Full wwPDB X-ray Structure Validation Report ⓘ

Nov 14, 2023 – 06:20 pm GMT

PDB ID	:	6YUL
Title	:	CK2 alpha bound to Macrocycle
Authors	:	Kraemer, A.; Hanke, T.; Kurz, C.; Celik, I.; Knapp, S.; Structural Genomics Consortium (SGC)
Deposited on	:	2020-04-27
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:

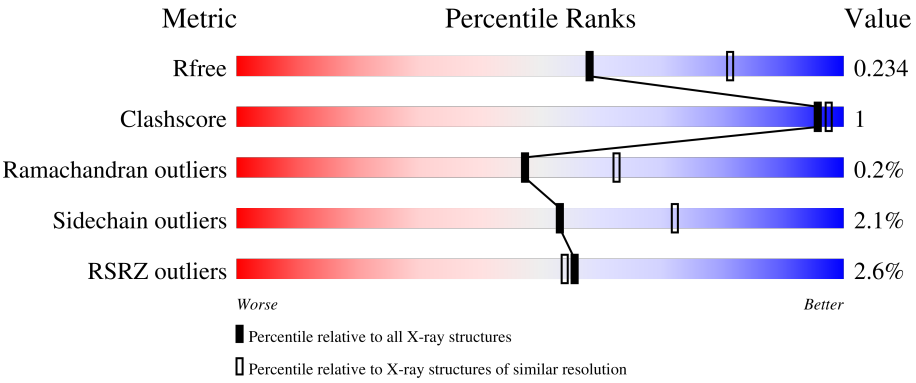
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 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))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (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 <=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	391	2% 81% 15%
1	GGG	391	3% 81% 15%

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
2	SO4	GGG	401	-	-	-	X

2 Entry composition (i)

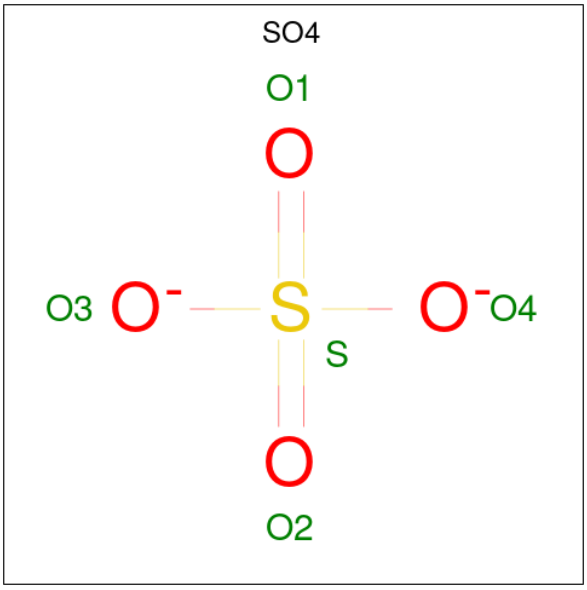
There are 4 unique types of molecules in this entry. The entry contains 5594 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	331	Total	C	N	O	S	0	0	0
			2722	1745	477	489	11			
1	GGG	331	Total	C	N	O	S	0	0	0
			2728	1750	478	489	11			

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



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

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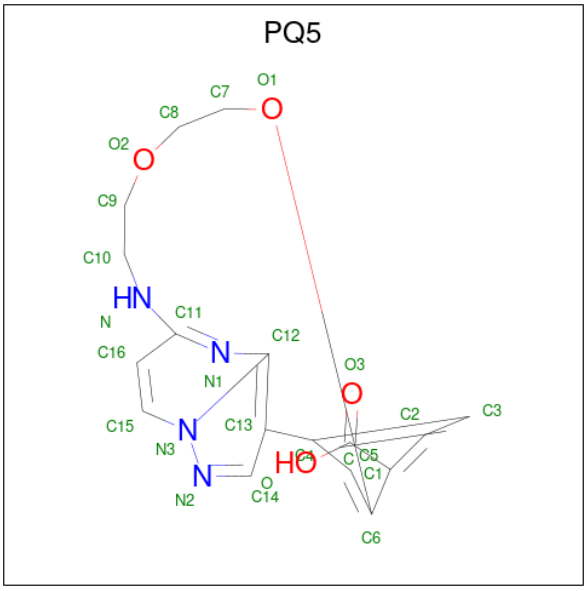
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	AAA	1	Total O S 5 4 1	0	0
2	GGG	1	Total O S 5 4 1	0	0
2	GGG	1	Total O S 5 4 1	0	0
2	GGG	1	Total O S 5 4 1	0	0
2	GGG	1	Total O S 5 4 1	0	0
2	GGG	1	Total O S 5 4 1	0	0

