



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:57 AM UTC

PDB ID : 1OEC / pdb_00001oec
Title : FGFr2 kinase domain
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Deposited on : 2003-03-24
Resolution : 2.40 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

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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

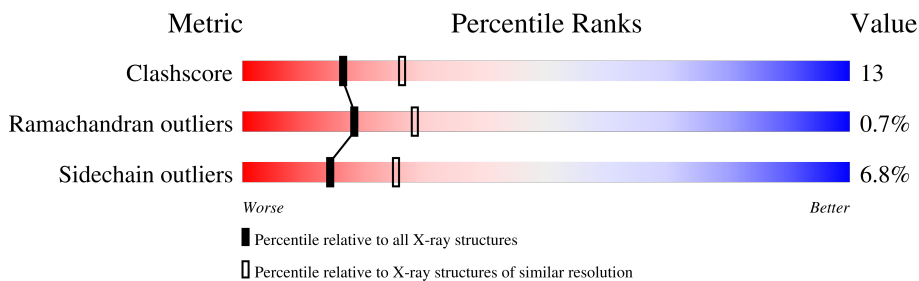
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	316	

2 Entry composition [i](#)

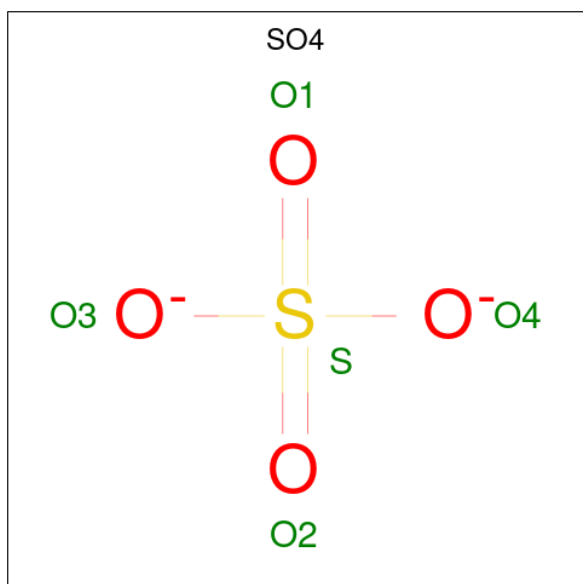
There are 4 unique types of molecules in this entry. The entry contains 2414 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FIBROBLAST GROWTH FACTOR RECEPTOR 2.

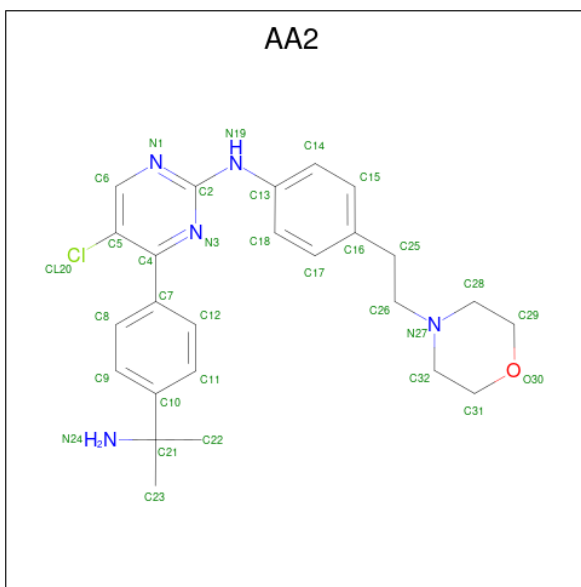
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	1
			2211	1406	379	406	20			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 4-ARYL-2-PHENYLAMINO PYRIMIDINE (CCD ID: AA2) (formula: C₂₅H₃₀ClN₅O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			32	25	1	5	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	161	Total	O	0	0
			161	161		

