



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2024 – 06:14 PM EDT

PDB ID : 8CPA  
Title : COMPARISON OF THE STRUCTURES OF THREE CARBOXYPEPTIDASE A-PHOSPHONATE COMPLEXES DETERMINED BY X-RAY CRYSTALLOGRAPHY  
Authors : Kim, H.; Lipscomb, W.N.  
Deposited on : 1991-05-21  
Resolution : 2.00 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>.

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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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

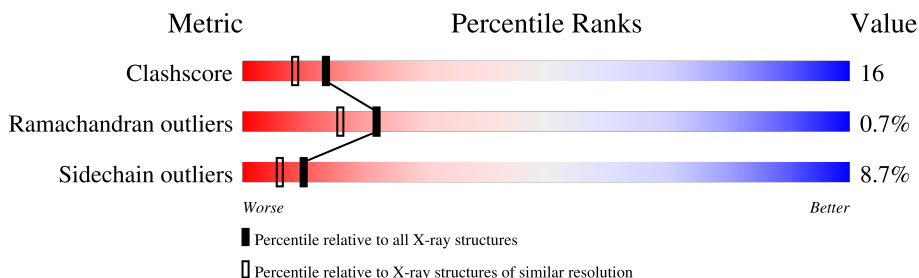
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	307	 69% 23% 7%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2724 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 CARBOXYPEPTIDASE A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2437	1561	406	465	5			

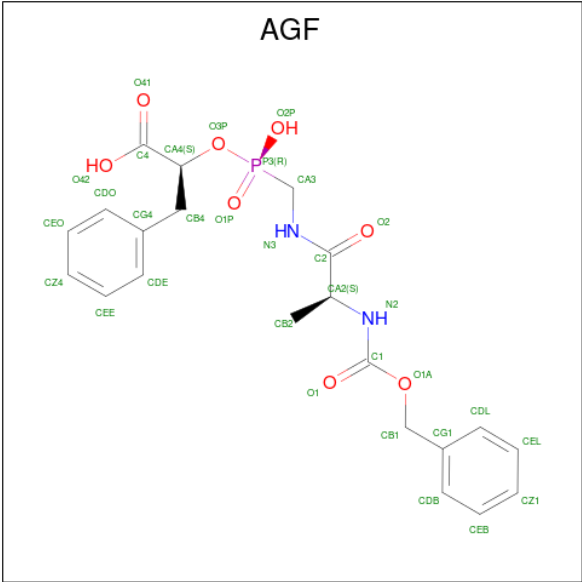
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	GLN	GLU	conflict	UNP P00730
A	31	GLU	GLN	conflict	UNP P00730
A	89	ASN	ASP	conflict	UNP P00730
A	93	ASN	ASP	conflict	UNP P00730
A	114	ASN	ASP	conflict	UNP P00730
A	122	GLU	GLN	conflict	UNP P00730
A	185	ASN	ASP	conflict	UNP P00730
A	228	ALA	GLU	conflict	UNP P00730
A	305	VAL	LEU	conflict	UNP P00730

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is O-(((1R)-((N-(PHENYL-METHOXY-CARBONYL)-ALANYL)-AMINO) METHYL)HYDROXYPHOSPHINYL)3-L-PHENYLLACTATE (three-letter code: AGF) (formula: C<sub>21</sub>H<sub>25</sub>N<sub>2</sub>O<sub>8</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			32	21	2	8	1		

- Molecule 4 is water.

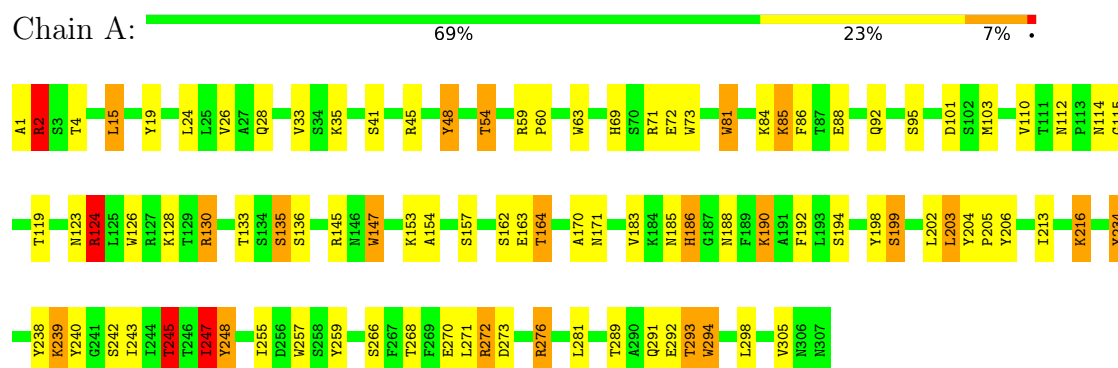
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	254	Total	O	0	0
			254	254		

### 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. 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.

Note EDS was not executed.

