Full wwPDB X-ray Structure Validation Report (i)

Jan 15, 2024 – 11:52 am GMT

PDB ID	:	6Z84
Title	:	CK2 alpha bound to chemical probe SGC-CK2-1 derivative
Authors	:	Kraemer, A.; Wells, C.; Drewry, D.H.; Pickett, J.E.; Axtman, A.D.; Knapp, S.; Structural Genomics Consortium (SGC)
Deposited on	:	2020-06-02
Resolution	:	2.50 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:

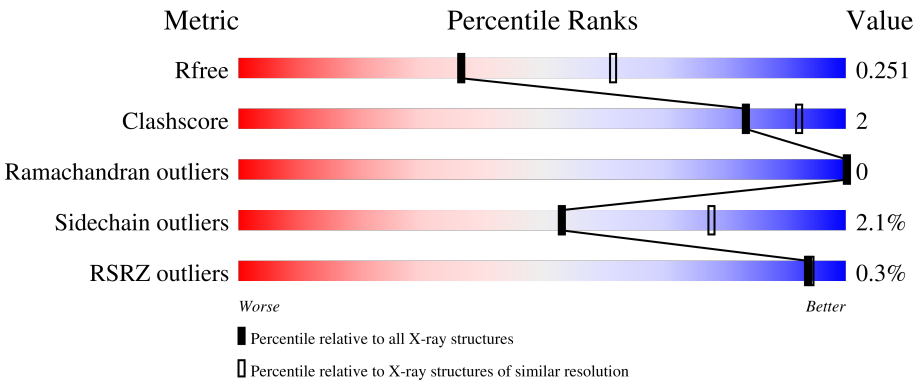
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	338	88% 9% •
1	BBB	338	91% 6% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5708 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.

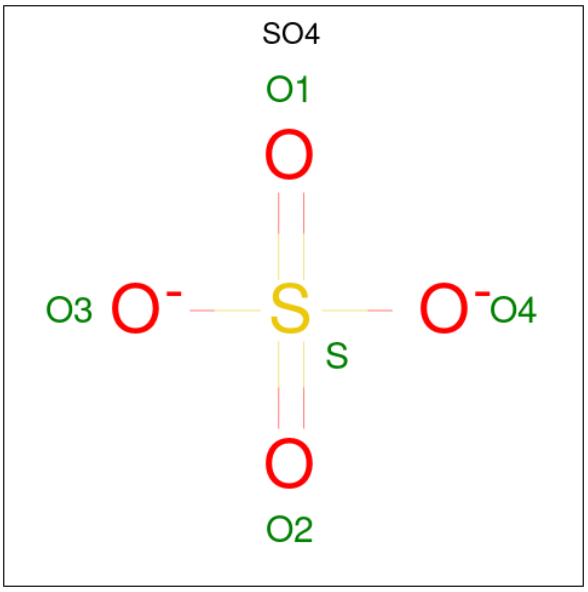
- Molecule 1 is a protein called Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	326	2697	1735	468	483	11	0	0	0
1	BBB	329	2718	1750	468	489	11	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	0	SER	-	expression tag	UNP P68400
BBB	0	SER	-	expression tag	UNP P68400

- 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

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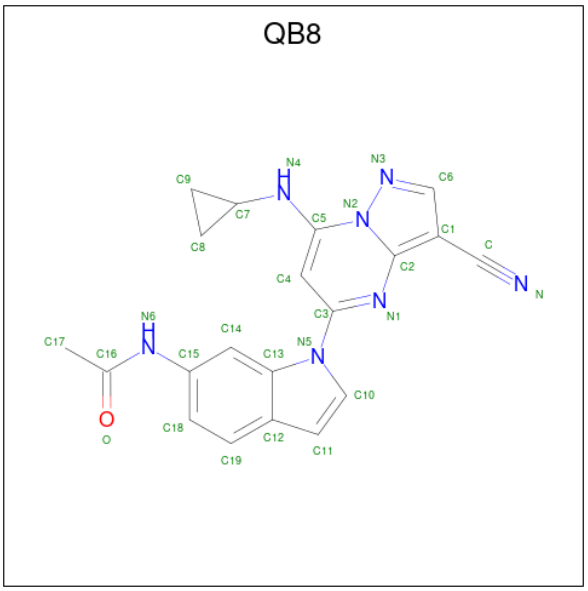
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
2	AAA	1	5	4	1		0	0
			Total	O	S			
2	AAA	1	5	4	1		0	0
			Total	O	S			
2	AAA	1	5	4	1		0	0
			Total	O	S			
2	AAA	1	5	4	1		0	0
			Total	O	S			
2	AAA	1	5	4	1		0	0
			Total	O	S			
2	AAA	1	5	4	1		0	0
			Total	O	S			
2	AAA	1	5	4	1		0	0
			Total	O	S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