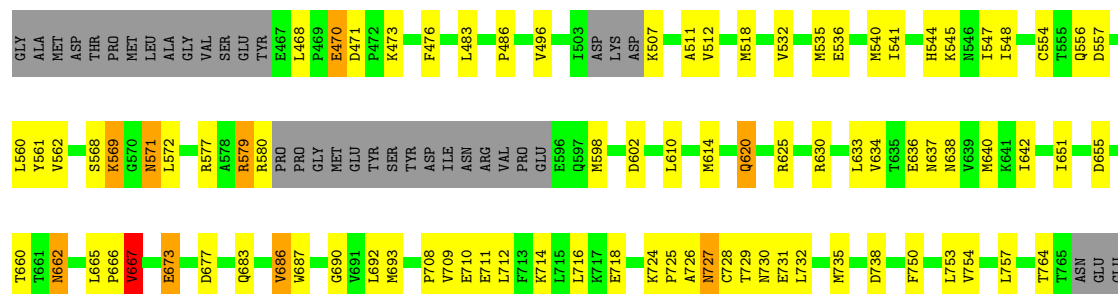
3 Residue-property plots

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: FIBROBLAST GROWTH FACTOR RECEPTOR 2

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	69.76 Å 80.50 Å 120.17 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.40	Depositor
% Data completeness (in resolution range)	98.0 (100.00-2.40)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.211 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2414	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

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: SO4, AA2

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	0.44	1/2255 (0.0%)	1.01	15/3046 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	764	THR	C-N	-5.41	1.25	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	620	GLN	OE1-CD-NE2	-9.80	112.80	122.60
1	A	568	SER	N-CA-C	7.95	119.94	111.28
1	A	638	ASN	N-CA-C	7.32	121.16	111.28
1	A	677	ASP	N-CA-C	7.09	121.64	112.92
1	A	620	GLN	CG-CD-NE2	6.62	126.33	116.40
1	A	511	ALA	N-CA-C	6.53	118.55	109.15
1	A	662	ASN	N-CA-C	6.19	119.96	111.54
1	A	667	VAL	N-CA-C	6.07	116.81	110.62
1	A	471	ASP	CA-C-N	6.01	125.49	119.24
1	A	471	ASP	C-N-CA	6.01	125.49	119.24
1	A	507	LYS	CA-C-N	5.98	125.36	118.85
1	A	507	LYS	C-N-CA	5.98	125.36	118.85
1	A	636	GLU	N-CA-C	-5.96	102.10	110.50
1	A	476	PHE	CA-C-N	5.49	125.81	119.93
1	A	476	PHE	C-N-CA	5.49	125.81	119.93

There are no chirality outliers.

There are no planarity outliers.