#### • Molecule 1: CARBOXYPEPTIDASE A



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.40Å 65.90Å 74.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.186 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2724	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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

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	0.80	1/2503 (0.0%)	1.57	48/3402 (1.4%)

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	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	72	GLU	CD-OE1	-5.04	1.20	1.25

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	272	ARG	NE-CZ-NH1	14.96	127.78	120.30
1	A	124	ARG	NE-CZ-NH2	-14.14	113.23	120.30
1	A	238	TYR	CB-CG-CD2	-8.84	115.69	121.00
1	A	272	ARG	NE-CZ-NH2	-8.50	116.05	120.30
1	A	294	TRP	CD1-CG-CD2	8.36	112.99	106.30
1	A	147	TRP	CD1-CG-CD2	8.35	112.98	106.30
1	A	145	ARG	NE-CZ-NH2	-8.21	116.20	120.30
1	A	257	TRP	CD1-CG-CD2	7.87	112.60	106.30
1	A	147	TRP	CE2-CD2-CG	-7.86	101.01	107.30
1	A	124	ARG	CA-CB-CG	7.77	130.49	113.40
1	A	124	ARG	NE-CZ-NH1	7.62	124.11	120.30
1	A	130	ARG	NE-CZ-NH1	7.48	124.04	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	272	ARG	CB-CG-CD	7.42	130.89	111.60
1	A	81	TRP	CD1-CG-CD2	7.38	112.20	106.30
1	A	294	TRP	CE2-CD2-CG	-7.31	101.45	107.30
1	A	73	TRP	CD1-CG-CD2	7.29	112.13	106.30
1	A	63	TRP	CD1-CG-CD2	7.26	112.11	106.30
1	A	145	ARG	NE-CZ-NH1	6.96	123.78	120.30
1	A	257	TRP	CE2-CD2-CG	-6.89	101.78	107.30
1	A	124	ARG	CG-CD-NE	-6.71	97.71	111.80
1	A	2	ARG	NE-CZ-NH1	-6.54	117.03	120.30
1	A	73	TRP	CE2-CD2-CG	-6.45	102.14	107.30
1	A	63	TRP	CE2-CD2-CG	-6.40	102.18	107.30
1	A	81	TRP	CE2-CD2-CG	-6.33	102.24	107.30
1	A	147	TRP	CG-CD2-CE3	6.29	139.56	133.90
1	A	126	TRP	CD1-CG-CD2	6.26	111.31	106.30
1	A	294	TRP	CB-CG-CD1	-6.15	119.00	127.00
1	A	206	TYR	CB-CG-CD1	-5.98	117.41	121.00
1	A	203	LEU	CA-CB-CG	5.94	128.96	115.30
1	A	147	TRP	CB-CG-CD1	-5.66	119.65	127.00
1	A	126	TRP	CE2-CD2-CG	-5.57	102.84	107.30
1	A	185	ASN	O-C-N	-5.52	113.87	122.70
1	A	276	ARG	NE-CZ-NH2	-5.51	117.55	120.30
1	A	185	ASN	N-CA-CB	-5.31	101.04	110.60
1	A	294	TRP	CG-CD1-NE1	-5.30	104.80	110.10
1	A	276	ARG	NE-CZ-NH1	5.29	122.95	120.30
1	A	186	HIS	CA-C-N	5.28	126.76	116.20
1	A	245	THR	N-CA-CB	-5.28	100.27	110.30
1	A	240	TYR	CB-CG-CD1	-5.19	117.89	121.00
1	A	72	GLU	OE1-CD-OE2	-5.18	117.09	123.30
1	A	186	HIS	O-C-N	-5.17	114.41	123.20
1	A	247	ILE	CB-CG1-CD1	-5.13	99.52	113.90
1	A	147	TRP	CG-CD1-NE1	-5.09	105.01	110.10
1	A	257	TRP	CG-CD2-CE3	5.08	138.47	133.90
1	A	257	TRP	CG-CD1-NE1	-5.08	105.02	110.10
1	A	81	TRP	CG-CD1-NE1	-5.05	105.05	110.10
1	A	73	TRP	CG-CD1-NE1	-5.03	105.07	110.10
1	A	69	HIS	CB-CG-CD2	-5.02	115.22	130.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	19	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	A	234	TYR	Sidechain
1	A	259	TYR	Sidechain
1	A	48	TYR	Sidechain

## 5.2 Too-close contacts

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	2437	0	2352	77	0
2	A	1	0	0	0	0
3	A	32	0	23	3	0
4	A	254	0	0	5	0
All	All	2724	0	2375	77	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 16.

