



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:57 PM UTC

PDB ID : 6YUM / pdb_00006yum
Title : CK2 alpha bound to unclosed Macrocycle
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Deposited on : 2020-04-27
Resolution : 2.75 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)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

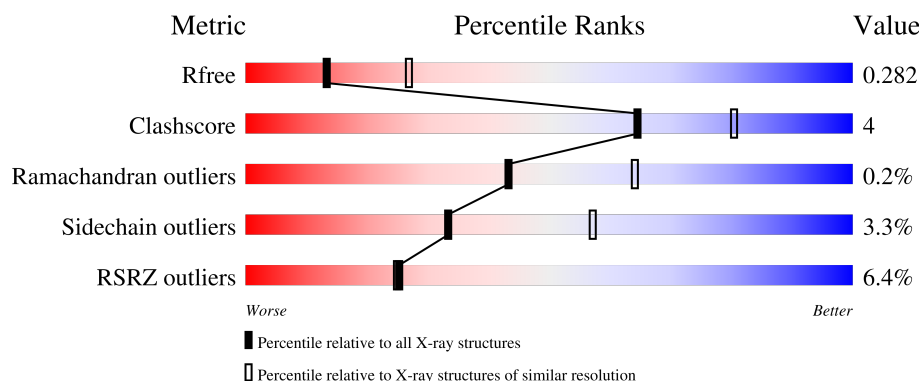
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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}	180053	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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 $\leq 5\%$. 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	 4% 75% 9% 15%
1	GGG	391	 7% 72% 10% 17%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5421 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
			2689	1729	463	486	11			
1	GGG	325	Total	C	N	O	S	0	0	0
			2634	1693	460	470	11			

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



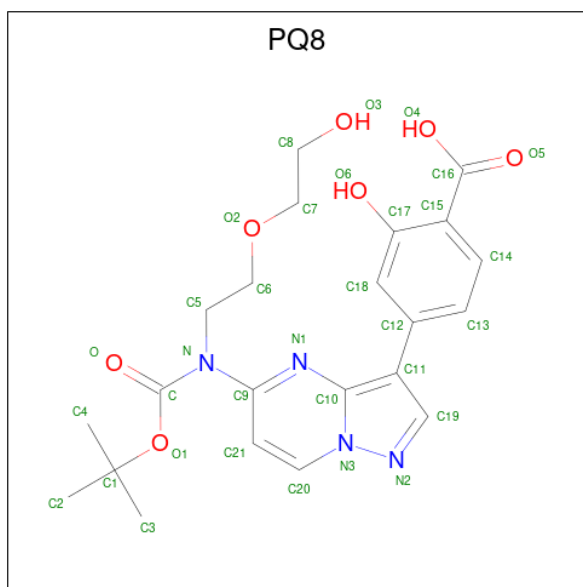
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AAA	1	Total	O	S	0	0
			5	4	1		
2	AAA	1	Total	O	S	0	0
			5	4	1		
2	AAA	1	Total	O	S	0	0
			5	4	1		
2	GGG	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 3 is 4-[5-[2-(2-hydroxyethoxy)ethyl-[(2-methylpropan-2-yl)oxycarbonyl]amino]pyrazolo[1,5-a]pyrimidin-3-yl]-2-oxidanyl-benzoic acid (CCD ID: PQ8) (formula: $C_{22}H_{26}N_4O_7$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	AAA	1	Total	C	N	O	0	0
			33	22	4	7		
3	GGG	1	Total	C	N	O	0	0
			33	22	4	7		

- Molecule 4 is water.

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

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	125.48Å 125.48Å 124.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.36 – 2.75 44.36 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.36-2.75) 99.8 (44.36-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.263 , 0.284 0.262 , 0.282	Depositor DCC
R_{free} test set	1407 reflections (5.31%)	wwPDB-VP
Wilson B-factor (Å ²)	70.0	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.003 for -h,-l,-k 0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5421	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: PQ8, SO4

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	0.88	0/2764	1.01	0/3757
1	GGG	0.91	1/2705 (0.0%)	1.00	0/3674
All	All	0.89	1/5469 (0.0%)	1.01	0/7431

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	GGG	238	ASN	C-O	5.65	1.30	1.24

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	2689	0	2516	20	0
1	GGG	2634	0	2474	21	0
2	AAA	15	0	0	0	0
2	GGG	15	0	0	0	0
3	AAA	33	0	0	0	0
3	GGG	33	0	0	0	0
4	AAA	1	0	0	0	0
4	GGG	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5421	0	4990	41	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 4.

