Full wwPDB X-ray Structure Validation Report (i)

Nov 16, 2022 – 06:18 pm GMT

PDB ID	:	7Z9O
Title	:	ATAD2 in complex with PepLite-Tyr
Authors	:	Turberville, S.; Martin, M.P.; Hope, I.; Noble, M.E.M.
Deposited on	:	2022-03-21
Resolution	:	1.47 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 (i) 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 (i)) were used in the production of this report:

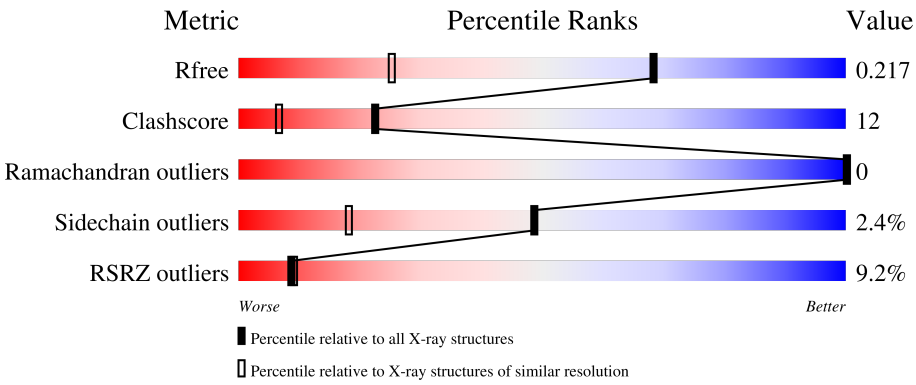
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.47 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	4690 (1.50-1.46)
Clashscore	141614	4955 (1.50-1.46)
Ramachandran outliers	138981	4846 (1.50-1.46)
Sidechain outliers	138945	4844 (1.50-1.46)
RSRZ outliers	127900	4614 (1.50-1.46)

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 <=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	AAA	130	9% 80% 17%

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	IK3	AAA	1208	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 1318 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.

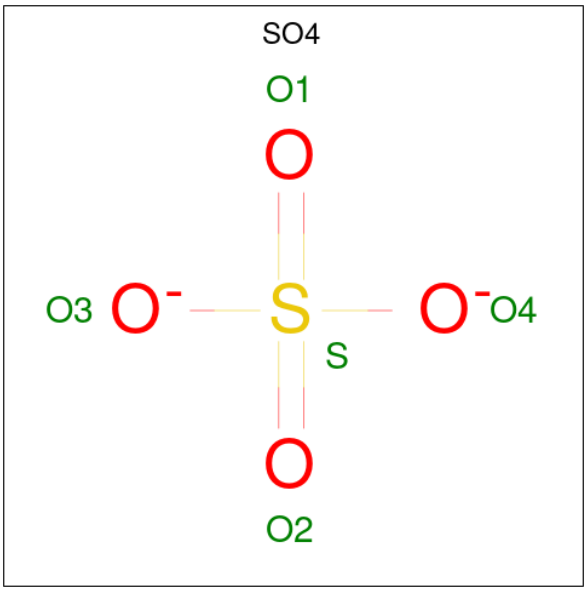
- Molecule 1 is a protein called ATPase family AAA domain-containing protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	130	1092	685	190	212	5	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	979	SER	-	expression tag	UNP Q6PL18
AAA	980	MET	-	expression tag	UNP Q6PL18

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

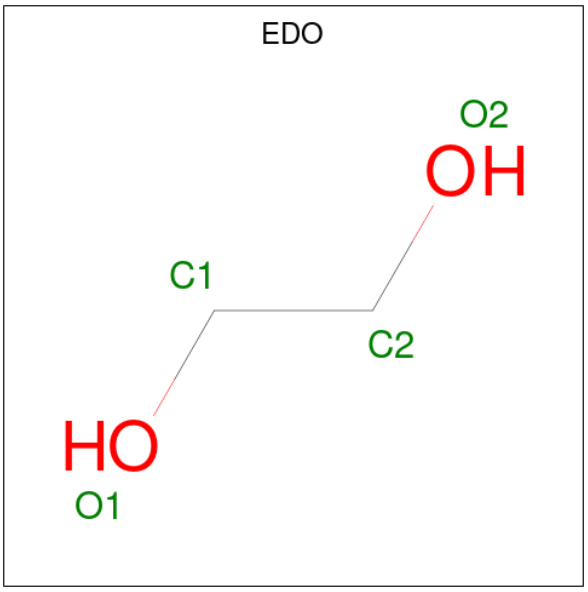


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	AAA	1	5	4	1	0	0
2	AAA	1	5	4	1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