- Molecule 3 is {N}-[1-[3-cyano-7-(cyclopropylamino)pyrazolo[1,5-a]pyrimidin-5-yl]indol-6-yl] ethanamide (three-letter code: QB8) (formula: $C_{20}H_{17}N_7O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	AAA	1	28	20	7	1	0	0
			Total	C	N	O		
3	BBB	1	28	20	7	1	0	0

- Molecule 4 is water.

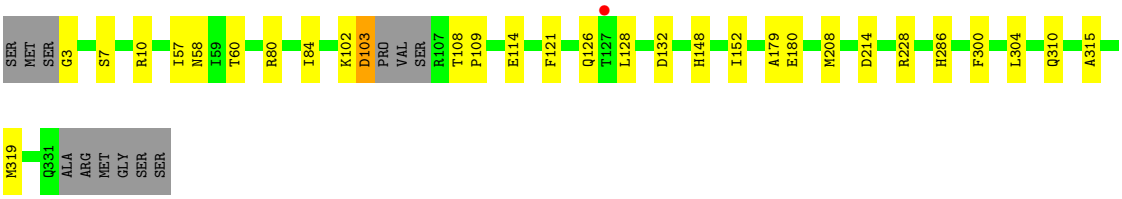
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	AAA	90	90	90	0	0
			Total	O		
4	BBB	87	87	87	0	0

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.

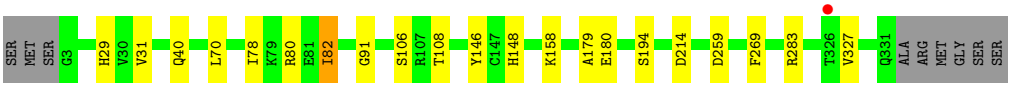
• Molecule 1: Casein kinase II subunit alpha

Chain AAA:



• Molecule 1: Casein kinase II subunit alpha

Chain BBB:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	126.35Å 126.35Å 124.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.67 – 2.50 44.67 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.67-2.50) 100.0 (44.67-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.40 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.215 , 0.250 0.219 , 0.251	Depositor DCC
R_{free} test set	1850 reflections (5.21%)	wwPDB-VP
Wilson B-factor (Å^2)	38.8	Xtriage
Anisotropy	0.630	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 39.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.004 for -h,-l,-k 0.000 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5708	wwPDB-VP
Average B, all atoms (Å^2)	43.0	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 30.65 % 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 1.2621e-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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, QB8

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	0.59	0/2770	0.68	0/3755
1	BBB	0.59	0/2793	0.68	0/3789
All	All	0.59	0/5563	0.68	0/7544

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 (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	2697	0	2589	16	0
1	BBB	2718	0	2610	10	0
2	AAA	40	0	0	0	0
2	BBB	20	0	0	1	0
3	AAA	28	0	0	0	0
3	BBB	28	0	0	0	0
4	AAA	90	0	0	2	0
4	BBB	87	0	0	1	0
All	All	5708	0	5199	26	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 2.

