:C:216:ARG:NE	1:D:387:ASP:OD2	2.46	0.48
1:D:324:THR:HG22	1:D:419:LEU:HB2	1.95	0.48
1:D:282:LYS:HE2	1:D:284:VAL:CG2	2.43	0.48
1:B:218:ASP:HA	1:B:504:ARG:HH21	1.77	0.48
1:D:245:LEU:HD22	1:D:254:GLN:HB3	1.95	0.48
1:B:268:MET:HG3	1:B:270:TYR:CE2	2.49	0.48
1:D:243:ALA:HB3	1:D:245:LEU:HG	1.94	0.48
1:B:336:TYR:HD1	1:B:360:PHE:CE2	2.32	0.48
1:B:391:ILE:O	1:B:415:VAL:HA	2.13	0.48
1:D:452:ARG:HH11	1:D:542:MET:CE	2.25	0.48
1:D:212:ARG:NH2	1:D:214:ARG:HH21	2.12	0.48
1:B:199:ALA:O	1:B:287:LEU:HD12	2.14	0.48
1:B:214:ARG:HD3	1:B:221:LEU:HD21	1.95	0.48
1:C:332:THR:HG23	1:C:336:TYR:CE2	2.49	0.48
1:C:423:ASP:CG	1:C:425:PRO:HD2	2.34	0.48
1:D:419:LEU:HD12	1:D:427:THR:HG23	1.96	0.48
1:C:393:ILE:O	1:C:417:SER:HA	2.14	0.48
1:C:277:THR:HB	1:C:280:GLY:O	2.14	0.47
1:C:342:LEU:O	1:C:342:LEU:HD12	2.14	0.47
1:B:476:GLY:O	1:B:547:LEU:HD13	2.15	0.47
1:D:205:GLU:HB3	1:D:282:LYS:HG3	1.96	0.47
1:B:320:MET:CB	1:B:415:VAL:HG23	2.40	0.47
1:B:326:PRO:O	1:B:331:LYS:NZ	2.47	0.47
1:B:331:LYS:HD2	1:B:418:THR:OG1	2.15	0.47
1:B:543:ARG:O	1:B:547:LEU:HG	2.14	0.47
1:B:395:GLU:OE1	1:B:420:HIS:NE2	2.45	0.47
1:C:331:LYS:HA	1:C:451:GLN:NE2	2.30	0.47
1:D:458:CYS:SG	1:D:496:CYS:HB3	2.53	0.47
1:D:309:TYR:HB3	1:D:512:PRO:HG3	1.97	0.46
1:B:563:VAL:HG23	1:B:564:THR:N	2.30	0.46
1:B:203:HIS:HB2	1:B:214:ARG:HB2	1.97	0.46
1:B:208:GLU:HB2	1:B:279:PHE:CE2	2.51	0.46
1:C:378:ALA:HA	1:C:381:ARG:HG2	1.97	0.46
1:C:208:GLU:HB2	1:C:279:PHE:CZ	2.51	0.46
1:C:396:ILE:HG13	1:C:419:LEU:HD21	1.96	0.46
1:D:396:ILE:HG22	1:D:401:THR:HG22	1.98	0.46
1:C:205:GLU:OE2	1:C:212:ARG:NE	2.42	0.46
1:B:190:ILE:O	1:B:215:TYR:OH	2.30	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:331:LYS:HB2	3:B:602:ADP:O2B	2.15	0.46
1:C:541:THR:HG22	1:C:542:MET:N	2.29	0.46
1:B:275:LEU:HD11	1:C:383:PHE:HE1	1.81	0.46
1:C:272:VAL:HG12	1:C:285:LEU:CD2	2.46	0.46
1:D:352:ALA:HB1	1:D:368:MET:CE	2.46	0.46
1:B:544:GLN:HA	1:B:547:LEU:HD12	1.98	0.45
1:C:441:VAL:O	1:C:445:VAL:HG22	2.16	0.45
1:B:208:GLU:HB2	1:B:279:PHE:CZ	2.50	0.45
1:B:329:SER:OG	1:B:451:GLN:O	2.33	0.45
1:B:374:LEU:HD11	1:B:379:ALA:HB2	1.99	0.45
1:B:454:ALA:HB1	1:B:559:GLU:HB3	1.99	0.45
1:C:303:GLU:CG	1:C:304:PRO:HD2	2.46	0.45
1:D:477:VAL:CG1	1:D:478:SER:N	2.79	0.45
1:D:533:GLU:OE2	1:D:536:ARG:NH1	2.50	0.45