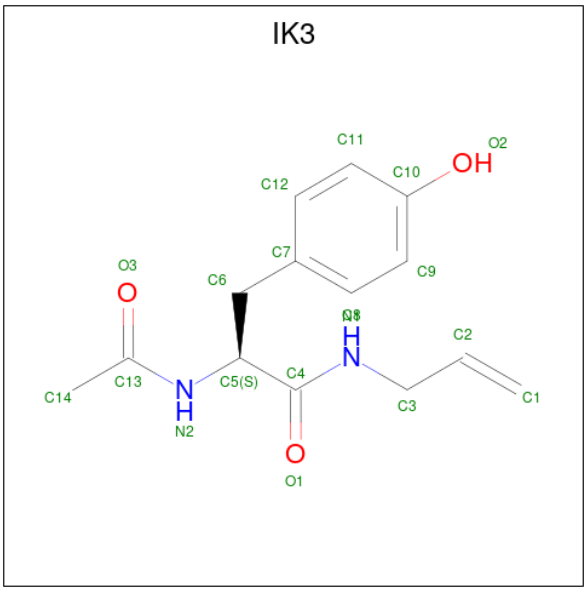
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
3	AAA	1	1	1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	AAA	1	4	2	2	0	0
			Total	C	O		
4	AAA	1	4	2	2	0	0
			Total	C	O		
4	AAA	1	4	2	2	0	0
			Total	C	O		
4	AAA	1	4	2	2	0	0

- Molecule 5 is (2 {S})-2-acetamido-3-(4-hydroxyphenyl)- {N}-prop-2-enyl-propanamide (three-letter code: IK3) (formula: $C_{14}H_{18}N_2O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	AAA	1	19	14	2	3	0	0

- Molecule 6 is water.

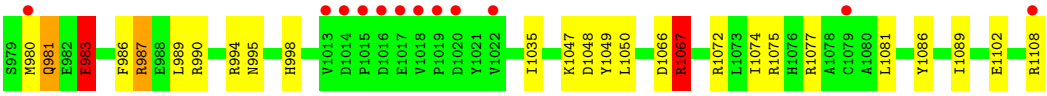
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	AAA	180	180	180	0	0

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: ATPase family AAA domain-containing protein 2

Chain AAA:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	79.30Å 79.30Å 138.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	61.52 – 1.47 61.52 – 1.47	Depositor EDS
% Data completeness (in resolution range)	99.3 (61.52-1.47) 99.3 (61.52-1.47)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.75 (at 1.47Å)	Xtriage
Refinement program	REFMAC 5.8.0258, REFMAC 5.8.0258	Depositor
R, R_{free}	0.201 , 0.218 0.201 , 0.217	Depositor DCC
R_{free} test set	2213 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	24.4	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	1318	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.30% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: IK3, SO4, CL, EDO

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	1.95	4/1110 (0.4%)	1.36	13/1498 (0.9%)

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	AAA	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	983	GLU	CD-OE2	47.19	1.77	1.25
1	AAA	983	GLU	CD-OE1	35.41	1.64	1.25
1	AAA	983	GLU	CG-CD	8.79	1.65	1.51
1	AAA	1102	GLU	CD-OE2	6.56	1.32	1.25

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AAA	1108	ARG	NE-CZ-NH2	-14.53	113.04	120.30
1	AAA	1108	ARG	NE-CZ-NH1	-12.49	114.06	120.30
1	AAA	1108	ARG	NH1-CZ-NH2	12.26	132.88	119.40
1	AAA	983	GLU	CG-CD-OE2	-11.13	96.03	118.30
1	AAA	1067	ARG	NE-CZ-NH1	-8.34	116.13	120.30
1	AAA	990	ARG	NE-CZ-NH2	-8.05	116.27	120.30
1	AAA	987	ARG	NE-CZ-NH2	-6.34	117.13	120.30
1	AAA	994	ARG	CG-CD-NE	-6.05	99.09	111.80
1	AAA	994	ARG	NE-CZ-NH2	-5.76	117.42	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	994	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	AAA	1049	TYR	CB-CG-CD2	-5.46	117.72	121.00
1	AAA	1077	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	AAA	986	PHE	CB-CG-CD1	5.01	124.31	120.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AAA	983	GLU	Sidechain

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	1092	0	1081	23	0
2	AAA	10	0	0	1	0
3	AAA	1	0	0	0	0
4	AAA	16	0	24	5	0
5	AAA	19	0	0	3	0
6	AAA	180	0	0	11	1
All	All	1318	0	1105	26	1

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 12.

