



# Full wwPDB X-ray Structure Validation Report i

Oct 27, 2021 – 07:07 am BST

PDB ID : 7O4A  
Title : Crystal structure of Penicillin-Binding Protein 1 (PBP1) from *Staphylococcus aureus* in complex with piperacillin  
Authors : Martinez Caballero, S.; Hermoso, J.A.  
Deposited on : 2021-04-05  
Resolution : 3.03 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 i symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

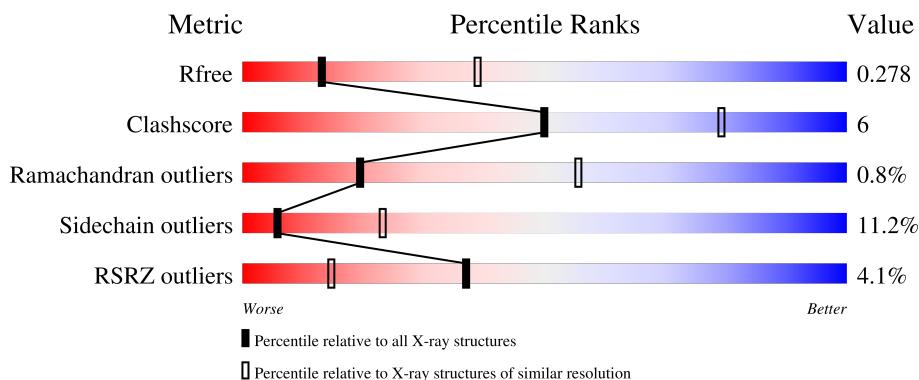
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## X-RAY DIFFRACTION

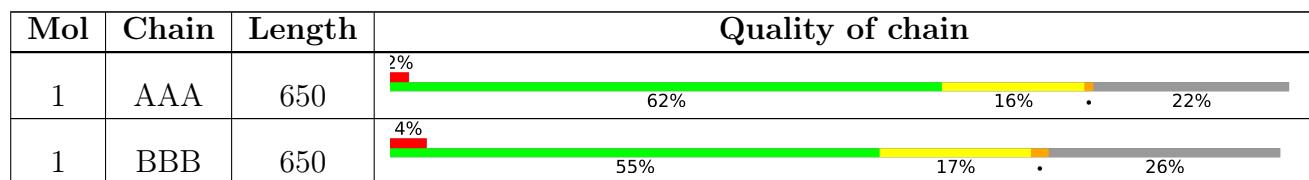
The reported resolution of this entry is 3.03 Å.

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	2399 (3.04-3.00)
Clashscore	141614	2734 (3.04-3.00)
Ramachandran outliers	138981	2640 (3.04-3.00)
Sidechain outliers	138945	2643 (3.04-3.00)
RSRZ outliers	127900	2287 (3.04-3.00)

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.



## 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7840 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.

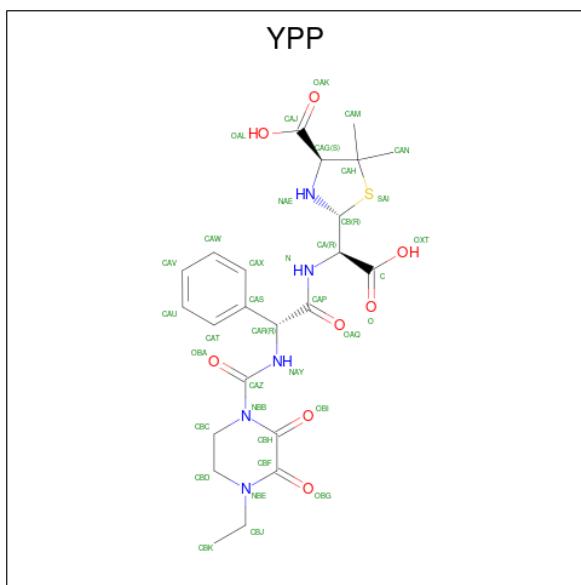
- Molecule 1 is a protein called Penicillin-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	510	4012	2542	690	764	16	0	0	0
1	BBB	478	3756	2383	641	716	16	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	64	MET	-	initiating methionine	UNP A0A0H2WVW5
BBB	64	MET	-	initiating methionine	UNP A0A0H2WVW5

- Molecule 2 is Hydrolyzed piperacillin (three-letter code: YPP) (formula: C<sub>23</sub>H<sub>29</sub>N<sub>5</sub>O<sub>8</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	AAA	1	36	23	5	7	1	0	0

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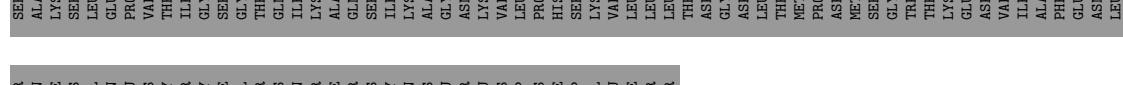
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	BBB	1	36	23	5	7	1	0	0

