



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:06 AM UTC

PDB ID : 3SYQ / pdb_00003syq
Title : Crystal structure of the G protein-gated inward rectifier K⁺ channel GIRK2 (Kir3.2) R201A mutant in complex with PIP2
Authors : Whorton, M.R.; MacKinnon, R.
Deposited on : 2011-07-18
Resolution : 3.44 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

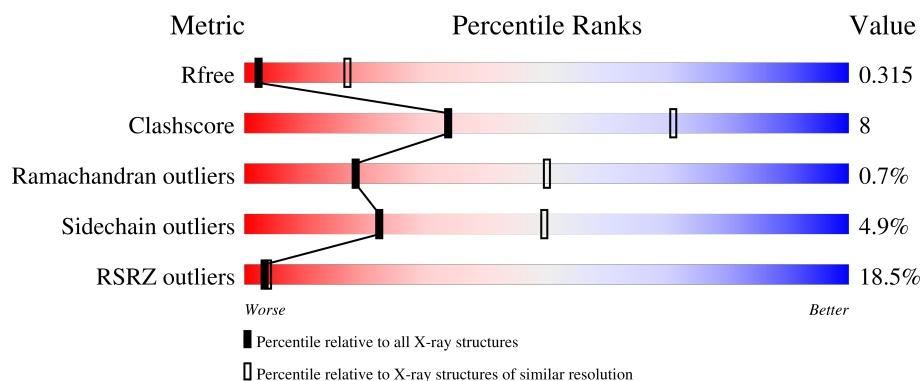
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.44 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	1736 (3.50-3.38)
Clashscore	190562	1808 (3.50-3.38)
Ramachandran outliers	187476	1776 (3.50-3.38)
Sidechain outliers	187428	1777 (3.50-3.38)
RSRZ outliers	180081	1736 (3.50-3.38)

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	A	340	17% 68% 16% • 14%
1	B	340	14% 68% 16% • 14%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4525 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 G protein-activated inward rectifier potassium channel 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	0	0
			2235	1448	362	412	13			
1	B	293	Total	C	N	O	S	0	0	0
			2255	1463	365	414	13			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	MET	-	expression tag	UNP P48542
A	51	ALA	-	expression tag	UNP P48542
A	201	ALA	ARG	engineered mutation	UNP P48542
A	260	THR	SER	SEE REMARK 999	UNP P48542
A	313	MET	ILE	SEE REMARK 999	UNP P48542
A	344	LEU	MET	SEE REMARK 999	UNP P48542
A	381	SER	-	expression tag	UNP P48542
A	382	ASN	-	expression tag	UNP P48542
A	383	SER	-	expression tag	UNP P48542
A	384	LEU	-	expression tag	UNP P48542
A	385	GLU	-	expression tag	UNP P48542
A	386	VAL	-	expression tag	UNP P48542
A	387	LEU	-	expression tag	UNP P48542
A	388	PHE	-	expression tag	UNP P48542
A	389	GLN	-	expression tag	UNP P48542
B	50	MET	-	expression tag	UNP P48542
B	51	ALA	-	expression tag	UNP P48542
B	201	ALA	ARG	engineered mutation	UNP P48542
B	260	THR	SER	SEE REMARK 999	UNP P48542
B	313	MET	ILE	SEE REMARK 999	UNP P48542
B	344	LEU	MET	SEE REMARK 999	UNP P48542
B	381	SER	-	expression tag	UNP P48542
B	382	ASN	-	expression tag	UNP P48542
B	383	SER	-	expression tag	UNP P48542
B	384	LEU	-	expression tag	UNP P48542

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Chain	Residue	Modelled	Actual	Comment	Reference
B	385	GLU	-	expression tag	UNP P48542
B	386	VAL	-	expression tag	UNP P48542
B	387	LEU	-	expression tag	UNP P48542
B	388	PHE	-	expression tag	UNP P48542
B	389	GLN	-	expression tag	UNP P48542