- Molecule 3 is 7,10-Dioxa-13,17,18,21-tetrazatetracyclo[12.5.2.12,6.017,20]docosa-1(20),2(22),3,5,14(21),15,18-heptaene-5-carboxylic acid (three-letter code: PQ5) (formula: $C_{17}H_{16}N_4O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AAA	1	Total C N O 25 17 4 4	0	0
3	GGG	1	Total C N O 25 17 4 4	0	0

- Molecule 4 is water.

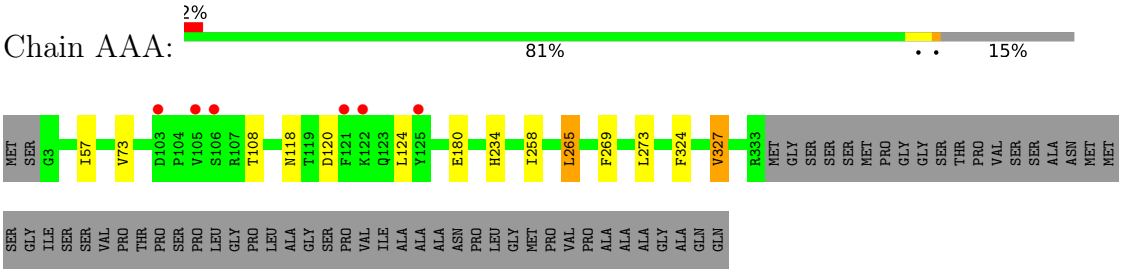
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	29	Total O 29 29	0	0
4	GGG	15	Total O 15 15	0	0

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.

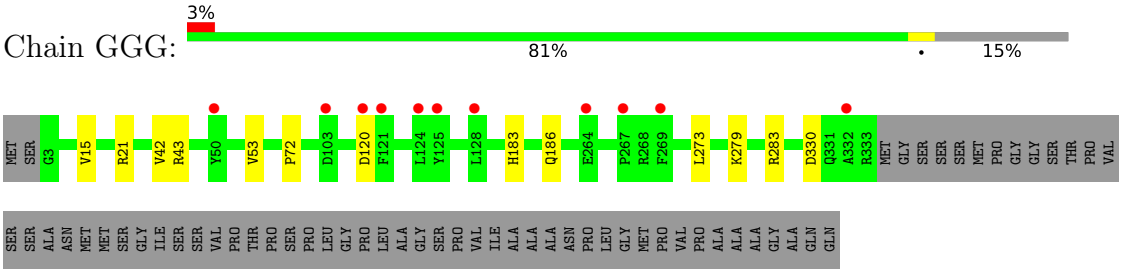
• Molecule 1: Casein kinase II subunit alpha

Chain AAA:



• Molecule 1: Casein kinase II subunit alpha

Chain GGG:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	128.65Å 128.65Å 125.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.48 – 2.40 45.48 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (45.48-2.40) 100.0 (45.48-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.13 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.217 , 0.232 0.221 , 0.234	Depositor DCC
R_{free} test set	2065 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å^2)	57.4	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 34.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,-l,-k 0.000 for l,-k,h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5594	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.03 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.1994e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, PQ5

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	0.60	0/2795	0.69	0/3791
1	GGG	0.61	0/2801	0.70	0/3798
All	All	0.60	0/5596	0.70	0/7589

There are no bond length outliers.

There are no bond angle outliers.