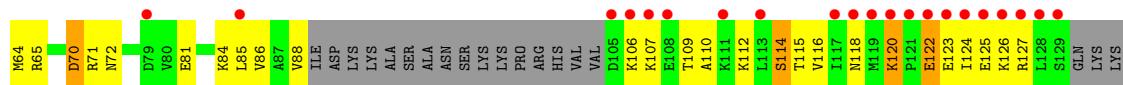
### 3 Residue-property plots [\(i\)](#)

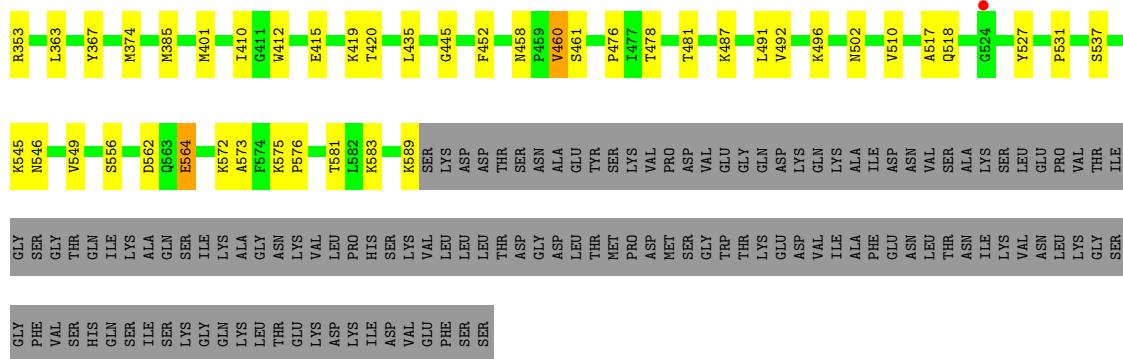
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: Penicillin-binding protein 1



- Molecule 1: Penicillin-binding protein 1





## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	178.69Å    178.69Å    223.65Å 90.00°    90.00°    120.00°	Depositor
Resolution (Å)	47.39 – 3.03 47.40 – 3.03	Depositor EDS
% Data completeness (in resolution range)	63.3 (47.39-3.03) 63.4 (47.40-3.03)	Depositor EDS
$R_{merge}$	0.33	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle^1$	2.74 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
$R$ , $R_{free}$	0.212 , 0.278 0.216 , 0.278	Depositor DCC
$R_{free}$ test set	1339 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	74.2	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7840	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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:  
YPP

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	AAA	0.68	1/4096 (0.0%)	0.88	1/5506 (0.0%)
1	BBB	0.69	1/3834 (0.0%)	0.87	1/5154 (0.0%)
All	All	0.69	2/7930 (0.0%)	0.87	2/10660 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	314	SER	CB-OG	7.98	1.52	1.42
1	AAA	314	SER	CB-OG	7.75	1.52	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	314	SER	CA-CB-OG	7.55	131.58	111.20
1	BBB	314	SER	CA-CB-OG	7.41	131.21	111.20

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts i

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AAA	4012	0	3998	42	0
1	BBB	3756	0	3724	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AAA	36	0	27	2	0
2	BBB	36	0	27	2	0
All	All	7840	0	7776	90	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 6.

