



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2024 – 11:03 PM EDT

PDB ID : 6MYN
Title : Crystal structure of murine NF-kappaB inducing kinase (NIK) bound to inhibitor R7
Authors : Harris, S.F.; Smith, M.; Barker, J.
Deposited on : 2018-11-01
Resolution : 2.74 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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

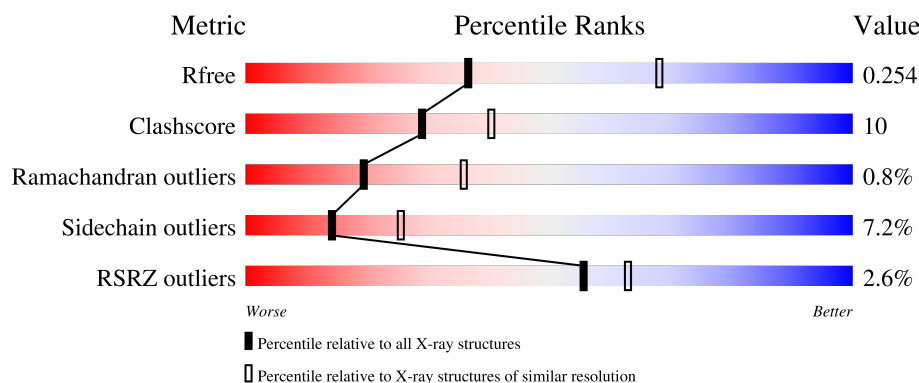
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.74 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	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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	347	
1	B	347	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5280 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 Mitogen-activated protein kinase kinase kinase 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	S	0	2	0
			2525	1598	449	457	21			
1	B	328	Total	C	N	O	S	0	1	0
			2557	1618	454	464	21			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



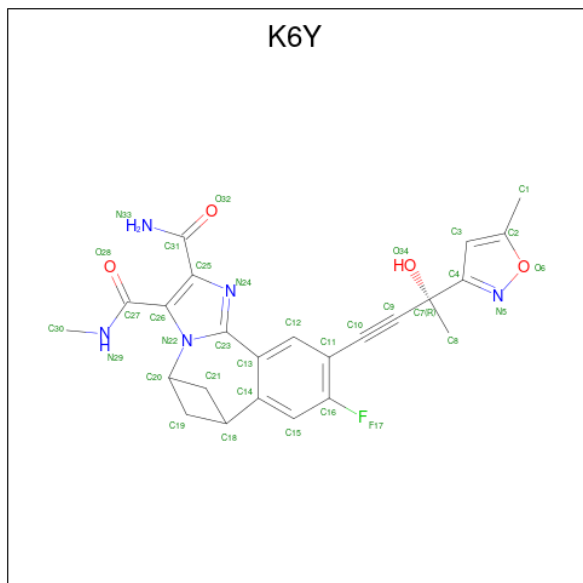
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 3 is (5s,7s)-9-fluoro-10-[(3R)-3-hydroxy-3-(5-methyl-1,2-oxazol-3-yl)but-1-yn-1-yl]-N 3 -methyl-6,7-dihydro-5H-5,7-methanoimidazo[2,1-a][2]benzazepine-2,3-dicarboxamide (three-letter code: K6Y) (formula: C₂₄H₂₂FN₅O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			34	24	1	5	4		
3	B	1	Total	C	F	N	O	0	0
			34	24	1	5	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	59	Total	O	0	0
			59	59		
4	B	46	Total	O	0	0
			46	46		

4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	143.22Å 143.22Å 46.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.19 – 2.74 42.19 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.8 (42.19-2.74) 99.9 (42.19-2.74)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.73Å)	Xtriage
Refinement program	PHENIX 1.12-2829_final	Depositor
R, R_{free}	0.179 , 0.255 0.179 , 0.254	Depositor DCC
R_{free} test set	2604 reflections (10.36%)	wwPDB-VP
Wilson B-factor (Å ²)	58.3	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5280	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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: K6Y, 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	A	0.52	0/2584	0.65	0/3493
1	B	0.50	1/2618 (0.0%)	0.64	0/3540
All	All	0.51	1/5202 (0.0%)	0.64	0/7033

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	586	CYS	CB-SG	-5.31	1.73	1.81

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	2525	0	2519	50	0
1	B	2557	0	2557	51	0
2	A	10	0	0	1	0
2	B	15	0	0	1	0
3	A	34	0	0	3	0
3	B	34	0	0	1	0
4	A	59	0	0	4	0
4	B	46	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5280	0	5076	98	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 10.