- # PIO

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	4	Total K 4 4	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	87.61Å 208.49Å 117.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.39 – 3.44 49.39 – 3.44	Depositor EDS
% Data completeness (in resolution range)	80.5 (49.39-3.44) 80.5 (49.39-3.44)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.78 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.299 , 0.323 0.295 , 0.315	Depositor DCC
R_{free} test set	577 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	117.3	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 53.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	4525	wwPDB-VP
Average B, all atoms (Å ²)	138.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.51% 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

5.1 Standard geometry

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

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	0.45	0/2283	0.81	0/3108
1	B	0.47	0/2303	0.80	0/3131
All	All	0.46	0/4586	0.80	0/6239

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	A	2235	0	2141	38	0
1	B	2255	0	2182	33	0
2	A	31	0	14	3	0
3	A	4	0	0	0	0
All	All	4525	0	4337	68	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 8.

All (68) 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:B:204:THR:HG21	1:B:230:ARG:HG3	1.62	0.81
1:A:90:LYS:HA	2:A:400:PIO:O6	1.82	0.79
1:A:209:THR:HG22	1:A:357:HIS:HB3	1.66	0.78
1:A:98:PHE:HD1	1:A:187:MET:HE3	1.56	0.71
1:A:371:GLU:O	1:A:375:LEU:HG	1.88	0.71
1:A:211:ALA:O	1:A:332:ILE:HA	1.96	0.65
1:A:91:TRP:HD1	2:A:400:PIO:H1	1.65	0.62
1:A:293:GLU:HG2	1:A:370:LYS:HD2	1.81	0.62
1:A:233:HIS:ND1	1:A:234:ILE:HG22	2.16	0.60
1:A:313:MET:HB2	1:A:320:THR:HG22	1.83	0.60
1:A:225:ARG:HG3	1:A:226:VAL:H	1.67	0.60
1:A:86:LEU:HA	1:A:89:LEU:HD12	1.84	0.59
1:B:291:PHE:HA	1:B:294:ILE:HD12	1.85	0.58
1:B:299:LEU:HD22	1:B:334:TRP:HB2	1.86	0.58
1:B:56:GLN:HE22	1:B:66:ASN:HB3	1.69	0.58
1:B:226:VAL:HG21	1:B:310:LEU:HD12	1.86	0.56
1:A:57:ARG:HH12	1:A:61:LYS:HG2	1.71	0.56
1:A:336:TYR:HA	1:A:361:GLU:HA	1.88	0.56
1:B:234:ILE:HG22	1:B:312:GLY:HA3	1.88	0.55
1:B:202:ALA:HB1	1:B:205:LEU:HD12	1.91	0.53
1:A:214:SER:HA	1:A:364:THR:HG21	1.90	0.53
1:B:85:THR:O	1:B:89:LEU:HG	2.10	0.52
1:A:150:GLU:OE2	1:A:160:ARG:NH2	2.43	0.52
1:B:61:LYS:HE2	1:B:209:THR:HA	1.91	0.52
1:B:199:LYS:HE2	1:B:324:ARG:HH22	1.73	0.51
1:B:299:LEU:HB3	1:B:300:PRO:HD3	1.92	0.51
1:A:317:THR:HG21	1:A:319:MET:HE2	1.92	0.51