1:B:303:GLU:HG3	1:B:304:PRO:HD2	1.99	0.45
1:C:314:ILE:HG22	1:C:342:LEU:HD21	1.99	0.45
1:B:238:ARG:NH2	1:B:242:MET:SD	2.90	0.45
1:D:452:ARG:NH1	1:D:542:MET:HE3	2.31	0.44
1:B:441:VAL:O	1:B:445:VAL:HG22	2.17	0.44
1:C:181:ALA:O	1:C:184:VAL:HG12	2.17	0.44
1:D:214:ARG:CD	1:D:221:LEU:HD21	2.37	0.44
1:B:445:VAL:HG23	1:B:513:MET:SD	2.57	0.44
1:C:351:THR:HG21	1:C:365:GLN:HG2	2.00	0.44
1:C:330:GLY:HA2	3:C:602:ADP:O2A	2.18	0.44
1:B:224:VAL:HG23	1:B:225:MET:HG3	2.00	0.43
1:D:347:GLU:HA	1:D:389:ASP:OD2	2.18	0.43
1:C:256:GLY:C	1:C:272:VAL:HG22	2.39	0.43
1:C:203:HIS:HB2	1:C:214:ARG:HB2	1.99	0.43
1:B:319:GLY:O	1:B:414:LEU:HA	2.18	0.43
1:B:369:HIS:NE2	1:B:371:ASP:HB2	2.34	0.43
1:B:370:GLU:HA	1:B:374:LEU:O	2.19	0.43
1:B:270:TYR:CB	1:B:287:LEU:HA	2.48	0.43
1:B:228:PRO:HG2	1:B:231:LEU:HD13	2.01	0.43
1:B:398:ASP:OD1	1:B:398:ASP:N	2.52	0.42
1:D:353:GLU:HG3	1:D:356:VAL:HA	2.00	0.42
1:D:477:VAL:CG2	1:D:547:LEU:CD2	2.94	0.42
1:D:452:ARG:NH1	1:D:542:MET:CE	2.82	0.42
1:B:278:LEU:CD1	1:C:356:VAL:HG21	2.49	0.42
1:C:458:CYS:HB3	1:C:461:CYS:SG	2.59	0.42
1:D:447:LEU:HD11	1:D:510:VAL:HG22	2.02	0.42
1:B:456:ARG:HH21	1:B:505:VAL:CG1	2.32	0.42

*Continued on next page...*



Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:353:GLU:HB2	1:B:356:VAL:HG22	2.00	0.42
1:C:351:THR:CG2	1:C:365:GLN:HG2	2.49	0.42
1:C:396:ILE:HG22	1:C:401:THR:HG22	2.02	0.42
1:D:388:PRO:O	1:D:413:HIS:ND1	2.52	0.42
1:B:212:ARG:NH2	1:B:214:ARG:NH1	2.67	0.42
1:D:383:PHE:O	1:D:388:PRO:HD3	2.19	0.42
1:C:276:PRO:O	1:D:366:VAL:HG12	2.19	0.42
1:D:547:LEU:CD1	1:D:547:LEU:N	2.82	0.42
1:C:186:LEU:HD12	1:C:186:LEU:O	2.19	0.41
1:D:487:CYS:HB3	1:D:550:LEU:HD21	2.01	0.41
1:D:249:GLU:OE2	1:D:251:ARG:HG3	2.19	0.41
1:D:250:ARG:CB	1:D:281:GLU:OE2	2.67	0.41
1:C:199:ALA:O	1:C:287:LEU:HD21	2.20	0.41
1:B:218:ASP:OD2	1:B:503:GLY:N	2.49	0.41
1:D:406:ILE:HG23	1:D:444:ALA:HB2	2.02	0.41
1:B:451:GLN:OE1	1:B:508:TYR:CE1	2.74	0.41
1:B:526:ASN:CG	1:B:527:THR:H	2.23	0.41
1:C:272:VAL:HG12	1:C:285:LEU:HD23	2.03	0.41
1:D:543:ARG:HH22	1:D:561:LEU:CD2	2.33	0.41
1:B:200:SER:N	1:B:216:ARG:O	2.51	0.41
1:D:376:PHE:O	1:D:380:LEU:HD13	2.21	0.41
1:C:352:ALA:HB2	1:C:383:PHE:CZ	2.56	0.40
1:C:372:ILE:HD11	1:C:374:LEU:HD13	2.04	0.40