All (41) 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:GGG:324:PHE:O	1:GGG:328:VAL:HG13	1.86	0.76
1:GGG:118:ASN:HD22	1:GGG:164:ILE:H	1.42	0.67
1:AAA:195:ARG:NH1	1:AAA:236:HIS:O	2.29	0.66
1:AAA:254:LEU:O	1:AAA:258:ILE:HG23	1.97	0.64
1:GGG:33:TRP:CZ3	1:GGG:100:ILE:HG22	2.39	0.57
1:GGG:84:ILE:HG23	1:GGG:152:ILE:HD13	1.86	0.57
1:AAA:84:ILE:HG23	1:AAA:152:ILE:HD13	1.86	0.57
1:GGG:163:MET:HE2	1:GGG:163:MET:HA	1.89	0.55
1:AAA:125:TYR:CZ	1:AAA:225:MET:HE3	2.42	0.55
1:GGG:118:ASN:ND2	1:GGG:164:ILE:H	2.05	0.54
1:AAA:163:MET:HA	1:AAA:163:MET:HE2	1.88	0.54
1:AAA:11:VAL:HG21	1:AAA:314:THR:HG21	1.91	0.52
1:AAA:281:TRP:HB3	1:AAA:298:LEU:HD22	1.90	0.52
1:AAA:249:LEU:HB3	1:AAA:307:TYR:CE2	2.44	0.52
1:AAA:267:PRO:O	1:AAA:270:ASN:ND2	2.43	0.52
1:AAA:299:ASP:O	1:AAA:303:LYS:HG3	2.09	0.52
1:AAA:125:TYR:CE2	1:AAA:225:MET:HE3	2.45	0.51
1:GGG:300:PHE:CZ	1:GGG:304:LEU:HD11	2.45	0.51
1:GGG:91:GLY:HA3	1:GGG:146:TYR:CE2	2.47	0.50
1:GGG:299:ASP:O	1:GGG:303:LYS:HG3	2.10	0.50
1:AAA:300:PHE:CZ	1:AAA:304:LEU:HD11	2.46	0.50
1:AAA:137:MET:HE1	1:AAA:218:LEU:HG	1.94	0.49
1:GGG:137:MET:HE1	1:GGG:218:LEU:HG	1.93	0.49
1:AAA:195:ARG:CZ	1:AAA:236:HIS:O	2.60	0.49
1:GGG:281:TRP:HB3	1:GGG:298:LEU:HD22	1.93	0.49
1:GGG:33:TRP:CE3	1:GGG:100:ILE:HG22	2.49	0.48
1:AAA:91:GLY:HA3	1:AAA:146:TYR:CE2	2.48	0.48
1:GGG:36:GLN:HB3	1:GGG:103:ASP:HA	1.96	0.47
1:AAA:11:VAL:HG21	1:AAA:314:THR:CG2	2.45	0.46
1:GGG:29:HIS:O	1:GGG:79:LYS:HE3	2.17	0.44
1:GGG:231:PRO:HD2	1:GGG:234:HIS:ND1	2.33	0.44
1:GGG:33:TRP:CH2	1:GGG:109:PRO:HB3	2.53	0.44
1:GGG:171:LEU:O	1:GGG:172:ARG:NH1	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GGG:108:THR:HA	1:GGG:109:PRO:HD3	1.87	0.42
1:GGG:265:LEU:HD23	1:GGG:265:LEU:HA	1.91	0.42
1:AAA:78:ILE:HD13	1:AAA:109:PRO:HG2	2.02	0.41
1:AAA:165:ASP:OD1	1:AAA:165:ASP:C	2.63	0.41
1:AAA:282:GLU:HA	1:AAA:285:VAL:HG23	2.03	0.41
1:GGG:165:ASP:OD1	1:GGG:165:ASP:C	2.63	0.41
1:AAA:273:LEU:HD12	1:AAA:273:LEU:HA	1.86	0.41
1:GGG:70:LEU:HD23	1:GGG:70:LEU:HA	1.93	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%)	320 (97%)	9 (3%)	0	100	100
1	GGG	321/391 (82%)	310 (97%)	10 (3%)	1 (0%)	36	56
All	All	650/782 (83%)	630 (97%)	19 (3%)	1 (0%)	43	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	GGG	193	ALA