1:A:243:LEU:O	1:A:259:GLN:HA	2.11	0.51
1:A:91:TRP:HB2	2:A:400:PIO:O11	2.11	0.51
1:A:95:LEU:O	1:A:99:VAL:HG23	2.12	0.49
1:B:150:GLU:OE2	1:B:160:ARG:NH2	2.46	0.49
1:A:209:THR:CG2	1:A:357:HIS:HB3	2.41	0.49
1:B:209:THR:HG22	1:B:357:HIS:HB3	1.94	0.48
1:A:202:ALA:HA	1:A:205:LEU:HD12	1.94	0.48
1:A:233:HIS:HA	1:A:315:GLU:HB2	1.94	0.48
1:A:236:GLU:CD	1:B:322:GLN:HE22	2.21	0.47
1:B:178:VAL:O	1:B:182:ILE:HD12	2.14	0.47
1:B:208:SER:HB3	1:B:225:ARG:HB3	1.96	0.47
1:A:208:SER:HB3	1:A:225:ARG:HB3	1.96	0.47
1:B:108:PHE:O	1:B:112:ILE:HG12	2.15	0.46
1:A:313:MET:CB	1:A:320:THR:HG22	2.46	0.46
1:B:247:LYS:HG3	1:B:255:ILE:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:PHE:CD1	1:A:187:MET:HE3	2.43	0.46
1:A:83:PHE:HD2	1:A:83:PHE:H	1.63	0.46
1:B:341:VAL:O	1:B:351:VAL:HA	2.16	0.46
1:B:202:ALA:HB2	1:B:321:CYS:HB2	1.98	0.45
1:A:108:PHE:O	1:A:112:ILE:HG12	2.16	0.45
1:B:314:VAL:HG23	1:B:319:MET:O	2.18	0.44
1:A:328:ILE:HG13	1:A:331:GLU:HG3	1.99	0.44
1:B:329:THR:HA	1:B:332:ILE:HD12	1.99	0.44
1:B:93:PHE:O	1:B:97:ILE:HG12	2.18	0.44
1:A:99:VAL:HA	1:B:178:VAL:HG21	1.99	0.44
1:A:98:PHE:HA	1:A:187:MET:HE2	2.01	0.43
1:A:335:GLY:HA2	1:A:364:THR:HB	2.01	0.43
1:B:245:LYS:HB3	1:B:304:LEU:HB3	1.99	0.43
1:A:338:PHE:HA	1:A:359:THR:HG22	2.01	0.43
1:A:270:ASP:OD1	1:B:260:THR:HA	2.20	0.42
1:B:278:PRO:HB3	1:B:356:PHE:CE1	2.54	0.42
1:B:243:LEU:HD11	1:B:304:LEU:HB2	2.00	0.42
1:B:242:LYS:HD2	1:B:259:GLN:HB3	2.02	0.42
1:A:83:PHE:CD2	1:A:83:PHE:N	2.88	0.41
1:A:83:PHE:HB3	1:A:193:VAL:HG11	2.01	0.41
1:B:199:LYS:CE	1:B:324:ARG:HH22	2.32	0.41
1:B:239:ILE:HG13	1:B:240:ARG:N	2.35	0.41
1:B:191:MET:O	1:B:192:PHE:C	2.64	0.41
1:B:249:THR:OG1	1:B:253:GLU:HB3	2.21	0.40
1:A:234:ILE:HG23	1:A:234:ILE:O	2.21	0.40
1:A:212:VAL:HG12	1:A:333:LEU:HB2	2.02	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	A	284/340 (84%)	264 (93%)	18 (6%)	2 (1%)	18	50
1	B	287/340 (84%)	268 (93%)	17 (6%)	2 (1%)	18	50
All	All	571/680 (84%)	532 (93%)	35 (6%)	4 (1%)	18	50

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	191	MET
1	A	234	ILE
1	A	156	GLY
1	B	156	GLY

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	234/305 (77%)	221 (94%)	13 (6%)	19	46
1	B	236/305 (77%)	226 (96%)	10 (4%)	26	53
All	All	470/610 (77%)	447 (95%)	23 (5%)	22	49

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	CYS
1	A	96	LEU
1	A	142	VAL
1	A	204	THR
1	A	226	VAL
1	A	262	ILE
1	A	270	ASP
1	A	276	VAL
1	A	311	GLU
1	A	317	THR
1	A	328	ILE
1	A	342	LEU