1:C:310:PHE:CD2	1:C:314:ILE:HD11	2.56	0.40
1:C:323:VAL:HG21	1:C:335:LEU:HD13	2.04	0.40
1:C:331:LYS:N	3:C:602:ADP:O1B	2.54	0.40
1:D:458:CYS:HB2	1:D:461:CYS:HB2	2.04	0.40
1:B:383:PHE:O	1:B:388:PRO:HD3	2.22	0.40
1:B:232:LYS:O	1:B:236:THR:HG23	2.22	0.40
1:C:297:MET:HE1	1:C:310:PHE:HD2	1.86	0.40
1:C:396:ILE:HG13	1:C:396:ILE:O	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	B	380/588 (65%)	373 (98%)	7 (2%)	0	100	100
1	C	377/588 (64%)	374 (99%)	3 (1%)	0	100	100
1	D	378/588 (64%)	373 (99%)	5 (1%)	0	100	100
All	All	1135/1764 (64%)	1120 (99%)	15 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	B	250/501 (50%)	247 (99%)	3 (1%)	71	85
1	C	273/501 (54%)	272 (100%)	1 (0%)	91	95
1	D	251/501 (50%)	251 (100%)	0	100	100
All	All	774/1503 (52%)	770 (100%)	4 (0%)	88	94

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	342	LEU
1	B	414	LEU
1	B	472	LEU
1	C	295	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	451	GLN
1	C	348	ASN
1	D	446	ASN
1	D	470	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 8 ligands modelled in this entry, 5 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
5	FMT	D	602	-	2,2,2	3.08	2 (100%)	1,1,1	2.22	1 (100%)
3	ADP	B	602	4	24,29,29	0.99	2 (8%)	29,45,45	1.44	4 (13%)
3	ADP	C	602	4	24,29,29	1.04	3 (12%)	29,45,45	1.54	6 (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
3	ADP	B	602	4	-	2/12/32/32	0/3/3/3
3	ADP	C	602	4	-	5/12/32/32	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	602	FMT	O1-C	3.52	1.40	1.22
3	B	602	ADP	C5-C4	2.60	1.47	1.40
5	D	602	FMT	O2-C	2.57	1.41	1.28
3	C	602	ADP	C5-C4	2.54	1.47	1.40
3	C	602	ADP	C2-N3	2.16	1.35	1.32
3	B	602	ADP	O4'-C1'	2.10	1.44	1.41
3	C	602	ADP	O4'-C1'	2.07	1.44	1.41

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	602	ADP	PA-O3A-PB	-4.12	118.68	132.83
3	B	602	ADP	N3-C2-N1	-3.43	123.31	128.68
3	C	602	ADP	N3-C2-N1	-3.30	123.52	128.68
3	B	602	ADP	PA-O3A-PB	-3.05	122.37	132.83
3	B	602	ADP	C3'-C2'-C1'	3.03	105.54	100.98
3	C	602	ADP	C3'-C2'-C1'	2.84	105.25	100.98
3	C	602	ADP	C4-C5-N7	-2.74	106.54	109.40
3	B	602	ADP	C4-C5-N7	-2.27	107.03	109.40
5	D	602	FMT	O2-C-O1	-2.22	102.58	126.69
3	C	602	ADP	O3B-PB-O2B	2.15	115.86	107.64
3	C	602	ADP	C2'-C3'-C4'	2.15	106.81	102.64

There are no chirality outliers.