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	AAA	2722	0	2610	8	0
1	GGG	2728	0	2618	6	0
2	AAA	25	0	0	0	0
2	GGG	25	0	0	0	0
3	AAA	25	0	0	0	0
3	GGG	25	0	0	1	0
4	AAA	29	0	0	0	0
4	GGG	15	0	0	0	0
All	All	5594	0	5228	12	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 1.

All (12) 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:120:ASP:O	1:AAA:124:LEU:N	2.35	0.60
1:AAA:73:VAL:HA	1:GGG:72:PRO:HG2	1.84	0.59
1:GGG:279:LYS:HA	1:GGG:283:ARG:NH1	2.30	0.47
1:AAA:73:VAL:CA	1:GGG:72:PRO:HG2	2.47	0.45
1:AAA:324:PHE:O	1:AAA:327:VAL:HG13	2.17	0.44
1:AAA:120:ASP:O	1:AAA:124:LEU:HB2	2.19	0.43
1:GGG:42:VAL:HG12	1:GGG:43:ARG:HG2	2.01	0.42
1:GGG:53:VAL:HG21	3:GGG:404:PQ5:C7	2.49	0.42
1:GGG:183:HIS:HD2	1:GGG:186:GLN:HE22	1.68	0.41
1:AAA:258:ILE:HD13	1:AAA:265:LEU:HG	2.03	0.41
1:AAA:265:LEU:HD23	1:AAA:265:LEU:HA	1.86	0.41
1:AAA:265:LEU:HD22	1:AAA:269:PHE:CD2	2.56	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	329/391 (84%)	321 (98%)	8 (2%)	0	100	100
1	GGG	329/391 (84%)	320 (97%)	8 (2%)	1 (0%)	41	55
All	All	658/782 (84%)	641 (97%)	16 (2%)	1 (0%)	47	62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	GGG	120	ASP

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	286/347 (82%)	278 (97%)	8 (3%)	43	63
1	GGG	286/347 (82%)	282 (99%)	4 (1%)	67	82
All	All	572/694 (82%)	560 (98%)	12 (2%)	53	72

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	57	ILE
1	AAA	108	THR
1	AAA	118	ASN
1	AAA	180	GLU
1	AAA	234	HIS
1	AAA	265	LEU
1	AAA	273	LEU
1	AAA	327	VAL
1	GGG	15	VAL
1	GGG	21	ARG
1	GGG	273	LEU
1	GGG	330	ASP

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)

12 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	SO4	AAA	401	-	4,4,4	0.43	0	6,6,6	0.10	0
2	SO4	AAA	404	-	4,4,4	0.34	0	6,6,6	0.07	0
2	SO4	AAA	405	-	4,4,4	0.32	0	6,6,6	0.09	0
3	PQ5	AAA	403	-	22,28,28	0.32	0	26,39,39	0.58	1 (3%)
2	SO4	GGG	406	-	4,4,4	0.37	0	6,6,6	0.10	0
2	SO4	AAA	402	-	4,4,4	0.34	0	6,6,6	0.07	0
2	SO4	GGG	402	-	4,4,4	0.36	0	6,6,6	0.11	0
2	SO4	GGG	403	-	4,4,4	0.34	0	6,6,6	0.06	0
2	SO4	GGG	405	-	4,4,4	0.36	0	6,6,6	0.07	0
3	PQ5	GGG	404	-	22,28,28	0.37	0	26,39,39	0.77	1 (3%)
2	SO4	AAA	406	-	4,4,4	0.36	0	6,6,6	0.09	0
2	SO4	GGG	401	-	4,4,4	0.38	0	6,6,6	0.04	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	PQ5	AAA	403	-	-	12/18/18/18	0/3/4/4
3	PQ5	GGG	404	-	-	10/18/18/18	0/3/4/4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	GGG	404	PQ5	C11-N1-C12	-3.46	114.44	117.59
3	AAA	403	PQ5	C11-N1-C12	-2.02	115.76	117.59