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	275/347 (79%)	266 (97%)	9 (3%)	33	57
1	GGG	268/347 (77%)	259 (97%)	9 (3%)	32	57
All	All	543/694 (78%)	525 (97%)	18 (3%)	33	57

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	8	ARG
1	AAA	47	ARG
1	AAA	94	ILE
1	AAA	180	GLU
1	AAA	252	GLU
1	AAA	258	ILE
1	AAA	270	ASN
1	AAA	283	ARG
1	AAA	294	SER
1	GGG	32	GLU
1	GGG	167	GLU
1	GGG	180	GLU
1	GGG	228	ARG
1	GGG	262	ASN
1	GGG	280	ARG
1	GGG	283	ARG
1	GGG	326	THR
1	GGG	328	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

8 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	PQ8	AAA	404	-	35,35,35	0.34	0	41,50,50	0.63	1 (2%)
3	PQ8	GGG	404	-	35,35,35	0.36	0	41,50,50	0.58	1 (2%)
2	SO4	AAA	401	-	4,4,4	0.33	0	6,6,6	0.08	0
2	SO4	AAA	403	-	4,4,4	0.33	0	6,6,6	0.08	0
2	SO4	AAA	402	-	4,4,4	0.34	0	6,6,6	0.08	0
2	SO4	GGG	401	-	4,4,4	0.33	0	6,6,6	0.06	0
2	SO4	GGG	402	-	4,4,4	0.35	0	6,6,6	0.08	0
2	SO4	GGG	403	-	4,4,4	0.34	0	6,6,6	0.08	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	PQ8	AAA	404	-	-	10/24/27/27	0/3/3/3
3	PQ8	GGG	404	-	-	4/24/27/27	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	AAA	404	PQ8	C11-C10-N1	2.66	130.84	125.03
3	GGG	404	PQ8	C11-C10-N1	2.54	130.60	125.03

There are no chirality outliers.

All (14) torsion outliers are listed below:

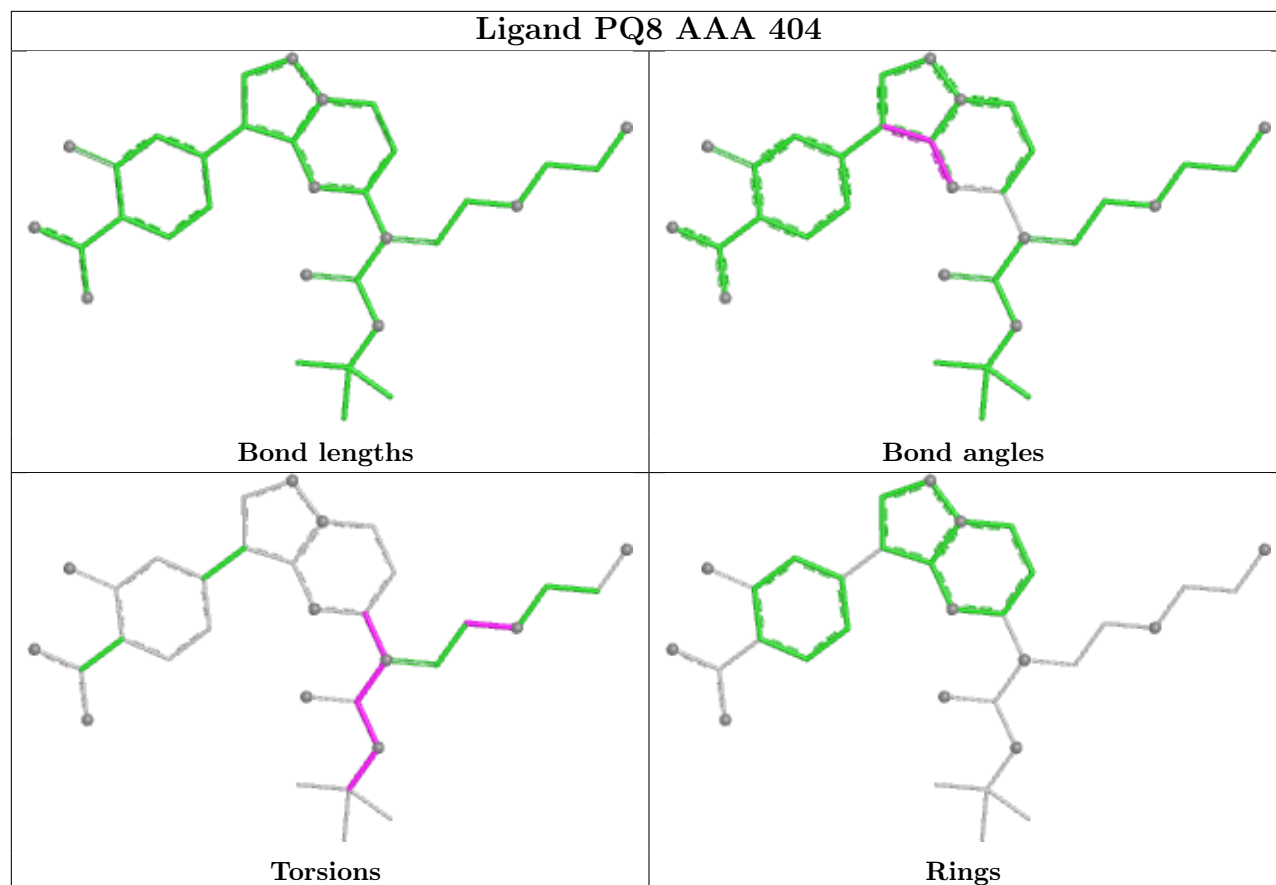
Mol	Chain	Res	Type	Atoms
3	AAA	404	PQ8	N1-C9-N-C5
3	AAA	404	PQ8	O-C-N-C9
3	AAA	404	PQ8	O1-C-N-C9
3	AAA	404	PQ8	N-C-O1-C1
3	AAA	404	PQ8	C2-C1-O1-C
3	AAA	404	PQ8	C3-C1-O1-C
3	AAA	404	PQ8	O-C-O1-C1
3	AAA	404	PQ8	C4-C1-O1-C
3	GGG	404	PQ8	O2-C7-C8-O3
3	GGG	404	PQ8	N-C5-C6-O2
3	GGG	404	PQ8	C5-C6-O2-C7
3	AAA	404	PQ8	C5-C6-O2-C7
3	AAA	404	PQ8	O-C-N-C5
3	GGG	404	PQ8	O-C-N-C5

There are no ring outliers.