All (98) 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:A:392:ASP:OD2	1:B:407:ARG:NH1	1.86	1.08
1:A:664:LYS:NZ	4:A:801:HOH:O	2.05	0.90
1:B:615:PRO:HG3	1:B:638:LYS:HG3	1.59	0.83
1:A:536:ASP:OD2	3:A:703:K6Y:F17	1.94	0.75
1:A:634:GLU:OE1	1:A:652:LYS:NZ	2.19	0.73
1:B:403:THR:HG21	1:B:407:ARG:HH21	1.53	0.72
1:B:405:GLN:HB2	1:B:406:PRO:HD3	1.73	0.70
1:A:453:ARG:HG3	1:A:503:GLU:HB3	1.74	0.69
1:A:615:PRO:HG3	1:A:638:LYS:HG3	1.75	0.68
1:B:600:GLN:HG3	1:B:675:ARG:HH21	1.62	0.64
1:A:658[A]:GLN:NE2	4:A:802:HOH:O	2.15	0.62
1:B:405:GLN:HB2	1:B:406:PRO:CD	2.29	0.62
1:B:506:GLU:O	1:B:510:THR:HG23	1.98	0.62
1:A:405:GLN:HB3	1:A:406:PRO:HD2	1.83	0.61
1:B:509:HIS:CE1	1:B:577:ALA:HB1	2.37	0.60
1:B:453:ARG:HH11	1:B:453:ARG:HA	1.67	0.59
1:B:666:PRO:HG2	1:B:669:GLY:HA2	1.85	0.59
1:A:347:VAL:HG11	1:A:395:TYR:HB2	1.85	0.58
1:B:489:LEU:O	4:B:801:HOH:O	2.17	0.57
1:A:404:HIS:CD2	1:A:405:GLN:HB2	2.40	0.57
1:B:455:VAL:HG21	1:B:535:CYS:HB3	1.86	0.57
1:A:655:LYS:NZ	1:A:659:GLU:OE2	2.36	0.56
1:A:432:LYS:HD3	1:A:466:TRP:CD2	2.41	0.56
1:B:386:GLU:HG3	1:B:389:LYS:HE2	1.87	0.55
1:B:410:ARG:NH1	1:B:418:ARG:NH2	2.54	0.55
1:A:455:VAL:HG21	1:A:535:CYS:HB3	1.88	0.55
1:B:600:GLN:HG3	1:B:675:ARG:NH2	2.21	0.55
1:B:404:HIS:HB2	1:B:418:ARG:HG2	1.89	0.55
1:B:397:GLU:OE1	1:B:432:LYS:NZ	2.41	0.53
1:A:428:CYS:HB2	1:A:471:MET:O	2.09	0.52
1:A:435:LEU:HD22	1:A:462:ARG:HD2	1.92	0.52
1:B:541:LEU:HD22	1:B:552:LEU:HD11	1.91	0.52
1:A:419:MET:HE3	1:A:420:LYS:C	2.30	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:SER:HB3	1:B:434:ARG:NH1	2.25	0.52
1:B:453:ARG:NH2	2:B:702:SO4:O3	2.43	0.52
1:A:552:LEU:HD13	1:A:575:CYS:HB2	1.92	0.51
1:A:514:LEU:HD23	1:A:541:LEU:HB3	1.91	0.51
1:B:514:LEU:HD11	1:B:579:VAL:HG22	1.92	0.51
1:B:601:TYR:HB2	1:B:602:PHE:CD2	2.46	0.51
1:B:449:LEU:HD22	1:B:507:TYR:HE2	1.77	0.49
1:A:387:LYS:HB2	1:A:426:PHE:CG	2.47	0.49
1:B:493:ARG:NH1	1:B:665:SER:O	2.45	0.49
1:A:386:GLU:HG2	1:B:484:LYS:HD3	1.94	0.49
1:A:397:GLU:OE2	1:A:407:ARG:NH2	2.46	0.48
1:A:529:GLY:HA3	1:A:667:TRP:CD2	2.48	0.48
1:A:401:TRP:CZ3	1:A:430:VAL:HG21	2.48	0.48
1:A:637:ARG:NH1	2:A:701:SO4:O2	2.43	0.48
1:B:544:GLN:O	1:B:547:GLY:N	2.31	0.47
1:A:405:GLN:HB3	1:A:406:PRO:CD	2.44	0.47
1:A:509:HIS:CE1	1:A:577:ALA:HB1	2.50	0.47
1:A:434:ARG:HB2	1:A:437:VAL:HG22	1.96	0.47
1:A:512:ARG:NH1	4:A:812:HOH:O	2.48	0.47
1:A:410:ARG:HD2	3:A:703:K6Y:O28	2.15	0.46
1:B:667:TRP:CZ2	1:B:668:LYS:HE2	2.50	0.46
1:A:340:VAL:O	1:A:344:GLN:HG3	2.17	0.45
1:A:655:LYS:O	1:A:659:GLU:HG3	2.17	0.45
1:B:398:GLU:HA	1:B:402:MET:HE3	1.98	0.45