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:BBB:78:ILE:O	1:BBB:82:ILE:HG23	1.86	0.76
1:AAA:80:ARG:HD3	1:AAA:179:ALA:O	1.86	0.75
1:BBB:106:SER:OG	1:BBB:108:THR:HG22	1.94	0.68
1:BBB:80:ARG:HD3	1:BBB:179:ALA:O	1.93	0.68
1:AAA:7:SER:O	1:AAA:208:MET:HE2	1.99	0.62
1:AAA:286:HIS:HB2	4:AAA:556:HOH:O	2.04	0.57
1:BBB:29:HIS:NE2	1:BBB:82:ILE:HD11	2.21	0.56
1:AAA:7:SER:H	1:AAA:208:MET:HE2	1.75	0.51
1:AAA:7:SER:O	1:AAA:208:MET:CE	2.60	0.49
1:BBB:91:GLY:HA3	1:BBB:146:TYR:CE2	2.49	0.48
1:BBB:80:ARG:HD2	4:BBB:510:HOH:O	2.14	0.47
1:AAA:102:LYS:O	1:AAA:103:ASP:HB2	2.15	0.47
1:BBB:283:ARG:NH1	2:BBB:401:SO4:O1	2.50	0.45
1:AAA:315:ALA:O	1:AAA:319:MET:HG3	2.17	0.45
1:AAA:3:GLY:N	4:AAA:505:HOH:O	2.51	0.44
1:AAA:84:ILE:HG12	1:AAA:152:ILE:HD12	2.00	0.44
1:AAA:126:GLN:HE22	1:AAA:228:ARG:CZ	2.30	0.44
1:AAA:108:THR:HA	1:AAA:109:PRO:HD3	1.89	0.43
1:AAA:128:LEU:HD22	1:AAA:132:ASP:HB3	2.00	0.43
1:AAA:148:HIS:HE1	1:AAA:214:ASP:OD2	2.03	0.42
1:AAA:10:ARG:HD2	1:AAA:310:GLN:O	2.20	0.42
1:BBB:70:LEU:HD13	1:BBB:78:ILE:HG12	2.02	0.41
1:BBB:148:HIS:HE1	1:BBB:214:ASP:OD2	2.04	0.41
1:AAA:58:ASN:OD1	1:AAA:60:THR:HB	2.21	0.41
1:AAA:300:PHE:CZ	1:AAA:304:LEU:HD11	2.56	0.41
1:BBB:158:LYS:HD3	1:BBB:194:SER:OG	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	322/338 (95%)	315 (98%)	7 (2%)	0	100	100
1	BBB	327/338 (97%)	320 (98%)	7 (2%)	0	100	100
All	All	649/676 (96%)	635 (98%)	14 (2%)	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	285/310 (92%)	280 (98%)	5 (2%)	59	81
1	BBB	288/310 (93%)	281 (98%)	7 (2%)	49	74
All	All	573/620 (92%)	561 (98%)	12 (2%)	53	78

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

Mol	Chain	Res	Type
1	AAA	57	ILE
1	AAA	103	ASP
1	AAA	114	GLU
1	AAA	121	PHE
1	AAA	180	GLU
1	BBB	31	VAL
1	BBB	40	GLN
1	BBB	82	ILE
1	BBB	180	GLU
1	BBB	259	ASP
1	BBB	269	PHE
1	BBB	327	VAL

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)

14 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	405	-	4,4,4	0.38	0	6,6,6	0.08	0
2	SO4	BBB	401	-	4,4,4	0.37	0	6,6,6	0.07	0
2	SO4	AAA	401	-	4,4,4	0.36	0	6,6,6	0.05	0
2	SO4	AAA	407	-	4,4,4	0.39	0	6,6,6	0.06	0
2	SO4	AAA	408	-	4,4,4	0.38	0	6,6,6	0.05	0
2	SO4	BBB	404	-	4,4,4	0.36	0	6,6,6	0.05	0
3	QB8	AAA	406	-	27,32,32	0.73	1 (3%)	30,47,47	0.97	2 (6%)
2	SO4	AAA	403	-	4,4,4	0.37	0	6,6,6	0.06	0
2	SO4	BBB	405	-	4,4,4	0.39	0	6,6,6	0.06	0
2	SO4	BBB	403	-	4,4,4	0.40	0	6,6,6	0.06	0
2	SO4	AAA	402	-	4,4,4	0.38	0	6,6,6	0.05	0
2	SO4	AAA	404	-	4,4,4	0.39	0	6,6,6	0.05	0
2	SO4	AAA	409	-	4,4,4	0.36	0	6,6,6	0.06	0
3	QB8	BBB	402	-	27,32,32	0.72	0	30,47,47	1.00	1 (3%)

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	QB8	BBB	402	-	-	2/10/16/16	0/5/5/5
3	QB8	AAA	406	-	-	2/10/16/16	0/5/5/5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	AAA	406	QB8	C4-C3	2.04	1.42	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	BBB	402	QB8	N1-C3-N5	2.98	118.39	114.66
3	AAA	406	QB8	N1-C3-N5	2.35	117.59	114.66
3	AAA	406	QB8	C5-C4-C3	2.27	120.85	118.09

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	AAA	406	QB8	O-C16-N6-C15
3	AAA	406	QB8	C17-C16-N6-C15
3	BBB	402	QB8	O-C16-N6-C15
3	BBB	402	QB8	C17-C16-N6-C15

There are no ring outliers.