All (90) 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:BBB:458:ASN:OD1	1:BBB:460:VAL:HG23	1.87	0.73
1:BBB:326:GLN:NE2	1:BBB:481:THR:OG1	2.30	0.65
1:AAA:260:VAL:O	1:AAA:264:GLN:HG2	1.97	0.64
1:BBB:314:SER:OG	2:BBB:801:YPP:NAE	2.34	0.60
1:BBB:71:ARG:NH1	1:BBB:243:THR:O	2.34	0.59
1:AAA:314:SER:OG	2:AAA:801:YPP:NAE	2.36	0.58
1:BBB:109:THR:HG22	1:BBB:158:LEU:HD22	1.86	0.58
1:BBB:260:VAL:O	1:BBB:264:GLN:HG2	2.03	0.58
1:BBB:236:ARG:NH2	1:BBB:237:GLY:O	2.38	0.57
1:AAA:71:ARG:NH1	1:AAA:243:THR:O	2.38	0.56
1:AAA:92:LYS:N	1:AAA:92:LYS:HD2	2.21	0.55
1:AAA:110:ALA:HA	1:AAA:124:ILE:HG21	1.88	0.55
1:AAA:240:VAL:HG13	1:AAA:456:VAL:HG22	1.87	0.55
1:AAA:143:THR:HG22	1:AAA:166:GLU:OE2	2.07	0.55
1:AAA:436:GLN:O	1:AAA:439:SER:OG	2.24	0.55
1:BBB:182:GLY:HA3	1:BBB:197:LEU:O	2.07	0.54
1:BBB:271:VAL:HG11	1:BBB:435:LEU:HD11	1.90	0.53
1:BBB:274:ASP:HB3	1:BBB:277:THR:OG1	2.09	0.53
1:AAA:335:LYS:HA	1:AAA:359:ILE:O	2.10	0.52
1:BBB:348:ILE:HD11	1:BBB:374:MET:SD	2.49	0.52
1:AAA:271:VAL:HG11	1:AAA:435:LEU:HD11	1.92	0.52
1:AAA:114:SER:O	1:AAA:115:THR:OG1	2.23	0.51
1:AAA:182:GLY:HA3	1:AAA:197:LEU:O	2.10	0.51
1:BBB:70:ASP:OD1	1:BBB:72:ASN:N	2.43	0.51
1:BBB:363:LEU:HG	1:BBB:367:TYR:CE2	2.46	0.51
1:BBB:114:SER:O	1:BBB:115:THR:OG1	2.24	0.51
1:AAA:326:GLN:HE22	1:AAA:478:THR:HG23	1.77	0.50
1:AAA:274:ASP:HB3	1:AAA:277:THR:OG1	2.12	0.50
1:BBB:326:GLN:HE22	1:BBB:478:THR:HG23	1.76	0.49
1:AAA:105:ASP:HB3	1:AAA:108:GLU:HB3	1.95	0.48
1:AAA:460:VAL:HG12	1:AAA:461:SER:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:88:VAL:HG21	1:BBB:160:GLY:O	2.13	0.48
1:BBB:106:LYS:HB3	1:BBB:125:GLU:OE2	2.12	0.48
1:BBB:518:GLN:HB3	1:BBB:527:TYR:HD2	1.78	0.48
1:BBB:518:GLN:HB3	1:BBB:527:TYR:CD2	2.48	0.48
1:BBB:138:PHE:O	1:BBB:142:GLY:HA3	2.14	0.48
1:BBB:289:PHE:HB2	1:BBB:295:LYS:O	2.13	0.47
1:BBB:107:LYS:CG	1:BBB:125:GLU:HG3	2.45	0.47
1:AAA:164:LEU:N	1:AAA:164:LEU:HD23	2.30	0.47
1:BBB:123:GLU:OE2	1:BBB:127:ARG:HG3	2.16	0.46
1:BBB:120:LYS:HE2	1:BBB:122:GLU:HG3	1.98	0.45
1:AAA:70:ASP:OD1	1:AAA:72:ASN:N	2.48	0.45
1:AAA:207:LEU:O	1:AAA:237:GLY:HA3	2.17	0.45
1:BBB:248:ILE:HD13	1:BBB:581:THR:HG23	1.98	0.45
1:AAA:491:LEU:O	1:AAA:492:VAL:C	2.55	0.45
1:AAA:150:LYS:HB2	1:AAA:163:LEU:HD13	1.99	0.44
1:BBB:289:PHE:HA	1:BBB:296:ASP:HB2	1.99	0.44
1:BBB:589:LYS:HE2	1:BBB:589:LYS:HB2	1.89	0.44
1:AAA:150:LYS:HA	1:AAA:163:LEU:CD1	2.48	0.44
1:AAA:206:TYR:N	1:AAA:206:TYR:CD1	2.85	0.44
1:AAA:487:LYS:O	1:AAA:491:LEU:HG	2.18	0.44
1:BBB:573:ALA:O	1:BBB:576:PRO:HG2	2.18	0.44
1:BBB:250:VAL:HG12	1:BBB:251:PHE:N	2.32	0.44
1:AAA:536:VAL:HG21	1:AAA:569:GLY:HA2	2.00	0.43
1:BBB:207:LEU:O	1:BBB:237:GLY:HA3	2.18	0.43
1:BBB:531:PRO:HG2	1:BBB:562:ASP:OD2	2.18	0.43
1:AAA:445:GLY:HA2	1:AAA:477:ILE:HG13	2.00	0.43
1:AAA:511:GLU:OE2	1:AAA:541:ASP:OD2	2.36	0.43
1:AAA:206:TYR:N	1:AAA:206:TYR:HD1	2.17	0.43
1:AAA:386:LYS:HD2	1:AAA:412:TRP:CD1	2.54	0.43
1:AAA:351:TRP:HB3	2:AAA:801:YPP:SAI	2.58	0.43
1:BBB:343:ILE:CD1	1:BBB:419:LYS:HG3	2.49	0.43
1:BBB:491:LEU:O	1:BBB:492:VAL:C	2.56	0.43
1:BBB:340:HIS:HA	1:BBB:349:SER:HA	2.01	0.42
1:BBB:206:TYR:N	1:BBB:206:TYR:CD1	2.86	0.42
1:AAA:166:GLU:OE2	1:AAA:168:GLU:OE2	2.38	0.42
1:BBB:348:ILE:CD1	1:BBB:374:MET:SD	3.08	0.42
1:AAA:302:ALA:HA	1:AAA:307:GLN:OE1	2.20	0.42
1:BBB:206:TYR:N	1:BBB:206:TYR:HD1	2.17	0.42
1:BBB:351:TRP:HB3	2:BBB:801:YPP:SAI	2.59	0.42
1:BBB:313:GLY:HA3	1:BBB:517:ALA:HB2	2.02	0.42
1:AAA:326:GLN:NE2	1:AAA:481:THR:OG1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:263:TYR:HB3	1:AAA:558:ALA:HB1	2.01	0.41
1:AAA:250:VAL:HG12	1:AAA:251:PHE:N	2.34	0.41
1:AAA:313:GLY:HA3	1:AAA:517:ALA:HB2	2.03	0.41
1:AAA:560:LYS:HG2	1:AAA:561:ASN:HD22	1.86	0.41
1:AAA:573:ALA:O	1:AAA:576:PRO:HG2	2.21	0.41
1:AAA:163:LEU:HD23	1:AAA:163:LEU:HA	1.83	0.41
1:BBB:445:GLY:O	1:BBB:476:PRO:HD2	2.21	0.41
1:AAA:412:TRP:CD2	1:AAA:418:GLN:HG2	2.55	0.41
1:AAA:542:ALA:HB3	1:AAA:582:LEU:HD11	2.03	0.41
1:BBB:107:LYS:HG2	1:BBB:125:GLU:CG	2.50	0.41
1:BBB:575:LYS:N	1:BBB:576:PRO:HD2	2.36	0.41
1:AAA:267:ASP:OD1	1:AAA:300:LYS:NZ	2.53	0.40
1:BBB:65:ARG:HD3	1:BBB:169:ARG:HH11	1.85	0.40
1:BBB:458:ASN:HB3	1:BBB:461:SER:OG	2.21	0.40
1:BBB:110:ALA:HA	1:BBB:124:ILE:HG21	2.03	0.40
1:BBB:289:PHE:CB	1:BBB:296:ASP:HB2	2.52	0.40
1:BBB:180:LEU:HD11	1:BBB:452:PHE:CD2	2.57	0.40
1:BBB:263:TYR:OH	1:BBB:572:LYS:HD2	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	AAA	506/650 (78%)	448 (88%)	54 (11%)	4 (1%)	19 55
1	BBB	470/650 (72%)	416 (88%)	50 (11%)	4 (1%)	17 53
All	All	976/1300 (75%)	864 (88%)	104 (11%)	8 (1%)	19 55