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Mol	Chain	Res	Type
1	A	359	THR
1	B	56	GLN
1	B	61	LYS
1	B	142	VAL
1	B	190	CYS
1	B	204	THR
1	B	240	ARG
1	B	255	ILE
1	B	280	ILE
1	B	314	VAL
1	B	343	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	GLN
1	A	184	ASN
1	A	258	ASN
1	A	298	GLN
1	B	56	GLN
1	B	176	GLN
1	B	197	GLN
1	B	288	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	$\# Z > 2$
2	PIO	A	400	-	31,31,47	0.71	0	44,47,65	0.84	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
2	PIO	A	400	-	-	11/26/50/68	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

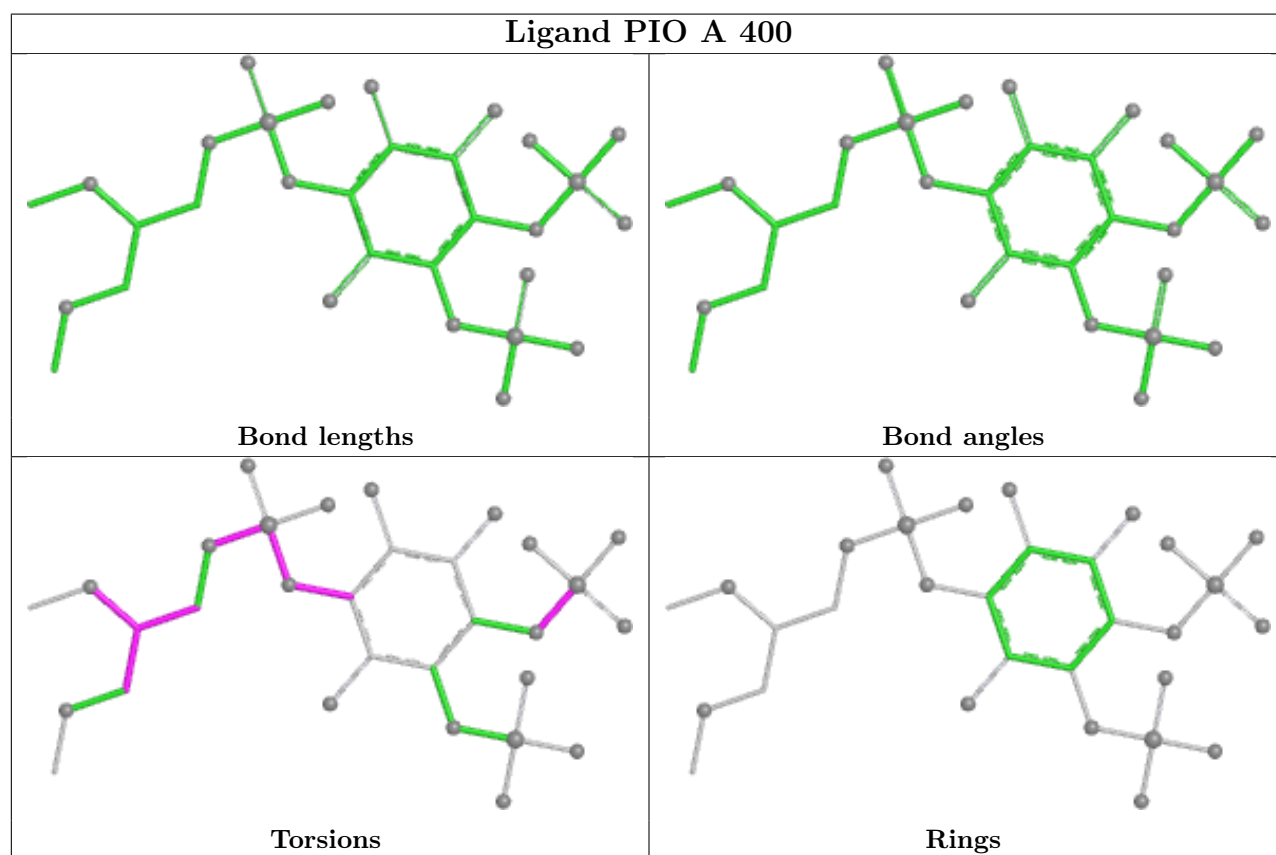
Mol	Chain	Res	Type	Atoms
2	A	400	PIO	C2-C1-O1-P1
2	A	400	PIO	C6-C1-O1-P1
2	A	400	PIO	C1-O1-P1-O13
2	A	400	PIO	C1C-O13-P1-O12
2	A	400	PIO	C1C-C2C-O2C-C1A
2	A	400	PIO	C3C-C2C-O2C-C1A
2	A	400	PIO	C1C-C2C-C3C-O3C
2	A	400	PIO	C1-O1-P1-O12
2	A	400	PIO	O2C-C2C-C3C-O3C
2	A	400	PIO	O13-C1C-C2C-O2C
2	A	400	PIO	C4-O4-P4-O42