All (77) 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:289:THR:O	1:A:293:THR:HG22	1.43	1.15
1:A:213:ILE:HG12	1:A:216:LYS:HE3	1.13	1.05
1:A:186:HIS:HD2	1:A:188:ASN:H	1.03	0.98
1:A:213:ILE:HG12	1:A:216:LYS:CE	1.96	0.95
1:A:213:ILE:CG1	1:A:216:LYS:HE3	2.01	0.91
1:A:54:THR:HG22	1:A:59:ARG:HH12	1.33	0.91
1:A:234:TYR:OH	1:A:291:GLN:NE2	2.09	0.86
1:A:133:THR:O	1:A:136:SER:O	1.97	0.82
1:A:186:HIS:CD2	1:A:188:ASN:H	1.95	0.80
1:A:239:LYS:N	1:A:239:LYS:HE3	1.98	0.78
1:A:45:ARG:HH11	1:A:114:ASN:ND2	1.82	0.77
1:A:186:HIS:HD2	1:A:188:ASN:N	1.80	0.77
1:A:103:MET:SD	1:A:305:VAL:HG22	2.28	0.74
1:A:45:ARG:HH11	1:A:114:ASN:HD22	1.35	0.73
1:A:198:TYR:CZ	3:A:309:AGF:HD11	2.24	0.72
1:A:153:LYS:HG2	4:A:520:HOH:O	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:ARG:O	1:A:124:ARG:NH2	2.22	0.71
1:A:54:THR:HG22	1:A:59:ARG:NH1	2.06	0.69
1:A:153:LYS:HD3	1:A:154:ALA:N	2.06	0.69
1:A:153:LYS:HD3	1:A:153:LYS:C	2.13	0.68
1:A:247:ILE:HD12	1:A:248:TYR:H	1.59	0.68
1:A:239:LYS:HE3	1:A:239:LYS:H	1.58	0.67
1:A:255:ILE:HG13	1:A:266:SER:HB3	1.77	0.66
1:A:86:PHE:HE1	1:A:294:TRP:CZ3	2.15	0.63
1:A:242:SER:OG	1:A:245:THR:HB	1.99	0.63
1:A:289:THR:O	1:A:293:THR:CG2	2.36	0.61
1:A:198:TYR:O	1:A:199:SER:CB	2.53	0.57
1:A:170:ALA:O	1:A:171:ASN:HB2	2.06	0.56
1:A:26:VAL:HG22	1:A:33:VAL:HG13	1.87	0.55
1:A:128:LYS:HD2	1:A:163:GLU:HA	1.89	0.55
1:A:26:VAL:HA	1:A:33:VAL:CG1	2.38	0.54
1:A:54:THR:HG21	1:A:101:ASP:HA	1.90	0.54
1:A:35:LYS:HE2	1:A:48:TYR:CD2	2.42	0.54
1:A:157:SER:HB3	1:A:164:THR:HG22	1.89	0.53
1:A:186:HIS:CD2	1:A:188:ASN:N	2.67	0.50
1:A:183:VAL:HG12	1:A:183:VAL:O	2.09	0.50
1:A:183:VAL:O	1:A:183:VAL:CG1	2.59	0.50
1:A:45:ARG:NH1	1:A:114:ASN:ND2	2.57	0.50
1:A:103:MET:SD	1:A:305:VAL:CG2	3.00	0.50
1:A:135:SER:HB2	4:A:490:HOH:O	2.11	0.50
1:A:192:PHE:CD1	1:A:255:ILE:HD12	2.47	0.49
1:A:15:LEU:HD21	1:A:110:VAL:HG11	1.95	0.48
1:A:88:GLU:O	1:A:92:GLN:OE1	2.32	0.48
1:A:213:ILE:H	1:A:216:LYS:HZ2	1.62	0.48
1:A:192:PHE:HD1	1:A:255:ILE:CD1	2.27	0.47
1:A:128:LYS:HE3	1:A:162:SER:O	2.14	0.47
1:A:192:PHE:HD1	1:A:255:ILE:HD12	1.78	0.46
1:A:272:ARG:HD2	1:A:292:GLU:OE2	2.15	0.46
1:A:153:LYS:HD3	1:A:154:ALA:O	2.15	0.46
1:A:41:SER:OG	1:A:114:ASN:ND2	2.48	0.46
1:A:86:PHE:CE1	1:A:294:TRP:CZ3	3.02	0.45
1:A:115:GLY:O	1:A:119:THR:HG23	2.17	0.45
1:A:2:ARG:NH1	1:A:2:ARG:O	2.50	0.45
1:A:26:VAL:HA	1:A:33:VAL:HG13	1.99	0.44
1:A:85:LYS:NZ	4:A:496:HOH:O	2.41	0.44
1:A:147:TRP:N	1:A:147:TRP:CD1	2.85	0.44
1:A:204:TYR:HB2	1:A:205:PRO:CD	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:SER:CB	1:A:164:THR:HG22	2.48	0.44
1:A:153:LYS:CD	1:A:154:ALA:N	2.76	0.43
1:A:119:THR:HA	1:A:123:ASN:O	2.18	0.43
1:A:198:TYR:O	1:A:199:SER:HB3	2.18	0.43
1:A:190:LYS:NZ	4:A:450:HOH:O	2.49	0.43
1:A:2:ARG:HH11	1:A:2:ARG:HD3	1.53	0.43
1:A:243:ILE:HG23	1:A:247:ILE:HD11	2.00	0.43
1:A:35:LYS:HE2	1:A:48:TYR:CG	2.53	0.42
1:A:1:ALA:O	1:A:2:ARG:HB3	2.20	0.42
1:A:153:LYS:HE3	4:A:485:HOH:O	2.18	0.42
1:A:194:SER:O	1:A:268:THR:HG23	2.19	0.42
1:A:272:ARG:HA	1:A:273:ASP:HA	1.71	0.42
1:A:24:LEU:HD23	1:A:24:LEU:HA	1.83	0.42
1:A:24:LEU:O	1:A:28:GLN:HG3	2.21	0.41
1:A:198:TYR:CE1	3:A:309:AGF:HE11	2.56	0.41
1:A:270:GLU:OE1	3:A:309:AGF:O2P	2.39	0.41
1:A:2:ARG:O	1:A:2:ARG:HD3	2.20	0.41
1:A:81:TRP:CH2	1:A:85:LYS:HG2	2.56	0.41
1:A:4:THR:OG1	1:A:84:LYS:HE2	2.21	0.41
1:A:60:PRO:HB3	1:A:190:LYS:HD3	2.04	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	305/307 (99%)	287 (94%)	16 (5%)	2 (1%)	22 16