All (26) 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:AAA:983:GLU:OE1	1:AAA:983:GLU:CD	1.64	1.33
1:AAA:983:GLU:CD	1:AAA:983:GLU:OE2	1.77	1.20
1:AAA:998:HIS:HD2	4:AAA:1204:EDO:H11	1.01	1.11
1:AAA:998:HIS:CD2	4:AAA:1204:EDO:H11	1.90	1.05
1:AAA:981:GLN:HE21	1:AAA:981:GLN:H	1.24	0.86
1:AAA:1066:ASP:OD1	6:AAA:1302:HOH:O	2.00	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:1047:LYS:HG3	4:AAA:1205:EDO:H22	1.81	0.62
1:AAA:1086:TYR:OH	4:AAA:1205:EDO:H12	2.00	0.61
5:AAA:1208:IK3:C11	6:AAA:1379:HOH:O	2.48	0.61
1:AAA:998:HIS:HD2	4:AAA:1204:EDO:C1	1.95	0.59
1:AAA:1035:ILE:HD11	6:AAA:1323:HOH:O	2.04	0.57
1:AAA:983:GLU:OE2	6:AAA:1303:HOH:O	2.16	0.57
1:AAA:983:GLU:OE2	1:AAA:983:GLU:CG	2.54	0.56
1:AAA:1075:ARG:HH21	5:AAA:1208:IK3:C12	2.19	0.56
1:AAA:989:LEU:HD23	6:AAA:1318:HOH:O	2.06	0.56
1:AAA:1081[B]:LEU:C	1:AAA:1081[B]:LEU:HD23	2.27	0.54
1:AAA:995:ASN:ND2	6:AAA:1311:HOH:O	2.43	0.51
2:AAA:1207:SO4:O4	6:AAA:1304:HOH:O	2.18	0.51
5:AAA:1208:IK3:C14	5:AAA:1208:IK3:O1	2.62	0.48
1:AAA:1048:ASP:OD2	6:AAA:1305:HOH:O	2.20	0.47
1:AAA:1067:ARG:NH2	1:AAA:1072:ARG:HH12	2.12	0.47
1:AAA:981:GLN:HE21	1:AAA:981:GLN:N	2.03	0.47
1:AAA:1074:ILE:HG13	6:AAA:1374:HOH:O	2.16	0.46
1:AAA:987:ARG:NH2	6:AAA:1312:HOH:O	2.43	0.45
1:AAA:1050:LEU:HD21	1:AAA:1089:ILE:HD12	2.02	0.42
1:AAA:1035:ILE:CD1	6:AAA:1323:HOH:O	2.65	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AAA:1357:HOH:O	6:AAA:1425:HOH:O[12_564]	1.85	0.35

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	129/130 (99%)	129 (100%)	0	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	AAA	124/123 (101%)	121 (98%)	3 (2%)	49 18

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	980	MET
1	AAA	981	GLN
1	AAA	1067	ARG

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)

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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	$\#\|Z\| > 2$
4	EDO	AAA	1204	-	3,3,3	0.11	0	2,2,2	0.16	0
2	SO4	AAA	1207	-	4,4,4	0.37	0	6,6,6	0.08	0
4	EDO	AAA	1206	-	3,3,3	0.24	0	2,2,2	0.58	0
4	EDO	AAA	1205	-	3,3,3	0.06	0	2,2,2	0.61	0
2	SO4	AAA	1201	-	4,4,4	0.66	0	6,6,6	0.46	0
4	EDO	AAA	1203	-	3,3,3	0.36	0	2,2,2	0.44	0
5	IK3	AAA	1208	1	19,19,19	0.80	1 (5%)	24,24,24	1.68	5 (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
4	EDO	AAA	1204	-	-	1/1/1/1	-
4	EDO	AAA	1206	-	-	0/1/1/1	-
4	EDO	AAA	1205	-	-	1/1/1/1	-
4	EDO	AAA	1203	-	-	0/1/1/1	-
5	IK3	AAA	1208	1	-	7/16/16/16	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AAA	1208	IK3	C3-N1	-2.56	1.38	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	AAA	1208	IK3	C2-C3-N1	4.54	131.04	112.92
5	AAA	1208	IK3	C5-C4-N1	3.77	124.14	116.54
5	AAA	1208	IK3	O1-C4-N1	-3.40	115.70	122.99
5	AAA	1208	IK3	C4-C5-N2	2.87	118.97	111.16
5	AAA	1208	IK3	C5-N2-C13	2.31	128.35	121.48