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	400	PIO	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 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

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	A	292/340 (85%)	1.26	59 (20%) 3 3	95, 143, 212, 238	0
1	B	293/340 (86%)	0.89	49 (16%) 4 5	87, 128, 182, 228	0
All	All	585/680 (86%)	1.07	108 (18%) 3 4	87, 135, 195, 238	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	62	ASP	12.5
1	A	63	GLY	10.9
1	A	181	SER	8.6
1	B	184	ASN	8.4
1	A	184	ASN	8.0
1	A	64	LYS	7.5
1	A	324	ARG	7.2
1	A	367	LEU	6.5
1	A	65	CYS	6.5
1	A	203	GLU	6.4
1	B	375	LEU	6.4
1	B	376	ALA	6.3
1	B	65	CYS	5.9
1	A	183	VAL	5.9
1	B	315	GLU	5.8
1	B	114	TRP	5.5
1	A	177	SER	5.4
1	A	182	ILE	5.3
1	A	154	THR	5.1
1	B	378	ARG	5.1
1	A	179	LEU	5.1
1	A	146	LEU	5.0
1	A	348	PHE	5.0
1	B	142	VAL	5.0

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Mol	Chain	Res	Type	RSRZ
1	B	152	GLU	4.9
1	B	151	THR	4.8
1	A	266	TYR	4.7
1	B	377	ASN	4.7
1	A	232	SER	4.6
1	A	371	GLU	4.6
1	A	343	THR	4.4
1	A	342	LEU	4.4
1	A	349	TYR	4.3
1	A	60	ARG	4.3
1	A	153	THR	4.0
1	A	323	ALA	4.0
1	A	152	GLU	3.9
1	A	102	TYR	3.6
1	B	162	ILE	3.6
1	B	274	PHE	3.6
1	B	187	MET	3.5
1	B	192	PHE	3.4
1	A	299	LEU	3.3
1	B	310	LEU	3.3
1	B	60	ARG	3.2
1	A	352	ASP	3.2
1	B	177	SER	3.2
1	A	185	ALA	3.2
1	B	146	LEU	3.1
1	A	180	GLY	3.1
1	A	199	LYS	3.1
1	B	153	THR	3.0
1	A	151	THR	3.0
1	B	141	PHE	3.0
1	A	302	GLU	3.0
1	B	319	MET	3.0
1	B	231	ASN	3.0
1	B	82	ILE	3.0
1	B	188	VAL	3.0
1	A	330	SER	2.9
1	B	155	ILE	2.9
1	B	154	THR	2.9
1	A	202	ALA	2.8
1	B	367	LEU	2.8
1	B	316	ALA	2.8
1	B	183	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	141	PHE	2.7
1	A	340	PRO	2.7
1	A	293	GLU	2.7
1	B	239	ILE	2.6
1	B	233	HIS	2.6
1	B	257	LEU	2.6
1	A	157	TYR	2.6
1	B	235	VAL	2.6
1	B	58	TYR	2.5
1	A	366	SER	2.5
1	A	145	PHE	2.4
1	B	237	ALA	2.4
1	B	297	ALA	2.4
1	A	173	LEU	2.4
1	A	178	VAL	2.4
1	A	103	THR	2.3
1	B	266	TYR	2.3
1	A	273	LEU	2.3
1	B	372	LEU	2.3
1	A	201	ALA	2.3
1	B	260	THR	2.3
1	B	137	ASN	2.3
1	A	174	LEU	2.2
1	A	117	ALA	2.2
1	B	185	ALA	2.2
1	B	102	TYR	2.2
1	B	117	ALA	2.2
1	A	192	PHE	2.2
1	B	173	LEU	2.1
1	B	344	LEU	2.1
1	A	114	TRP	2.1
1	B	264	VAL	2.1
1	B	167	PRO	2.1
1	A	137	ASN	2.1
1	A	351	VAL	2.1
1	A	263	ASN	2.1
1	A	104	VAL	2.1
1	A	188	VAL	2.1
1	A	81	ASP	2.1
1	A	59	VAL	2.0
1	B	105	THR	2.0
1	A	82	ILE	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](#)