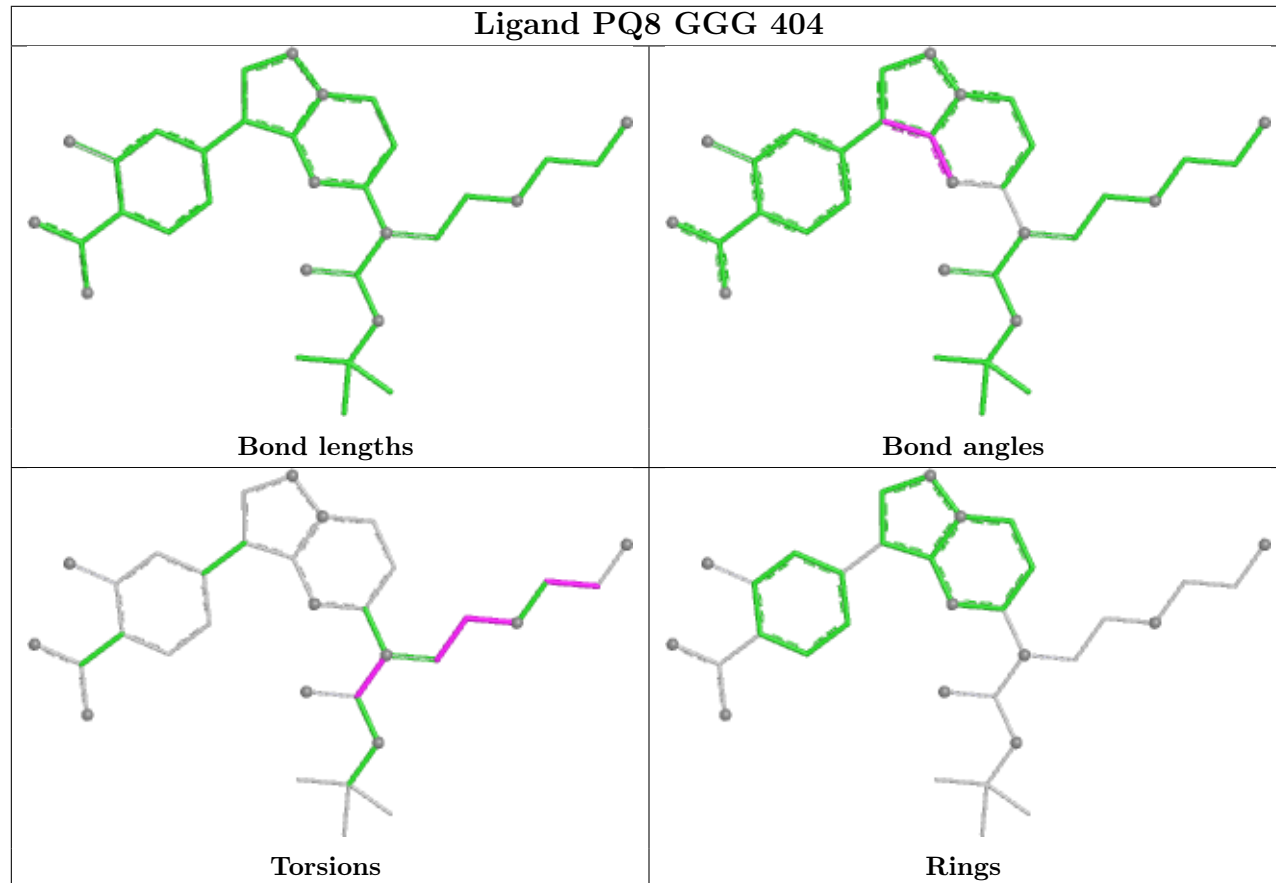
No monomer is involved in short contacts.

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.

Ligand PQ8 AAA 404



Ligand PQ8 GGG 404



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

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	331/391 (84%)	0.54	14 (4%) 40 39	55, 75, 100, 117	0
1	GGG	325/391 (83%)	0.66	28 (8%) 16 16	49, 73, 104, 123	0
All	All	656/782 (83%)	0.60	42 (6%) 25 25	49, 74, 102, 123	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	106	SER	3.4
1	GGG	52	GLU	3.3
1	GGG	232	PHE	3.0
1	GGG	71	LYS	3.0
1	GGG	286	HIS	2.9
1	AAA	117	ASN	2.9
1	AAA	36	GLN	2.8
1	AAA	204	VAL	2.8
1	GGG	288	GLU	2.8
1	GGG	267	PRO	2.7
1	GGG	105	VAL	2.7
1	AAA	61	ASN	2.6
1	GGG	233	PHE	2.6
1	GGG	107	ARG	2.6
1	GGG	268	ARG	2.6
1	GGG	236	HIS	2.6
1	GGG	160	HIS	2.5
1	GGG	73	VAL	2.5
1	AAA	103	ASP	2.5
1	GGG	266	ASP	2.5
1	AAA	193	ALA	2.5
1	GGG	110	ALA	2.5
1	AAA	3	GLY	2.4
1	AAA	123	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	GGG	47	ARG	2.4
1	AAA	74	LYS	2.3
1	AAA	73	VAL	2.3
1	GGG	281	TRP	2.3
1	GGG	61	ASN	2.3
1	GGG	34	GLY	2.3
1	GGG	46	GLY	2.2
1	AAA	125	TYR	2.2
1	GGG	331	GLN	2.2
1	GGG	225	MET	2.2
1	GGG	271	ASP	2.2
1	GGG	291	HIS	2.1
1	GGG	60	THR	2.1
1	AAA	328	VAL	2.1
1	GGG	240	ASP	2.0
1	GGG	128	LEU	2.0
1	AAA	323	TYR	2.0
1	GGG	305	LEU	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 oligosaccharides 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	GGG	403	5/5	0.62	0.09	136,138,140,144	0
2	SO4	AAA	402	5/5	0.85	0.11	108,110,111,113	0
2	SO4	AAA	401	5/5	0.89	0.07	74,75,78,79	0
3	PQ8	GGG	404	33/33	0.89	0.14	63,70,95,96	0
2	SO4	AAA	403	5/5	0.90	0.14	102,102,103,104	0