All (7) torsion outliers are listed below:

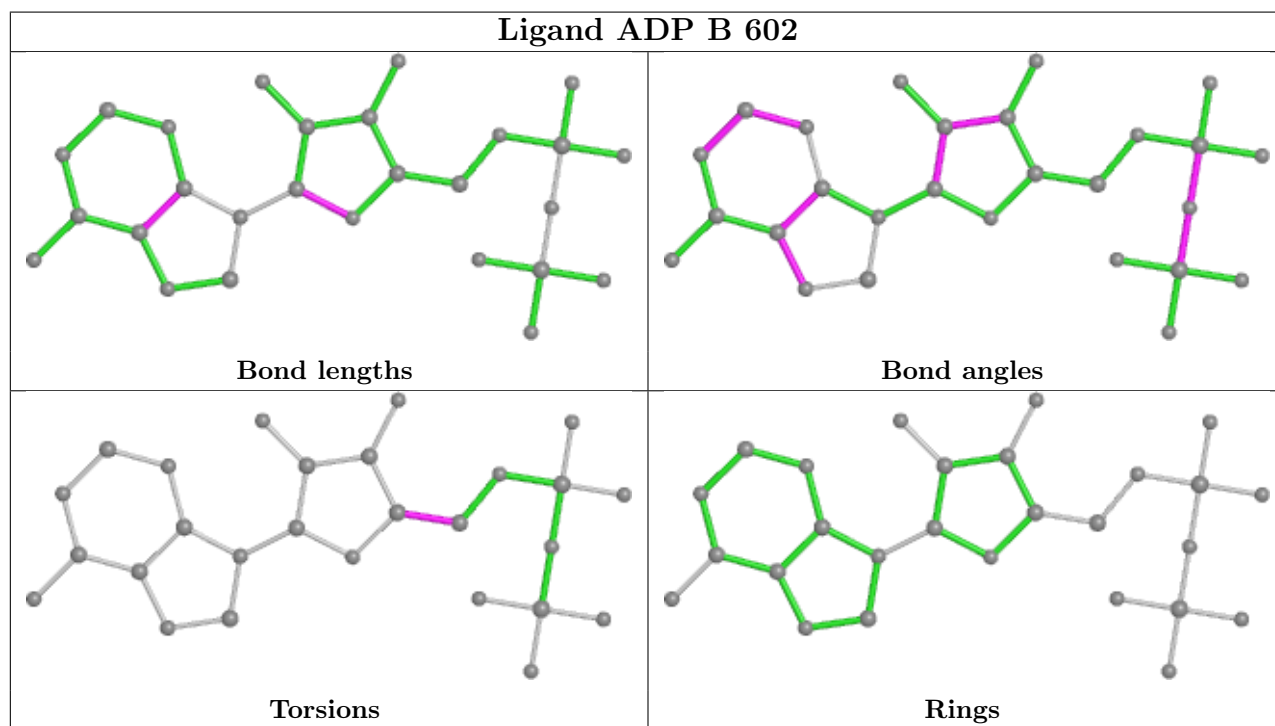
Mol	Chain	Res	Type	Atoms
3	C	602	ADP	C5'-O5'-PA-O1A
3	C	602	ADP	C5'-O5'-PA-O2A
3	C	602	ADP	C5'-O5'-PA-O3A
3	C	602	ADP	O4'-C4'-C5'-O5'
3	B	602	ADP	C3'-C4'-C5'-O5'
3	B	602	ADP	O4'-C4'-C5'-O5'
3	C	602	ADP	C3'-C4'-C5'-O5'

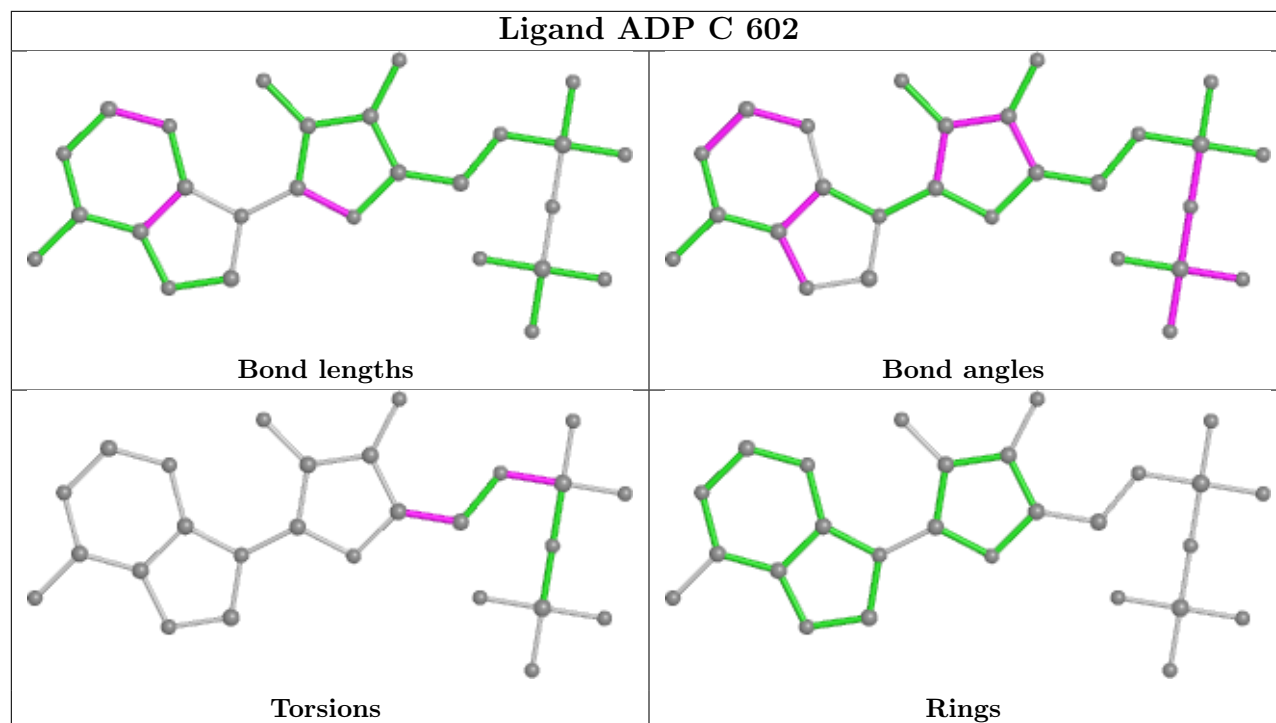
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	ADP	1	0
3	C	602	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 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	B	384/588 (65%)	-0.20	2 (0%) 91   90	63, 89, 113, 123	0
1	C	381/588 (64%)	-0.33	0 100   100	61, 78, 98, 118	0
1	D	384/588 (65%)	-0.17	0 100   100	66, 86, 122, 144	0
All	All	1149/1764 (65%)	-0.23	2 (0%) 95   95	61, 85, 115, 144	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	482	GLY	2.3
1	B	362	GLY	2.1

### 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, 95<sup>th</sup> 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.