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	2211	0	2201	53	0
2	A	10	0	0	0	0
3	A	32	0	30	5	0
4	A	161	0	0	3	0
All	All	2414	0	2231	58	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 (58) 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:729:THR:HG22	1:A:731:GLU:H	1.35	0.90
1:A:569:LYS:HB2	1:A:634:VAL:HG13	1.61	0.81
1:A:630:ARG:HH22	1:A:666:PRO:HG3	1.46	0.80
3:A:789:AA2:H17	4:A:2011:HOH:O	1.81	0.80
1:A:572:LEU:HD13	1:A:640:MET:HE1	1.63	0.78
1:A:470:GLU:HB2	1:A:556:GLN:HE21	1.50	0.77
3:A:789:AA2:H233	4:A:2064:HOH:O	1.89	0.71
1:A:535:MET:HE1	1:A:560:LEU:HD11	1.72	0.69
1:A:486:PRO:HA	1:A:496:VAL:HG12	1.73	0.69
1:A:468:LEU:HD12	1:A:468:LEU:H	1.58	0.68
1:A:625:ARG:HH21	1:A:662:ASN:HD22	1.41	0.65
1:A:630:ARG:NH2	1:A:666:PRO:HG3	2.13	0.63
1:A:729:THR:HB	1:A:732:LEU:HG	1.80	0.63
3:A:789:AA2:H18	3:A:789:AA2:N3	2.13	0.63
1:A:548:ILE:CD1	1:A:633:LEU:HD12	2.29	0.62
1:A:735:MET:HE1	1:A:757:LEU:HG	1.82	0.62
1:A:541:ILE:HA	1:A:620:GLN:HG2	1.82	0.61
1:A:726:ALA:O	1:A:727:ASN:HB2	2.00	0.61
3:A:789:AA2:H12	3:A:789:AA2:CL20	2.38	0.60
1:A:571:ASN:H	1:A:571:ASN:HD22	1.51	0.59
1:A:651:ILE:HD12	1:A:655:ASP:HA	1.86	0.58
1:A:728:CYS:SG	1:A:732:LEU:HB2	2.45	0.57
1:A:545:LYS:HD2	1:A:545:LYS:N	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:579:ARG:H	1:A:579:ARG:HD2	1.70	0.56
1:A:571:ASN:H	1:A:571:ASN:ND2	2.04	0.54
1:A:683:GLN:O	1:A:686:VAL:HG22	2.07	0.54
1:A:544:HIS:HB3	1:A:547:ILE:HG12	1.90	0.52
1:A:750:PHE:O	1:A:754:VAL:HG23	2.10	0.51
1:A:548:ILE:HD12	1:A:633:LEU:HD12	1.93	0.51
1:A:651:ILE:HG22	1:A:651:ILE:O	2.11	0.50
1:A:470:GLU:HB2	1:A:556:GLN:NE2	2.22	0.50
1:A:548:ILE:HD11	1:A:633:LEU:HD12	1.93	0.50
1:A:690:GLY:HA2	1:A:693:MET:HE3	1.96	0.48
1:A:726:ALA:O	1:A:727:ASN:CB	2.62	0.47
1:A:729:THR:HG22	1:A:731:GLU:N	2.18	0.47
1:A:535:MET:HE3	1:A:562:VAL:HG22	1.96	0.47
1:A:598:MET:HE2	1:A:602:ASP:HB3	1.97	0.47
3:A:789:AA2:CL20	3:A:789:AA2:C12	3.00	0.46
1:A:730:ASN:HB3	4:A:2128:HOH:O	2.15	0.46
1:A:724:LYS:HA	1:A:725:PRO:HD3	1.75	0.46
1:A:625:ARG:HH21	1:A:662:ASN:ND2	2.10	0.46
1:A:625:ARG:O	1:A:665:LEU:HD22	2.16	0.46
1:A:667:VAL:HG21	1:A:709:VAL:HB	1.98	0.46
1:A:483:LEU:HD13	1:A:518:MET:HE1	1.99	0.45
1:A:554:CYS:HB2	1:A:561:TYR:HB2	1.98	0.45
1:A:753:LEU:O	1:A:757:LEU:HB2	2.15	0.45
1:A:610:LEU:HD13	1:A:692:LEU:HD21	2.00	0.43
1:A:673:GLU:CD	1:A:673:GLU:H	2.26	0.42
1:A:708:PRO:HG2	1:A:711:GLU:HG2	2.00	0.42
1:A:716:LEU:HD12	1:A:716:LEU:HA	1.92	0.42
1:A:496:VAL:HG22	1:A:518:MET:HE3	2.01	0.42
1:A:729:THR:H	1:A:732:LEU:HD12	1.84	0.42
1:A:687:TRP:CD1	1:A:687:TRP:C	2.98	0.41
1:A:532:VAL:O	1:A:536:GLU:HG3	2.21	0.41
1:A:577:ARG:O	1:A:580:ARG:HG2	2.21	0.41
1:A:614:MET:SD	1:A:642:ILE:HD13	2.61	0.41
1:A:620:GLN:HA	1:A:620:GLN:OE1	2.20	0.40
1:A:714:LYS:HA	1:A:714:LYS:HD3	1.93	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	275/316 (87%)	263 (96%)	10 (4%)	2 (1%)	18	28

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	727	ASN
1	A	557	ASP

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	237/276 (86%)	221 (93%)	16 (7%)	14	25

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	470	GLU
1	A	473	LYS
1	A	512	VAL
1	A	540	MET
1	A	569	LYS
1	A	571	ASN
1	A	579	ARG
1	A	637	ASN
1	A	660	THR

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Mol	Chain	Res	Type
1	A	667	VAL
1	A	673	GLU
1	A	686	VAL
1	A	710	GLU
1	A	712	LEU
1	A	718	GLU
1	A	738	ASP