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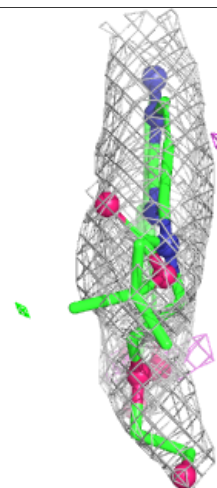
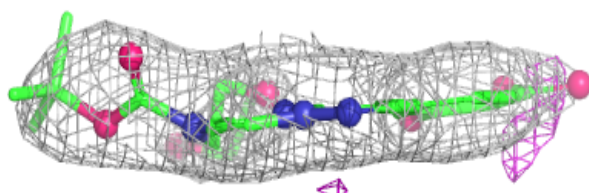
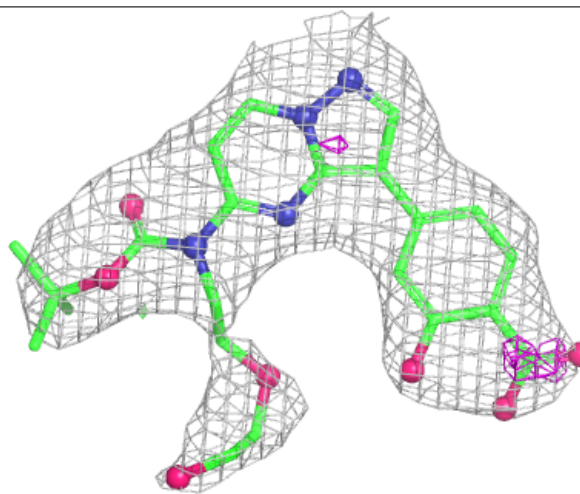
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PQ8	AAA	404	33/33	0.90	0.13	75,88,111,112	0
2	SO4	GGG	401	5/5	0.90	0.14	81,83,84,85	0
2	SO4	GGG	402	5/5	0.91	0.10	81,82,87,89	0

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.

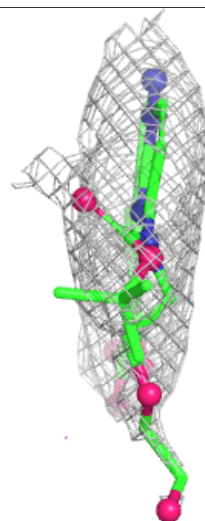
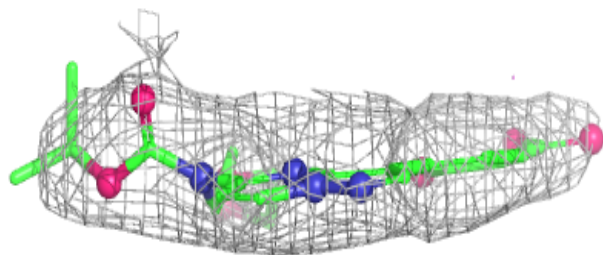
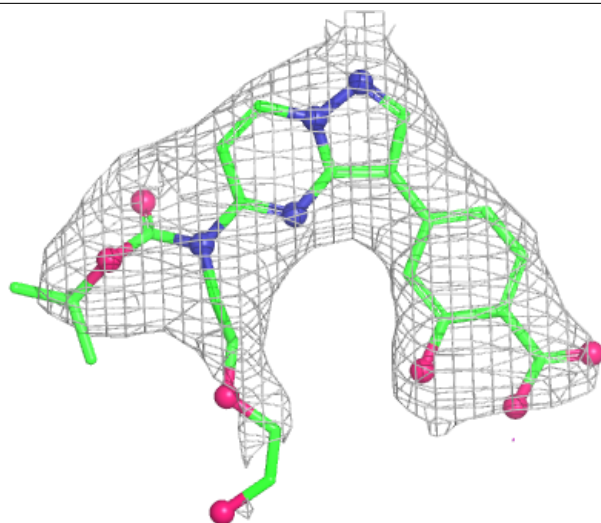
Electron density around PQ8 GGG 404:

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



Electron density around PQ8 AAA 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 [i](#)

There are no such residues in this entry.