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	AAA	403	PQ5	C12-C13-C4-C3
3	AAA	403	PQ5	C12-C13-C4-C5
3	AAA	403	PQ5	C14-C13-C4-C3
3	AAA	403	PQ5	C14-C13-C4-C5
3	GGG	404	PQ5	C12-C13-C4-C3
3	GGG	404	PQ5	C12-C13-C4-C5
3	GGG	404	PQ5	C14-C13-C4-C3
3	GGG	404	PQ5	C14-C13-C4-C5
3	AAA	403	PQ5	O1-C7-C8-O2
3	GGG	404	PQ5	O1-C7-C8-O2
3	AAA	403	PQ5	N-C10-C9-O2
3	AAA	403	PQ5	O3-C-C1-C6
3	GGG	404	PQ5	C7-C8-O2-C9
3	GGG	404	PQ5	N-C10-C9-O2
3	GGG	404	PQ5	O3-C-C1-C6
3	GGG	404	PQ5	C10-C9-O2-C8
3	AAA	403	PQ5	C8-C7-O1-C6
3	GGG	404	PQ5	C8-C7-O1-C6
3	AAA	403	PQ5	C7-C8-O2-C9
3	AAA	403	PQ5	C16-C11-N-C10
3	AAA	403	PQ5	N1-C11-N-C10
3	AAA	403	PQ5	C5-C6-O1-C7

There are no ring outliers.

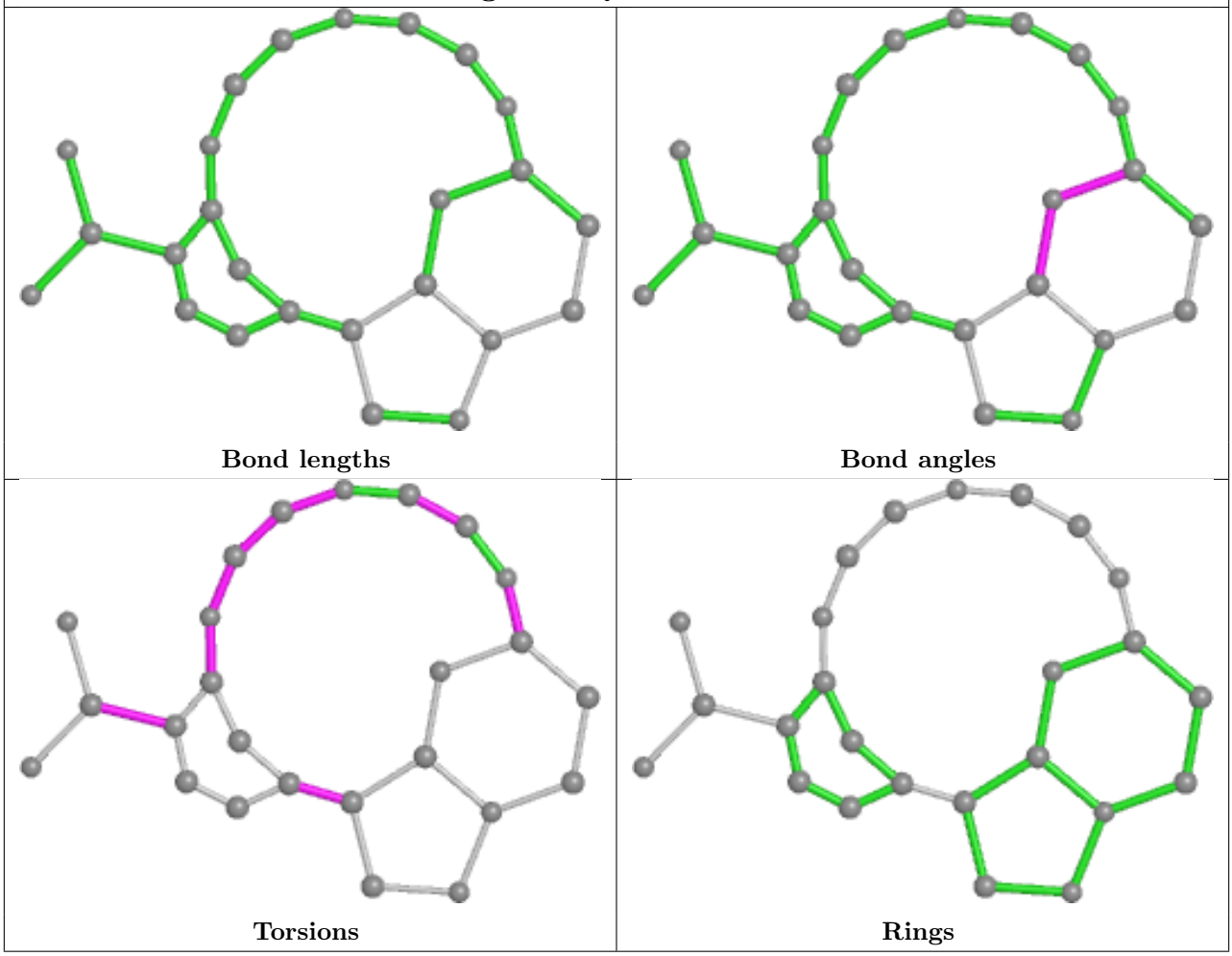
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	GGG	404	PQ5	1	0