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	526	GLY
1	AAA	593	ASP
1	AAA	132	LYS
1	BBB	299	LYS
1	BBB	564	GLU
1	AAA	545	LYS
1	BBB	545	LYS
1	BBB	160	GLY

### 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	AAA	430/552 (78%)	389 (90%)	41 (10%)	8 31
1	BBB	401/552 (73%)	349 (87%)	52 (13%)	4 18
All	All	831/1104 (75%)	738 (89%)	93 (11%)	6 23

All (93) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	64	MET
1	AAA	65	ARG
1	AAA	70	ASP
1	AAA	84	LYS
1	AAA	91	LYS
1	AAA	92	LYS
1	AAA	94	SER
1	AAA	98	LYS
1	AAA	99	LYS
1	AAA	114	SER
1	AAA	118	ASN
1	AAA	120	LYS
1	AAA	126	LYS
1	AAA	131	LYS
1	AAA	141	LYS
1	AAA	173	ASN

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Mol	Chain	Res	Type
1	AAA	179	HIS
1	AAA	183	ARG
1	AAA	207	LEU
1	AAA	208	SER
1	AAA	235	LYS
1	AAA	240	VAL
1	AAA	256	LEU
1	AAA	261	GLU
1	AAA	321	LEU
1	AAA	337	LYS
1	AAA	347	ARG
1	AAA	348	ILE
1	AAA	349	SER
1	AAA	409	GLN
1	AAA	412	TRP
1	AAA	420	THR
1	AAA	496	LYS
1	AAA	497	LYS
1	AAA	518	GLN
1	AAA	529	LYS
1	AAA	549	VAL
1	AAA	556	SER
1	AAA	587	VAL
1	AAA	589	LYS
1	AAA	591	LYS
1	BBB	64	MET
1	BBB	70	ASP
1	BBB	81	GLU
1	BBB	84	LYS
1	BBB	85	LEU
1	BBB	86	VAL
1	BBB	112	LYS
1	BBB	114	SER
1	BBB	116	VAL
1	BBB	118	ASN
1	BBB	120	LYS
1	BBB	122	GLU
1	BBB	126	LYS
1	BBB	141	LYS
1	BBB	143	THR
1	BBB	144	ASN
1	BBB	150	LYS