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	AAA	1208	IK3	C5-C4-N1-C3
5	AAA	1208	IK3	C14-C13-N2-C5
5	AAA	1208	IK3	O3-C13-N2-C5
5	AAA	1208	IK3	O1-C4-N1-C3
5	AAA	1208	IK3	N2-C5-C6-C7
5	AAA	1208	IK3	C1-C2-C3-N1
4	AAA	1204	EDO	O1-C1-C2-O2
5	AAA	1208	IK3	C4-C5-C6-C7
4	AAA	1205	EDO	O1-C1-C2-O2

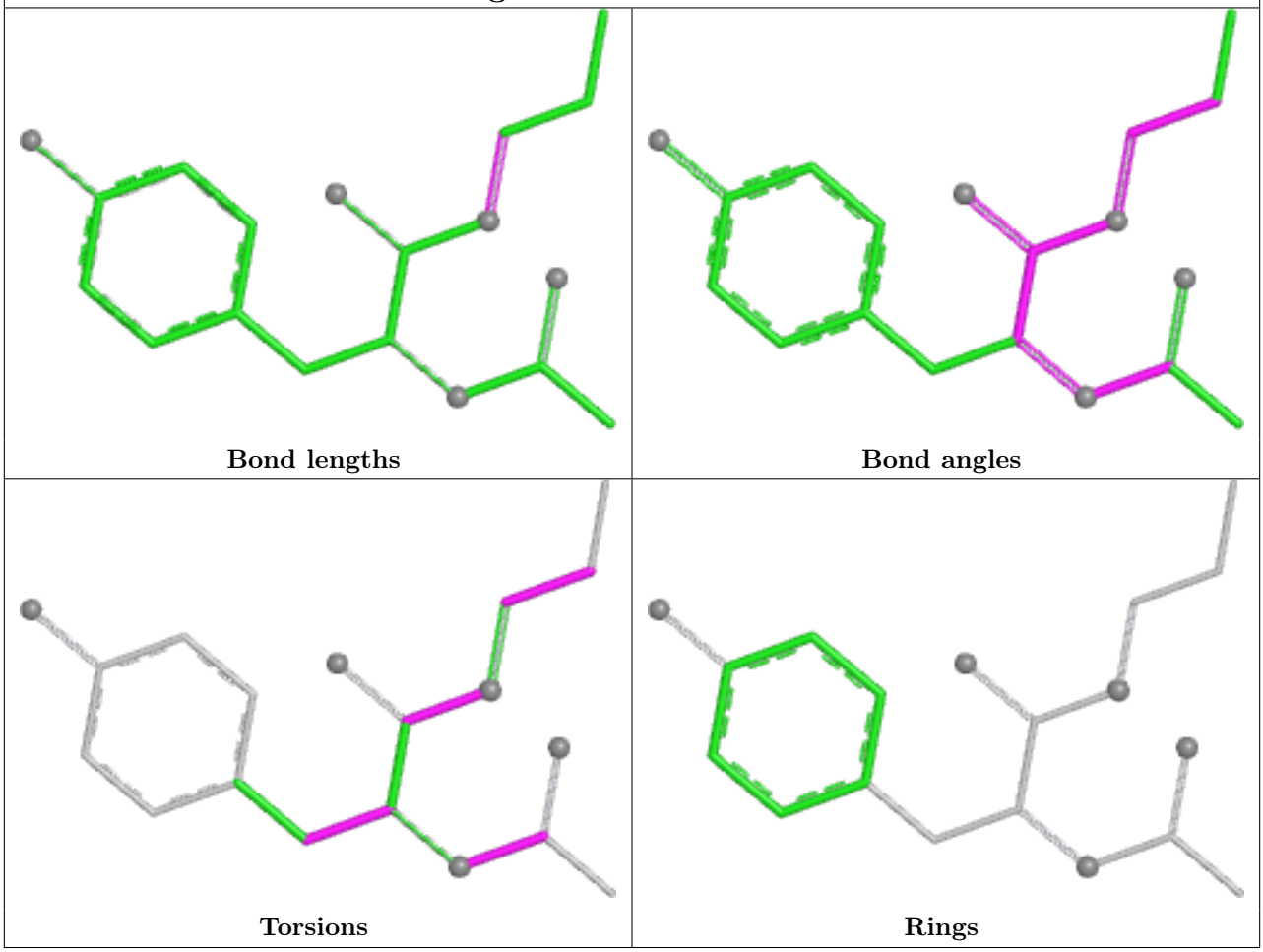
There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	AAA	1204	EDO	3	0
2	AAA	1207	SO4	1	0
4	AAA	1205	EDO	2	0
5	AAA	1208	IK3	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 then 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.