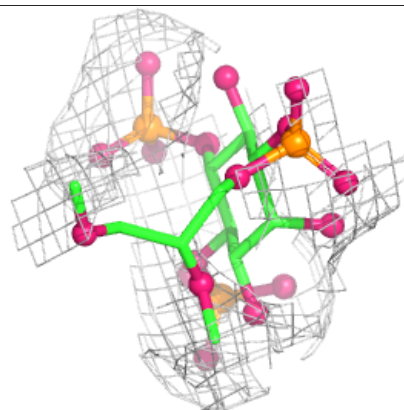
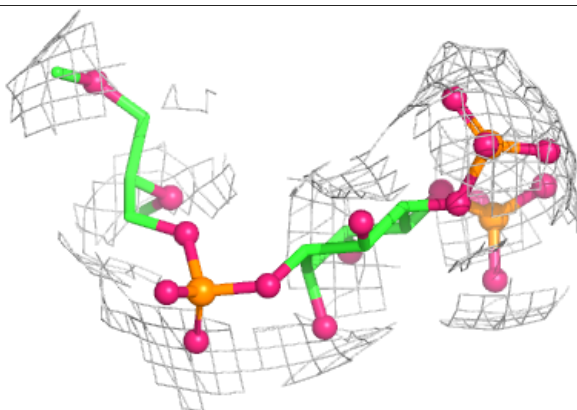
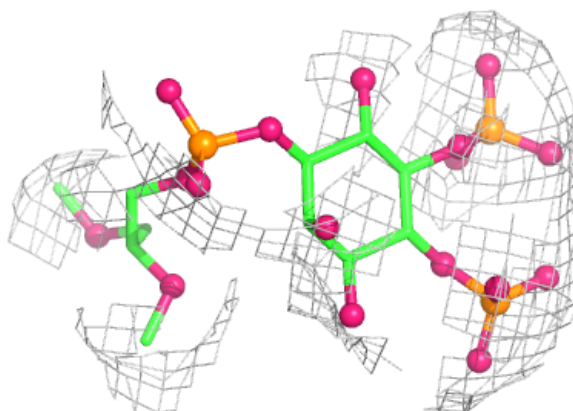
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PIO	A	400	31/47	0.33	0.15	161,164,165,165	0
3	K	A	501	1/1	0.85	0.16	101,101,101,101	1
3	K	A	502	1/1	0.85	0.09	167,167,167,167	1
3	K	A	504	1/1	0.92	0.07	103,103,103,103	1
3	K	A	503	1/1	0.98	0.04	96,96,96,96	1

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 PIO A 400:

$2mF_o - DF_c$ (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.