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Mol	Chain	Res	Type
1	BBB	159	PRO
1	BBB	163	LEU
1	BBB	166	GLU
1	BBB	179	HIS
1	BBB	189	ASP
1	BBB	192	GLU
1	BBB	208	SER
1	BBB	238	ASP
1	BBB	256	LEU
1	BBB	260	VAL
1	BBB	261	GLU
1	BBB	286	ARG
1	BBB	326	GLN
1	BBB	337	LYS
1	BBB	343	ILE
1	BBB	347	ARG
1	BBB	349	SER
1	BBB	353	ARG
1	BBB	385	MET
1	BBB	401	MET
1	BBB	410	ILE
1	BBB	412	TRP
1	BBB	415	GLU
1	BBB	420	THR
1	BBB	460	VAL
1	BBB	487	LYS
1	BBB	496	LYS
1	BBB	502	ASN
1	BBB	510	VAL
1	BBB	537	SER
1	BBB	546	ASN
1	BBB	549	VAL
1	BBB	556	SER
1	BBB	564	GLU
1	BBB	583	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 [\(i\)](#)

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
2	YPP	AAA	801	1	31,38,39	4.34	11 (35%)	39,55,57	3.06	17 (43%)
2	YPP	BBB	801	1	31,38,39	4.15	10 (32%)	39,55,57	3.01	16 (41%)

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	YPP	AAA	801	1	-	5/22/64/66	0/3/3/3
2	YPP	BBB	801	1	-	6/22/64/66	0/3/3/3

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	801	YPP	OBA-CAZ	10.81	1.42	1.23
2	AAA	801	YPP	OBA-CAZ	10.80	1.42	1.23
2	AAA	801	YPP	OBG-CBF	9.98	1.44	1.23
2	AAA	801	YPP	OAQ-CAP	9.78	1.42	1.23
2	AAA	801	YPP	OBI-CBH	9.57	1.43	1.23
2	BBB	801	YPP	OAQ-CAP	9.45	1.42	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	801	YPP	OBG-CBF	9.29	1.42	1.23
2	BBB	801	YPP	OBI-CBH	9.27	1.42	1.23
2	AAA	801	YPP	CBH-CBF	-8.10	1.40	1.53
2	BBB	801	YPP	CBH-CBF	-7.41	1.41	1.53
2	AAA	801	YPP	CBD-NBE	-7.18	1.34	1.47
2	BBB	801	YPP	CBD-NBE	-6.70	1.35	1.47
2	AAA	801	YPP	CBC-NBB	-5.02	1.39	1.48
2	BBB	801	YPP	CBC-NBB	-4.72	1.40	1.48
2	AAA	801	YPP	CBD-CBC	-2.94	1.40	1.51
2	AAA	801	YPP	CAH-SAI	-2.64	1.80	1.85
2	BBB	801	YPP	CBD-CBC	-2.35	1.42	1.51
2	AAA	801	YPP	CB-SAI	-2.27	1.79	1.84
2	AAA	801	YPP	CAS-CAR	-2.20	1.49	1.52
2	BBB	801	YPP	CAG-NAE	2.11	1.49	1.46
2	BBB	801	YPP	CB-SAI	-2.10	1.79	1.84

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	BBB	801	YPP	CA-N-CAP	-7.90	114.49	123.12
2	AAA	801	YPP	CA-N-CAP	-7.34	115.11	123.12
2	AAA	801	YPP	NAY-CAZ-NBB	7.04	124.28	114.04
2	BBB	801	YPP	NAY-CAZ-NBB	6.87	124.03	114.04
2	AAA	801	YPP	CBD-CBC-NBB	5.95	119.99	108.78
2	AAA	801	YPP	CBD-NBE-CBF	5.50	131.21	120.69
2	AAA	801	YPP	OBG-CBF-NBE	5.28	129.15	123.66
2	AAA	801	YPP	CBJ-NBE-CBF	-5.02	113.62	119.64
2	BBB	801	YPP	CBD-CBC-NBB	4.85	117.93	108.78
2	BBB	801	YPP	CBD-NBE-CBF	4.73	129.73	120.69
2	BBB	801	YPP	OAQ-CAP-N	-4.64	114.33	122.93
2	AAA	801	YPP	OAQ-CAP-N	-4.63	114.35	122.93
2	BBB	801	YPP	CBJ-NBE-CBF	-4.59	114.13	119.64
2	AAA	801	YPP	OBA-CAZ-NBB	4.40	124.72	119.78
2	AAA	801	YPP	OBA-CAZ-NAY	-4.31	110.99	123.05
2	BBB	801	YPP	CAN-CAH-SAI	-4.30	102.00	109.21
2	BBB	801	YPP	OBA-CAZ-NBB	4.29	124.59	119.78
2	BBB	801	YPP	OBA-CAZ-NAY	-4.18	111.36	123.05
2	BBB	801	YPP	CAR-NAY-CAZ	-4.14	113.35	121.17
2	BBB	801	YPP	OBG-CBF-NBE	4.09	127.92	123.66
2	AAA	801	YPP	CAR-NAY-CAZ	-3.76	114.05	121.17
2	BBB	801	YPP	CAM-CAH-SAI	3.46	115.02	109.21
2	AAA	801	YPP	CAN-CAH-SAI	-3.32	103.64	109.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	BBB	801	YPP	CAX-CAS-CAT	3.10	122.16	118.29
2	BBB	801	YPP	CAH-SAI-CB	-2.97	87.63	93.99
2	AAA	801	YPP	CAH-SAI-CB	-2.58	88.46	93.99
2	AAA	801	YPP	CAS-CAR-NAY	-2.55	106.28	112.89
2	BBB	801	YPP	CAR-CAP-N	2.50	123.29	116.82
2	AAA	801	YPP	CAM-CAH-SAI	2.49	113.39	109.21
2	AAA	801	YPP	CAR-CAP-N	2.46	123.19	116.82
2	BBB	801	YPP	CAG-CAH-SAI	2.29	108.34	103.81
2	AAA	801	YPP	CAG-CAH-SAI	2.24	108.25	103.81
2	AAA	801	YPP	CAX-CAS-CAT	2.14	120.96	118.29