Ligand IK3 AAA 1208



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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AAA	130/130 (100%)	0.74	12 (9%) 9 9	17, 27, 67, 95	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	1018	VAL	6.7
1	AAA	1019	PRO	5.6
1	AAA	1016	ASP	5.1
1	AAA	1014	ASP	5.1
1	AAA	1015	PRO	4.8
1	AAA	1013	VAL	4.6
1	AAA	1022	VAL	4.3
1	AAA	1017	GLU	3.9
1	AAA	980	MET	2.5
1	AAA	1079	CYS	2.5
1	AAA	1020	ASP	2.4
1	AAA	1108	ARG	2.2

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

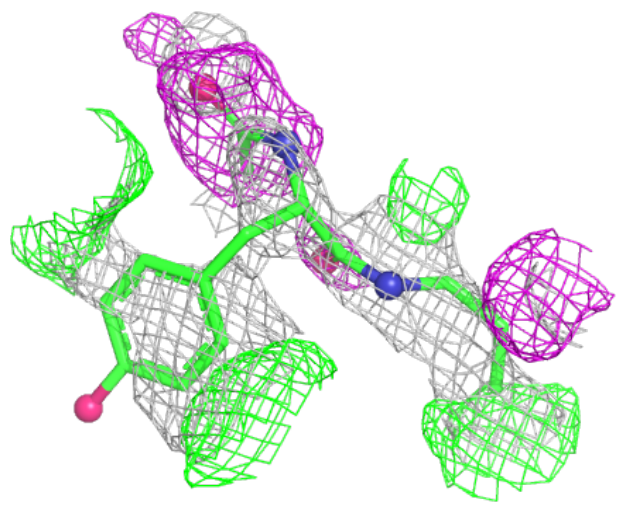
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

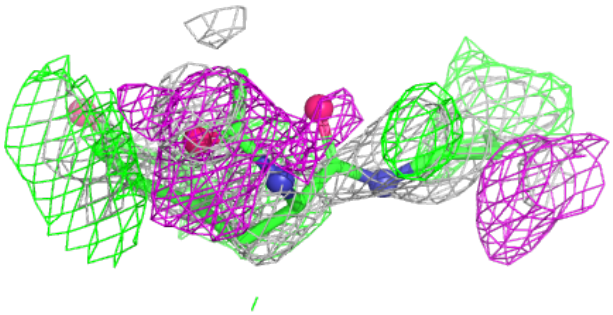
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	IK3	AAA	1208	19/19	0.52	0.45	46,73,99,108	0
4	EDO	AAA	1204	4/4	0.81	0.19	66,66,67,75	0
4	EDO	AAA	1205	4/4	0.85	0.29	45,51,53,71	0
2	SO4	AAA	1207	5/5	0.92	0.12	93,95,101,102	5
4	EDO	AAA	1206	4/4	0.94	0.14	51,59,63,64	0
3	CL	AAA	1202	1/1	0.95	0.13	76,76,76,76	0
2	SO4	AAA	1201	5/5	0.97	0.10	31,34,39,41	0
4	EDO	AAA	1203	4/4	0.97	0.08	24,26,30,31	0

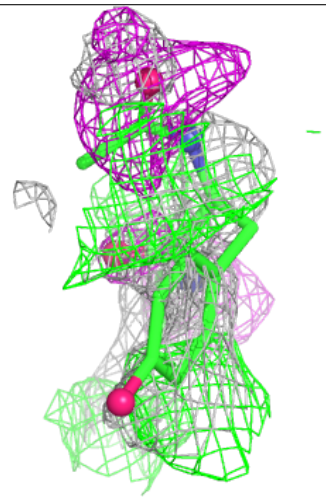
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around IK3 AAA 1208:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.