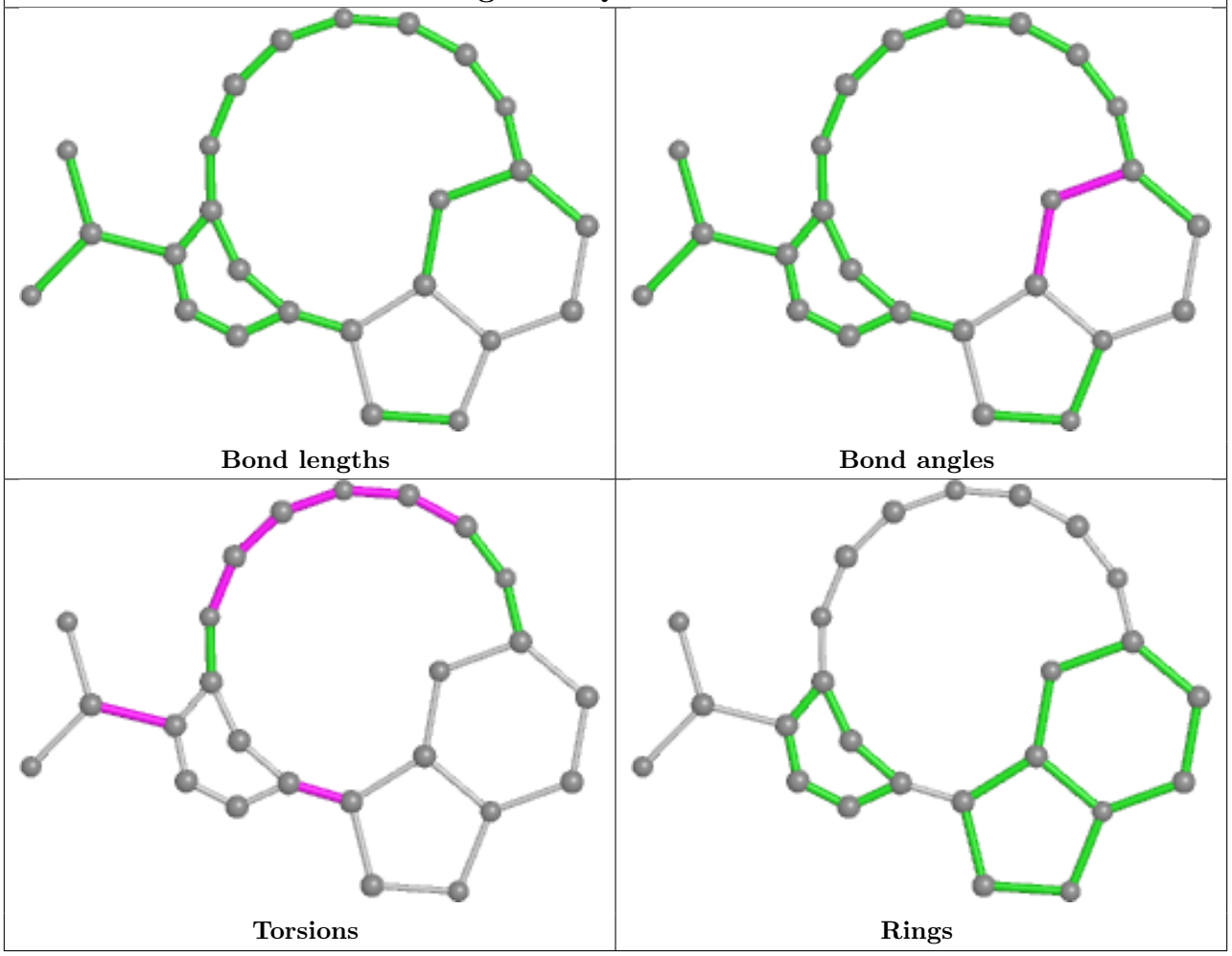
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 PQ5 AAA 403