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AAA	801	YPP	N-CAP-CAR-CAS
2	AAA	801	YPP	OAQ-CAP-CAR-CAS
2	AAA	801	YPP	CBK-CBJ-NBE-CBD
2	BBB	801	YPP	N-CAP-CAR-CAS
2	BBB	801	YPP	OAQ-CAP-CAR-CAS
2	BBB	801	YPP	OAQ-CAP-CAR-NAY
2	BBB	801	YPP	CBK-CBJ-NBE-CBD
2	BBB	801	YPP	N-CAP-CAR-NAY
2	AAA	801	YPP	CBK-CBJ-NBE-CBF
2	BBB	801	YPP	CBK-CBJ-NBE-CBF
2	AAA	801	YPP	CAP-CAR-NAY-CAZ

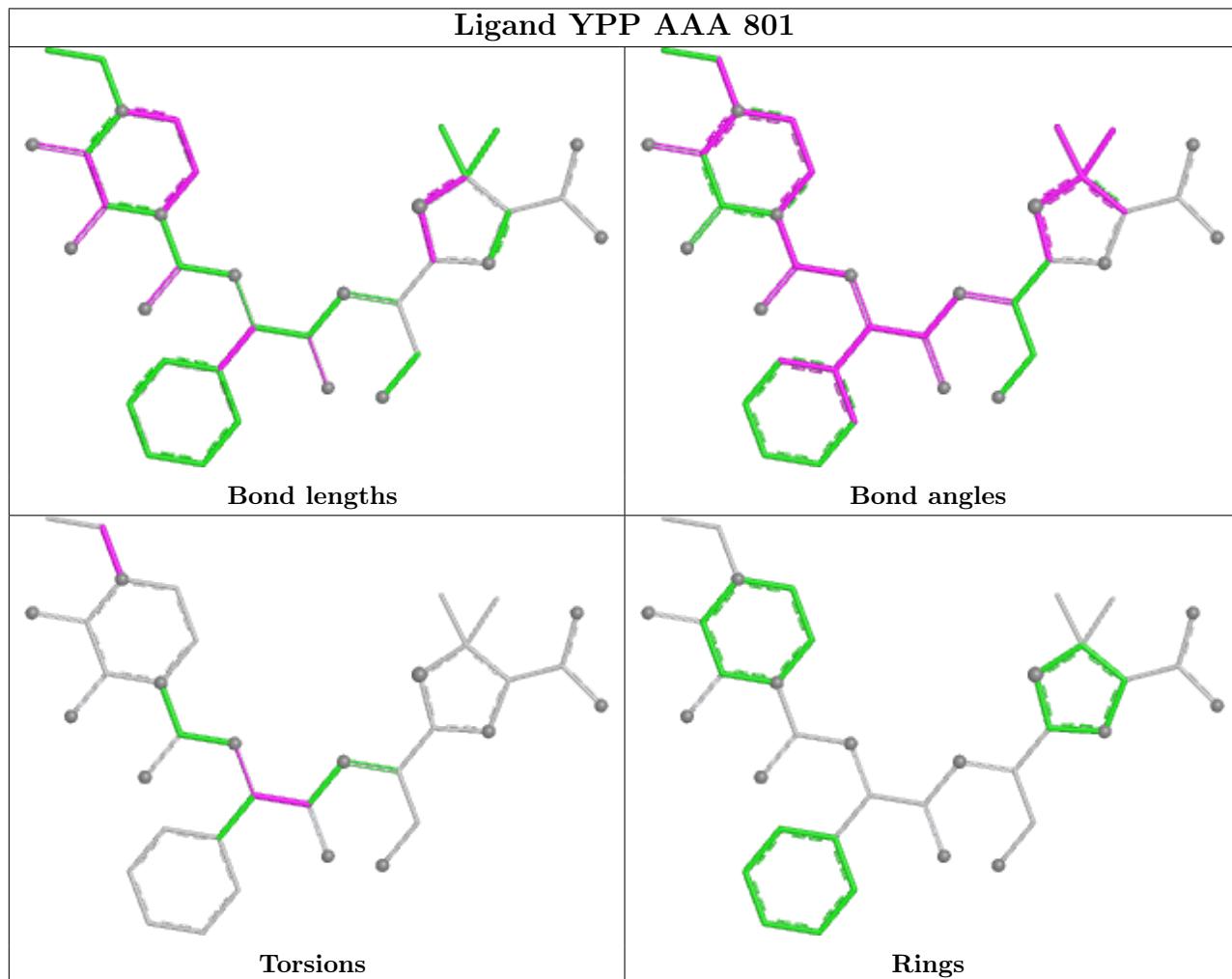
There are no ring outliers.