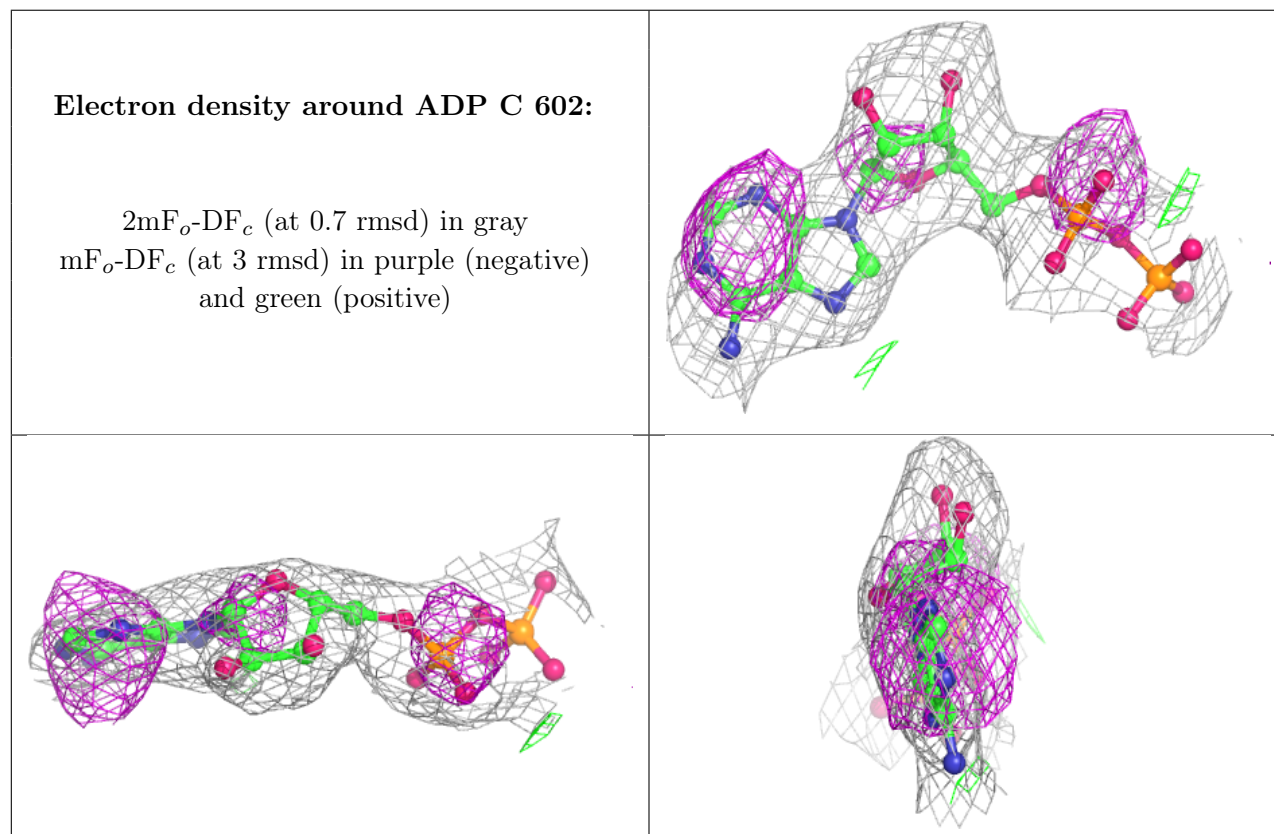
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	ADP	C	602	27/27	0.90	0.19	45,46,48,49	0

*Continued on next page...*

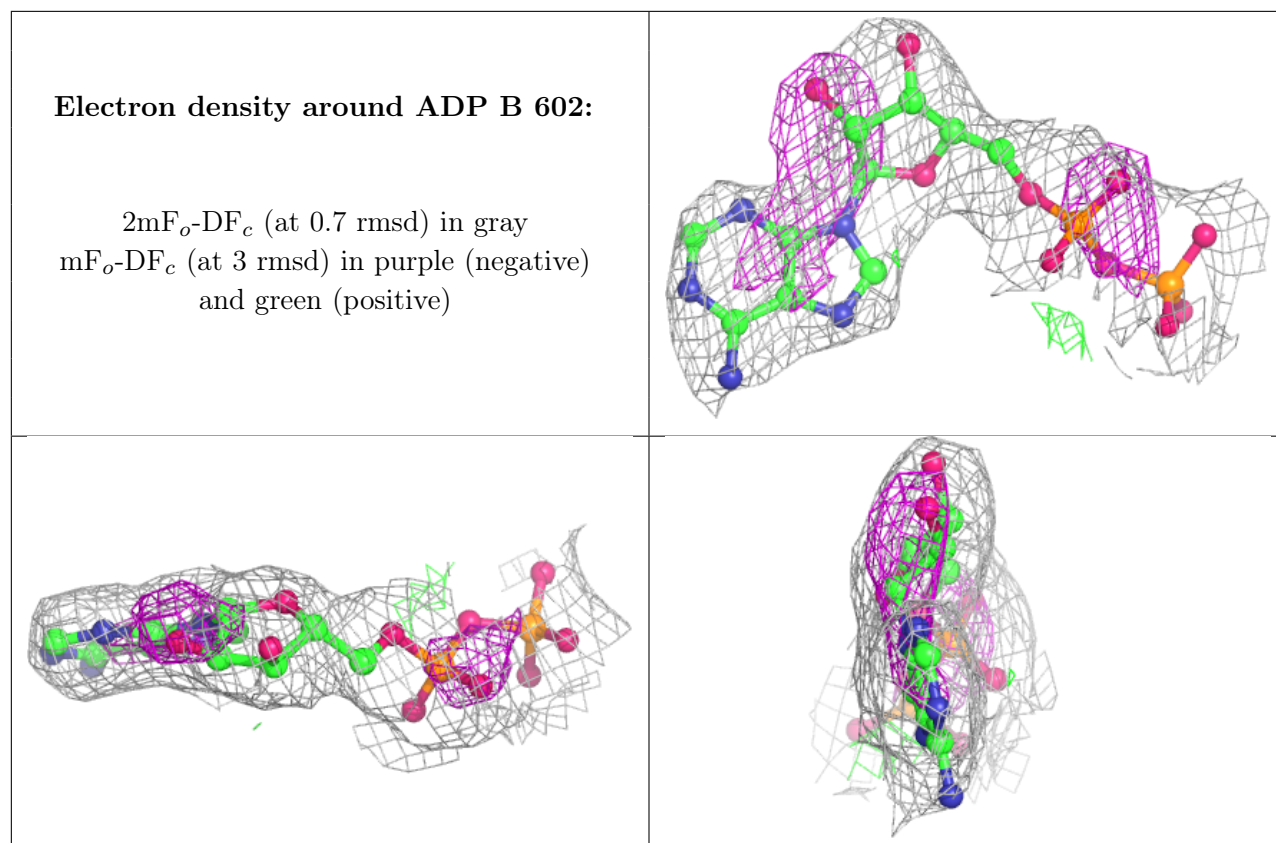
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MG	B	603	1/1	0.90	0.23	10,10,10,10	0
3	ADP	B	602	27/27	0.92	0.18	59,60,60,60	0
4	MG	C	603	1/1	0.97	0.09	10,10,10,10	0
5	FMT	D	602	3/3	0.97	0.25	16,16,16,16	0
2	ZN	D	601	1/1	0.99	0.03	16,16,16,16	0
2	ZN	B	601	1/1	0.99	0.03	16,16,16,16	0
2	ZN	C	601	1/1	0.99	0.06	16,16,16,16	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.