Ligand PQ5 GGG 404



5.7 Other polymers

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

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^{th} 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	331/391 (84%)	-0.00	6 (1%)	68	66	41, 57, 96, 147	0
1	GGG	331/391 (84%)	0.11	11 (3%)	46	45	40, 60, 101, 133	0
All	All	662/782 (84%)	0.05	17 (2%)	56	54	40, 58, 99, 147	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	103	ASP	4.8
1	AAA	125	TYR	4.8
1	GGG	125	TYR	4.7
1	AAA	105	VAL	3.8
1	GGG	332	ALA	3.3
1	GGG	128	LEU	3.2
1	GGG	50	TYR	3.2
1	AAA	106	SER	2.8
1	AAA	122	LYS	2.8
1	GGG	124	LEU	2.7
1	GGG	267	PRO	2.5
1	GGG	264	GLU	2.5
1	GGG	120	ASP	2.5
1	GGG	269	PHE	2.4
1	AAA	121	PHE	2.1
1	GGG	103	ASP	2.1
1	GGG	121	PHE	2.1

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

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)

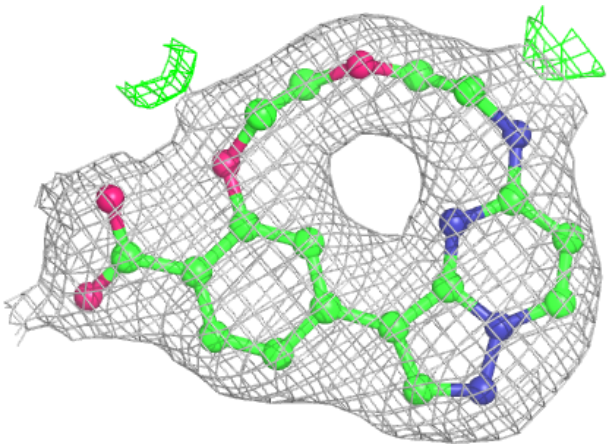
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

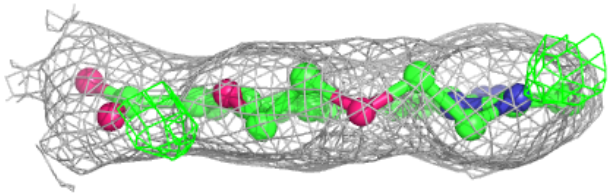
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	GGG	401	5/5	0.57	0.79	155,157,162,163	0
2	SO4	GGG	403	5/5	0.83	0.29	101,105,114,118	0
2	SO4	GGG	405	5/5	0.86	0.14	106,109,116,117	0
2	SO4	AAA	406	5/5	0.87	0.17	89,90,97,104	0
2	SO4	GGG	406	5/5	0.87	0.20	96,97,105,105	0
2	SO4	AAA	404	5/5	0.92	0.16	77,79,88,91	0
2	SO4	AAA	402	5/5	0.94	0.11	72,75,83,85	0
3	PQ5	AAA	403	25/25	0.94	0.13	45,49,61,63	0
2	SO4	GGG	402	5/5	0.96	0.13	69,70,76,79	0
3	PQ5	GGG	404	25/25	0.96	0.14	47,53,58,60	0
2	SO4	AAA	401	5/5	0.98	0.11	64,64,65,66	0
2	SO4	AAA	405	5/5	0.98	0.12	66,70,74,76	0