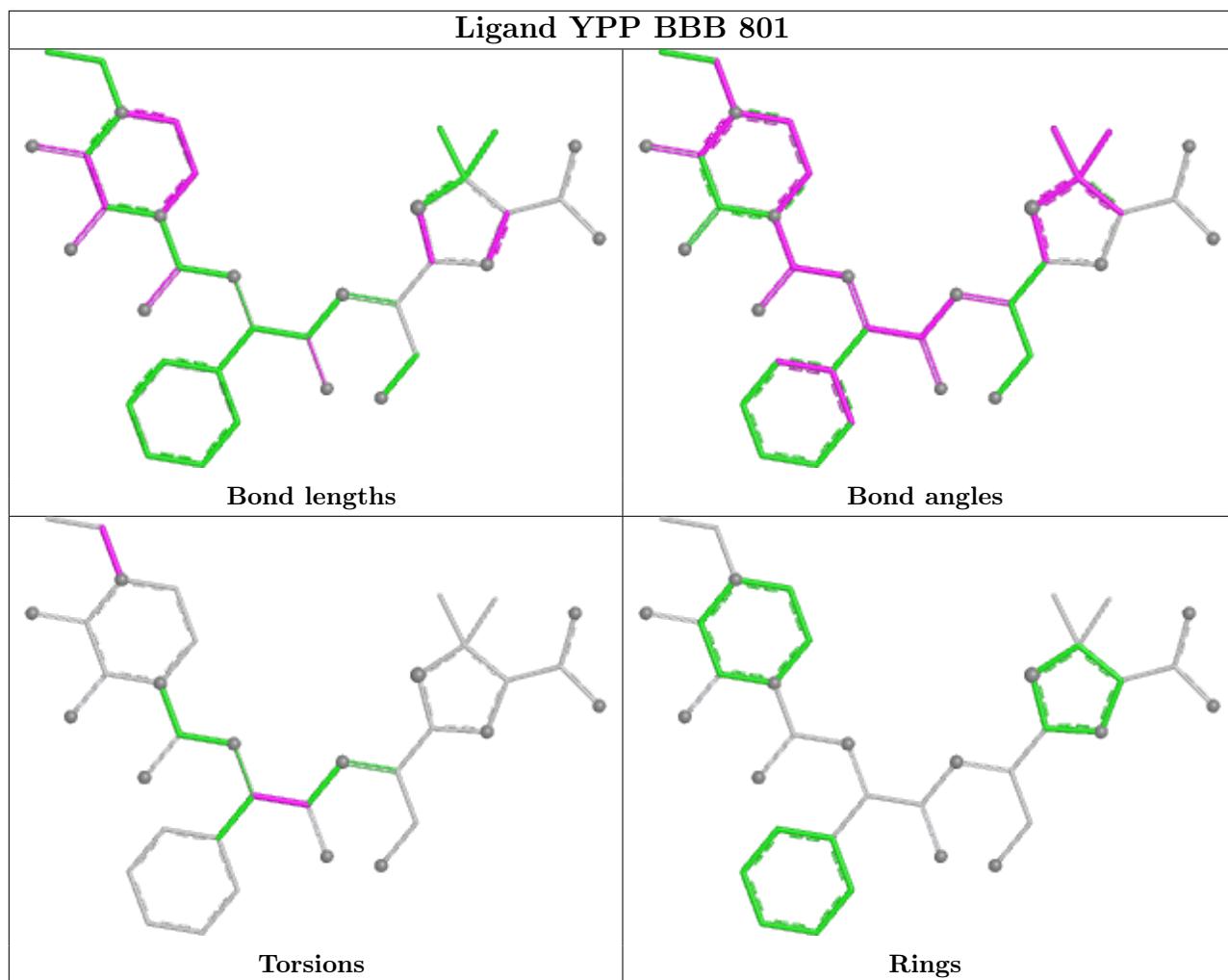
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	801	YPP	2	0
2	BBB	801	YPP	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	AAA	510/650 (78%)	-0.21	12 (2%) 59 30	47, 72, 120, 157	0
1	BBB	478/650 (73%)	0.11	29 (6%) 21 7	56, 95, 158, 214	0
All	All	988/1300 (76%)	-0.05	41 (4%) 37 15	47, 83, 144, 214	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	594	THR	4.8
1	AAA	593	ASP	4.5
1	BBB	113	LEU	4.4
1	BBB	120	LYS	3.6
1	BBB	119	MET	3.5
1	BBB	108	GLU	3.4
1	BBB	85	LEU	3.4
1	BBB	147	TYR	3.4
1	BBB	124	ILE	3.3
1	BBB	107	LYS	3.3
1	AAA	233	GLN	3.2
1	BBB	121	PRO	3.2
1	BBB	125	GLU	3.2
1	BBB	105	ASP	3.1
1	AAA	589	LYS	3.1
1	BBB	128	LEU	2.9
1	BBB	127	ARG	2.9
1	BBB	164	LEU	2.9
1	BBB	126	LYS	2.9
1	BBB	122	GLU	2.9
1	BBB	123	GLU	2.8
1	BBB	163	LEU	2.7
1	BBB	129	SER	2.7
1	BBB	524	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	AAA	126	LYS	2.5
1	BBB	160	GLY	2.4
1	BBB	79	ASP	2.3
1	AAA	590	SER	2.3
1	BBB	141	LYS	2.3
1	AAA	120	LYS	2.3
1	BBB	111	LYS	2.3
1	AAA	234	PRO	2.2
1	BBB	106	LYS	2.2
1	AAA	592	ASP	2.2
1	BBB	148	GLN	2.2
1	AAA	115	THR	2.1
1	BBB	261	GLU	2.1
1	BBB	118	ASN	2.1
1	AAA	122	GLU	2.1
1	AAA	119	MET	2.0
1	BBB	117	ILE	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 [\(i\)](#)