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	ARG

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Mol	Chain	Res	Type
1	A	199	SER

### 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	263/263 (100%)	240 (91%)	23 (9%)	10 6

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	15	LEU
1	A	54	THR
1	A	85	LYS
1	A	95	SER
1	A	112	ASN
1	A	124	ARG
1	A	130	ARG
1	A	135	SER
1	A	164	THR
1	A	190	LYS
1	A	202	LEU
1	A	203	LEU
1	A	216	LYS
1	A	239	LYS
1	A	245	THR
1	A	247	ILE
1	A	248	TYR
1	A	271	LEU
1	A	276	ARG
1	A	281	LEU
1	A	293	THR
1	A	298	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	HIS
1	A	112	ASN
1	A	114	ASN
1	A	186	HIS
1	A	291	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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z  > 2$
3	AGF	A	309	2	31,33,33	2.59	8 (25%)	39,44,44	1.73	11 (28%)

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	AGF	A	309	2	-	4/31/32/32	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	309	AGF	CA4-C4	-9.25	1.44	1.52
3	A	309	AGF	P3-O3P	5.13	1.65	1.57
3	A	309	AGF	P3-CA3	-4.25	1.68	1.82
3	A	309	AGF	CB1-CG1	-3.16	1.43	1.50
3	A	309	AGF	CA2-C2	-2.93	1.45	1.52
3	A	309	AGF	CB4-CG4	-2.92	1.44	1.51
3	A	309	AGF	O1A-CB1	-2.47	1.40	1.45
3	A	309	AGF	O1A-C1	-2.21	1.30	1.35

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	309	AGF	CB4-CA4-C4	-4.42	100.37	110.23
3	A	309	AGF	O3P-CA4-CB4	3.82	113.99	107.51
3	A	309	AGF	O1-C1-N2	-3.22	119.56	124.85
3	A	309	AGF	CG4-CB4-CA4	3.18	118.39	113.15
3	A	309	AGF	O1A-C1-N2	3.11	116.83	110.50
3	A	309	AGF	CA2-N2-C1	2.68	125.51	120.49
3	A	309	AGF	O2P-P3-O1P	2.55	118.57	110.07
3	A	309	AGF	O2P-P3-CA3	-2.30	100.81	106.71
3	A	309	AGF	CB1-O1A-C1	2.21	120.86	115.93
3	A	309	AGF	C2-CA2-N2	2.13	116.87	111.60
3	A	309	AGF	O2-C2-CA2	2.09	125.16	120.52

There are no chirality outliers.