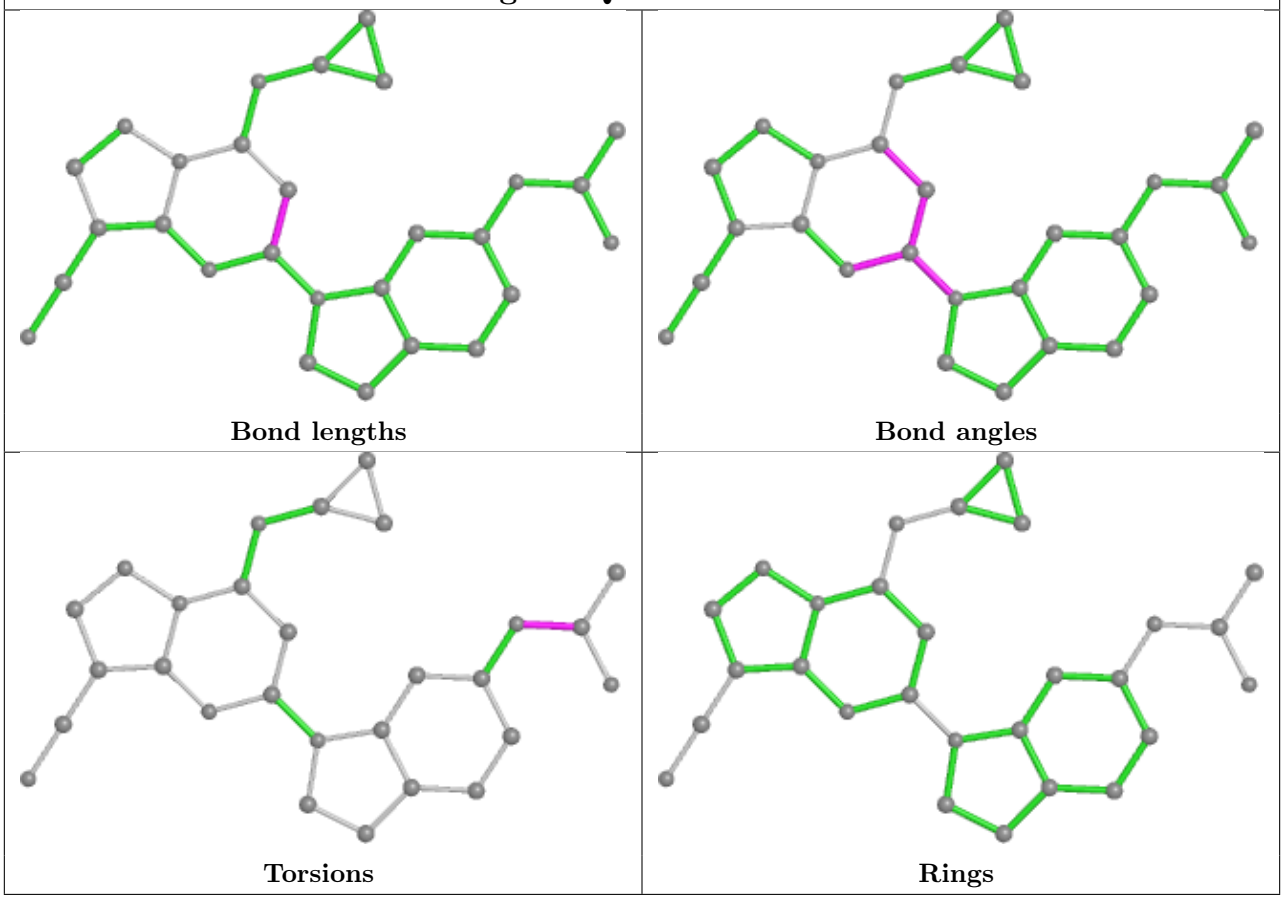
1 monomer is involved in 1 short contact:

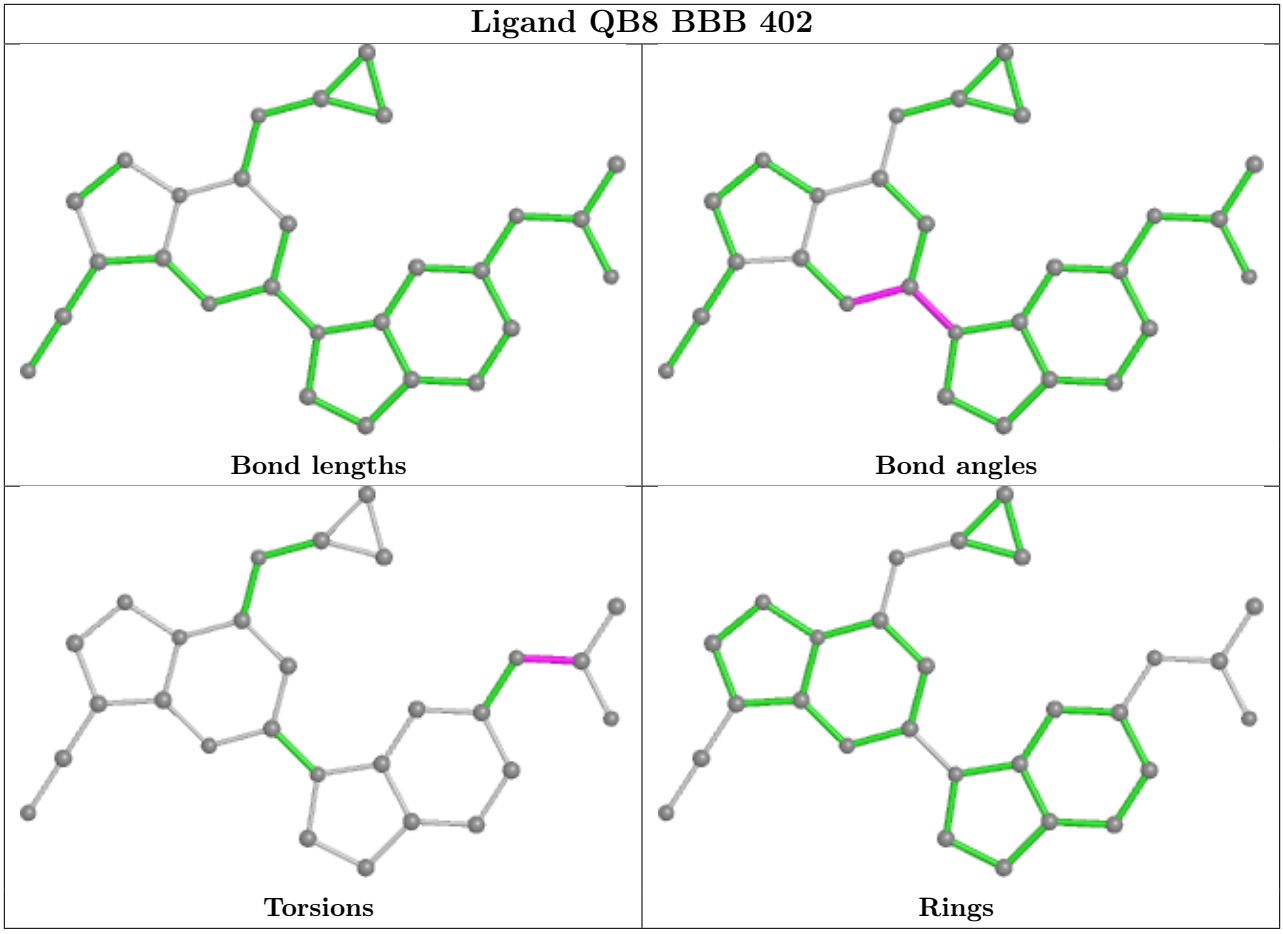
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	BBB	401	SO4	1	0

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 QB8 AAA 406





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	326/338 (96%)	-0.15	1 (0%)	94	94	28, 41, 70, 94	0
1	BBB	329/338 (97%)	-0.18	1 (0%)	94	94	28, 42, 64, 85	0
All	All	655/676 (96%)	-0.16	2 (0%)	94	94	28, 41, 67, 94	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	326	THR	2.2
1	AAA	127	THR	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, 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
2	SO4	AAA	401	5/5	0.85	0.18	90,93,95,97	0
2	SO4	BBB	404	5/5	0.90	0.17	87,88,90,90	0
2	SO4	AAA	409	5/5	0.93	0.12	73,73,75,78	0