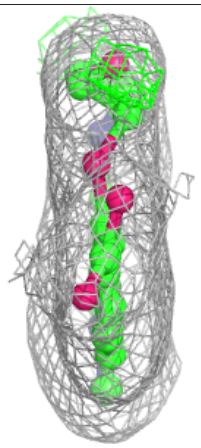
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PQ5 AAA 403:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

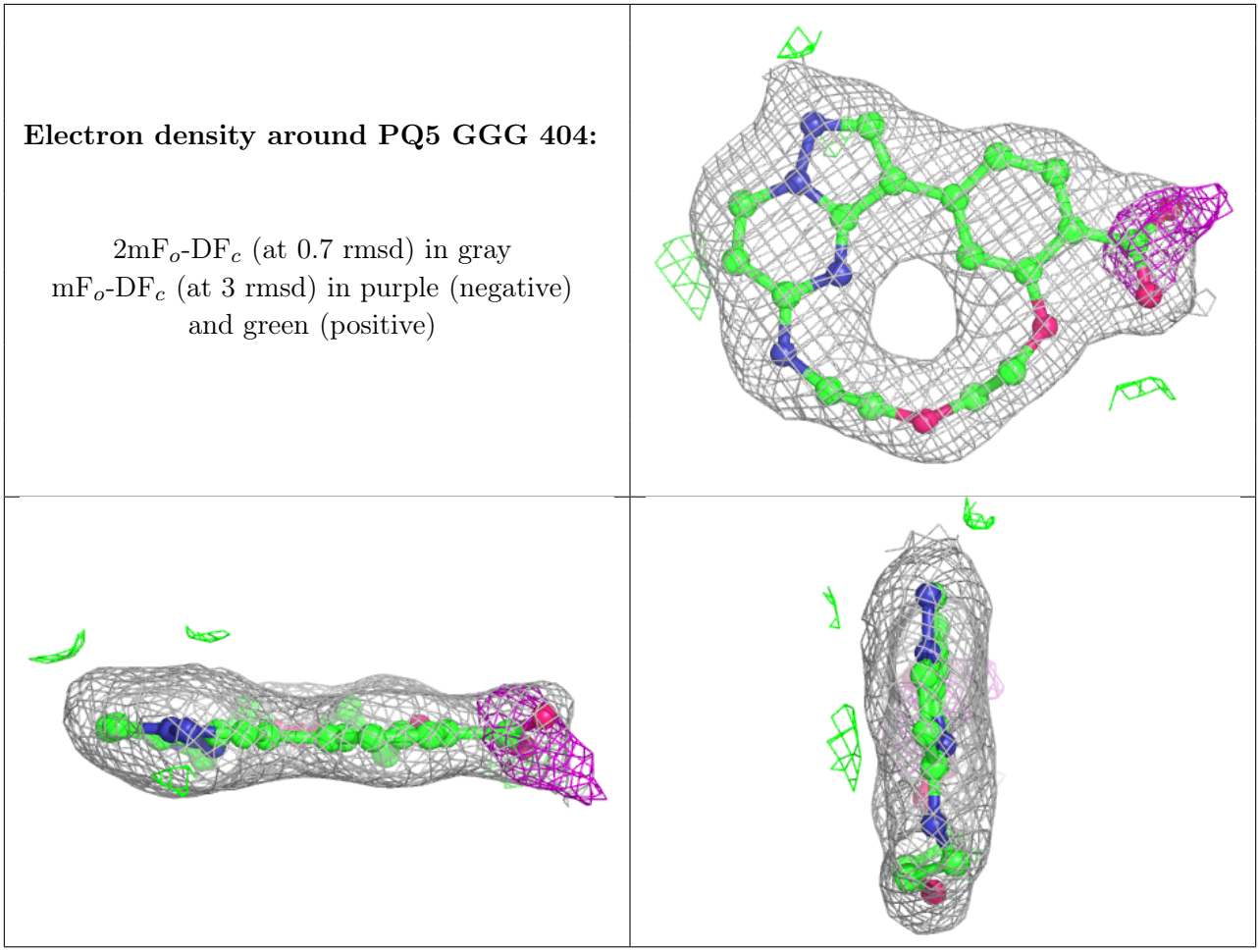






Electron density around PQ5 GGG 404:

$2mF_o$-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

There are no such residues in this entry.