All (4) torsion outliers are listed below:

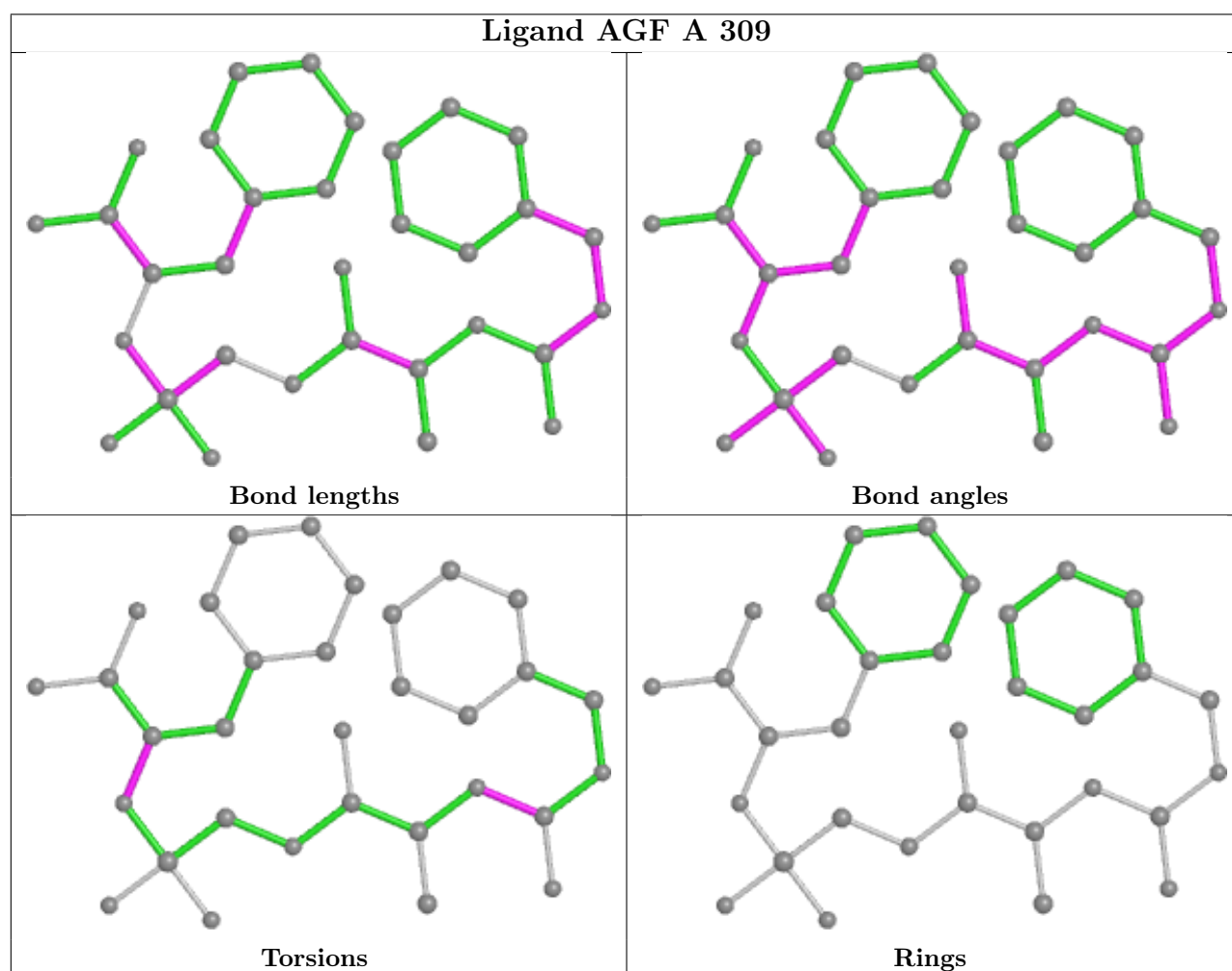
Mol	Chain	Res	Type	Atoms
3	A	309	AGF	C4-CA4-O3P-P3
3	A	309	AGF	CB4-CA4-O3P-P3
3	A	309	AGF	O1A-C1-N2-CA2
3	A	309	AGF	O1-C1-N2-CA2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	309	AGF	3	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 ⓘ

There are no chain breaks in this entry.



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.