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

Mol	Chain	Res	Type
1	A	549	ASN
1	A	556	GLN
1	A	571	ASN
1	A	631	ASN
1	A	652	ASN
1	A	662	ASN
1	A	730	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

3 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	$\# Z > 2$
3	AA2	A	789	-	34,35,35	1.46	4 (11%)	44,49,49	1.81	4 (9%)
2	SO4	A	782	-	4,4,4	0.61	0	6,6,6	0.23	0
2	SO4	A	781	-	4,4,4	0.56	0	6,6,6	0.12	0

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	AA2	A	789	-	-	3/19/27/27	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	789	AA2	C21-C10	2.86	1.56	1.51
3	A	789	AA2	C4-C5	2.53	1.44	1.39
3	A	789	AA2	C22-C21	2.44	1.56	1.53
3	A	789	AA2	C4-N3	2.41	1.38	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	789	AA2	N1-C2-N3	-7.62	119.05	126.42
3	A	789	AA2	C6-C5-C4	-5.62	117.52	120.43
3	A	789	AA2	C6-N1-C2	4.74	122.31	115.81
3	A	789	AA2	C5-C6-N1	-2.80	120.63	122.78

There are no chirality outliers.

All (3) torsion outliers are listed below:

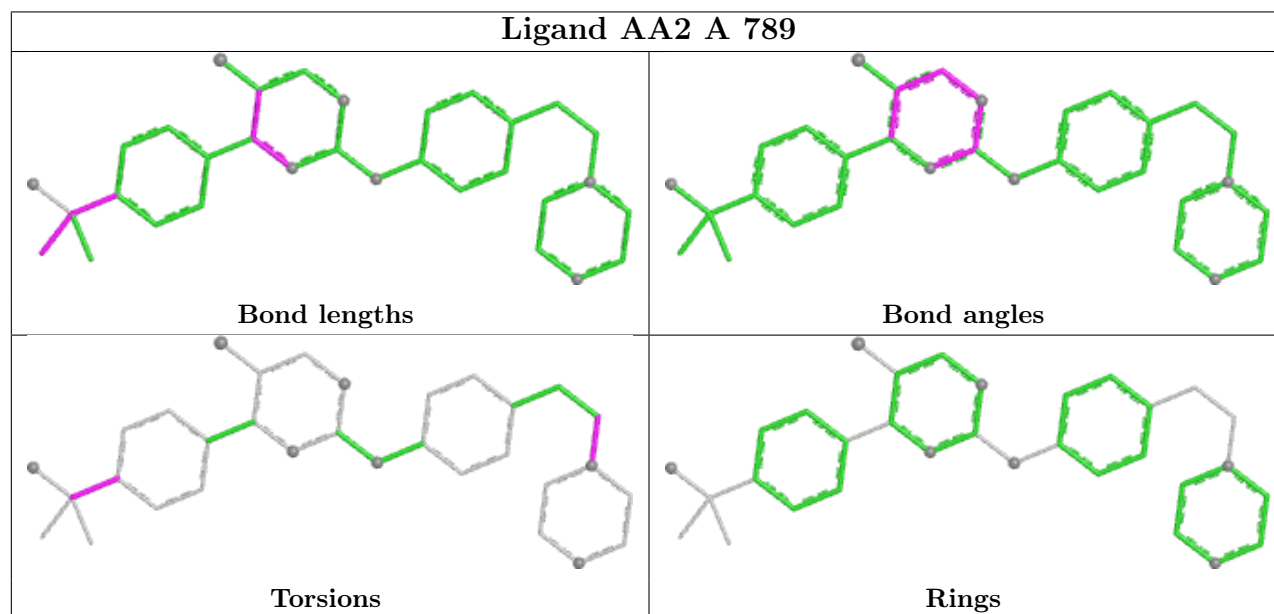
Mol	Chain	Res	Type	Atoms
3	A	789	AA2	C9-C10-C21-N24
3	A	789	AA2	C11-C10-C21-N24
3	A	789	AA2	C25-C26-N27-C28

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	789	AA2	5	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

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.