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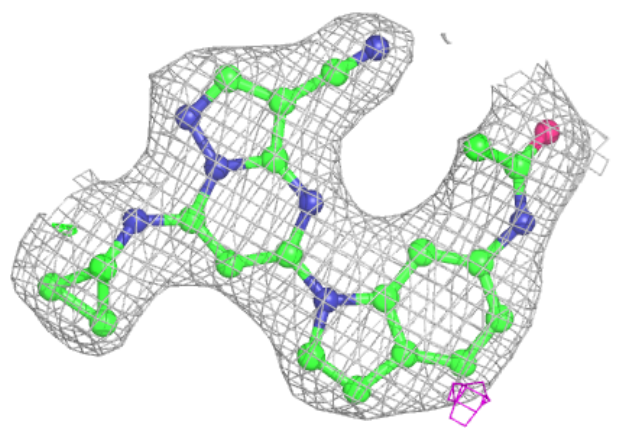
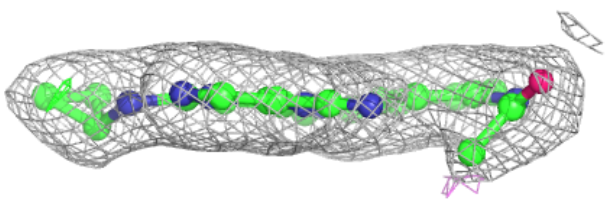
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	BBB	405	5/5	0.94	0.16	92,92,93,93	0
2	SO4	AAA	402	5/5	0.95	0.12	65,65,69,69	0
2	SO4	BBB	401	5/5	0.96	0.11	58,60,63,64	0
2	SO4	AAA	408	5/5	0.96	0.15	88,90,90,90	0
2	SO4	AAA	404	5/5	0.96	0.09	76,77,77,78	0
2	SO4	AAA	403	5/5	0.97	0.12	64,66,67,69	0
2	SO4	BBB	403	5/5	0.97	0.13	54,55,57,57	0
3	QB8	AAA	406	28/28	0.97	0.12	30,33,38,39	0
3	QB8	BBB	402	28/28	0.97	0.14	35,37,38,38	0
2	SO4	AAA	405	5/5	0.98	0.10	47,48,49,50	0
2	SO4	AAA	407	5/5	0.98	0.09	49,51,52,52	0

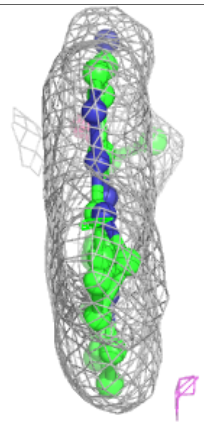
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around QB8 AAA 406:

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

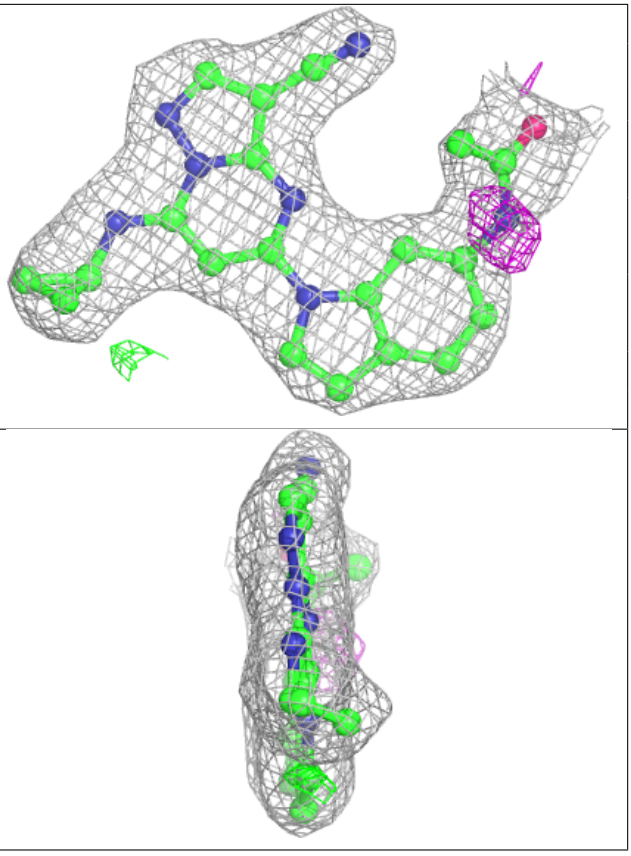


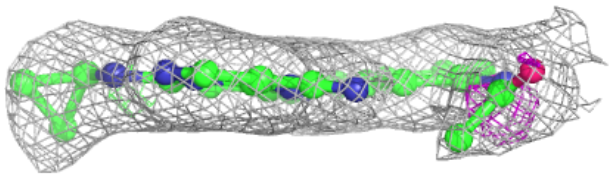




Electron density around QB8 BBB 402:

$2mF_o$-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.