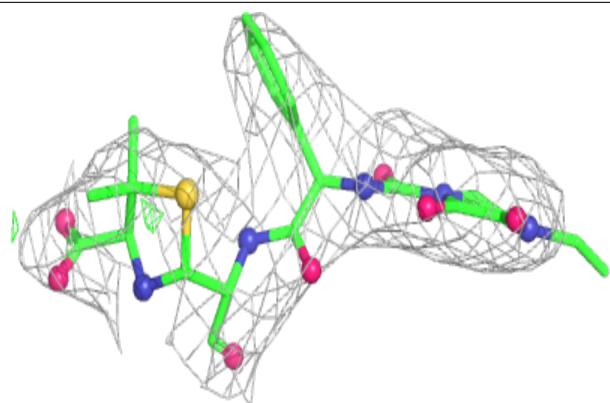
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q<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
2	YPP	BBB	801	36/37	0.92	0.25	87,101,120,128	0
2	YPP	AAA	801	36/37	0.94	0.23	54,76,116,121	0

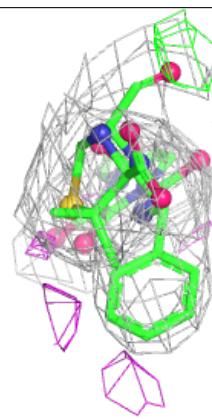
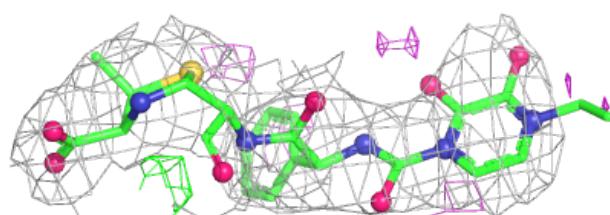
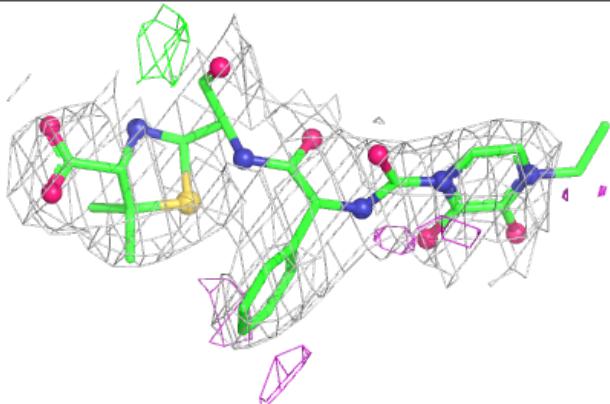
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around YPP BBB 801:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around YPP AAA 801:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.