1:B:476:GLY:HA3	1:B:526:SER:O	2.17	0.45
1:B:514:LEU:HD13	1:B:577:ALA:HA	1.99	0.45
1:B:552:LEU:HD12	1:B:552:LEU:HA	1.64	0.45
1:A:617:ILE:HG21	1:A:633:GLN:HG2	1.98	0.45
1:A:347:VAL:HA	1:A:381:GLY:O	2.17	0.45
1:B:378:ASP:CG	1:B:396:ARG:HH22	2.20	0.44
1:A:334:PRO:HB2	1:B:570:VAL:O	2.18	0.44
1:B:634:GLU:HG3	1:B:652:LYS:NZ	2.33	0.44
1:A:383:LEU:HD12	1:A:390:PRO:HD3	2.00	0.43
1:A:418:ARG:NH1	1:A:473:LEU:HD21	2.32	0.43
1:B:567:PRO:HG2	1:B:638:LYS:HG2	1.99	0.43
1:A:536:ASP:HA	3:A:703:K6Y:C9	2.48	0.43
1:B:590:HIS:CE1	1:B:596:HIS:CD2	3.07	0.43
1:A:394:GLU:HG2	4:A:805:HOH:O	2.19	0.42
1:B:509:HIS:CG	1:B:577:ALA:HB1	2.53	0.42
1:B:590:HIS:CE1	1:B:596:HIS:HD2	2.37	0.42
1:B:627:LEU:HD12	1:B:627:LEU:HA	1.56	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:MET:HE1	1:A:669:GLY:N	2.34	0.42
1:B:495:LEU:HB2	1:B:657:LEU:HD13	2.01	0.42
3:B:704:K6Y:O32	3:B:704:K6Y:N29	2.53	0.42
1:B:355:LEU:HD11	1:B:443:LEU:HD13	2.01	0.42
1:B:421:ASP:OD2	1:B:424:THR:HG23	2.20	0.42
1:B:509:HIS:CD2	1:B:577:ALA:HB1	2.55	0.42
1:A:407:ARG:HH11	1:A:417:HIS:CE1	2.38	0.42
1:A:578:LYS:NZ	1:A:640:PRO:O	2.47	0.42
1:B:355:LEU:HD12	1:B:355:LEU:O	2.19	0.42
1:B:387:LYS:HB3	1:B:426:PHE:CG	2.54	0.42
1:B:474:LEU:HD13	1:B:524:LEU:HB2	2.02	0.42
1:A:454:ILE:HD11	1:A:508:LEU:HG	2.02	0.41
1:B:347:VAL:HG11	1:B:395:TYR:HB2	2.01	0.41
1:A:627:LEU:HD11	1:A:652:LYS:HD2	2.01	0.41
1:A:630:GLN:O	1:A:634:GLU:HG3	2.20	0.41
1:B:428:CYS:HB2	1:B:471:MET:O	2.20	0.41
1:A:493:ARG:NH1	1:A:667:TRP:HA	2.36	0.41
1:B:544:GLN:O	1:B:546:ASP:N	2.54	0.41
1:A:419:MET:HG2	1:A:430:VAL:HG22	2.03	0.41
1:A:570:VAL:HG11	1:A:607:CYS:O	2.21	0.41
1:B:496:TYR:OH	1:B:530:SER:O	2.36	0.40
1:A:416:VAL:HA	1:A:430:VAL:O	2.22	0.40
1:B:629:ALA:O	1:B:633:GLN:HG3	2.22	0.40
1:A:455:VAL:HG21	1:A:524:LEU:HD12	2.04	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	318/347 (92%)	298 (94%)	18 (6%)	2 (1%)	25 44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	325/347 (94%)	303 (93%)	19 (6%)	3 (1%)	17	32
All	All	643/694 (93%)	601 (94%)	37 (6%)	5 (1%)	19	36

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	405	GLN
1	A	405	GLN
1	B	412	SER
1	B	674	PRO
1	A	536	ASP

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	271/289 (94%)	252 (93%)	19 (7%)	15	27
1	B	275/289 (95%)	255 (93%)	20 (7%)	14	25
All	All	546/578 (94%)	507 (93%)	39 (7%)	14	26

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	361	THR
1	A	385	THR
1	A	387	LYS
1	A	402	MET
1	A	403	THR
1	A	407	ARG
1	A	408	VAL
1	A	419	MET
1	A	423	GLN
1	A	430	VAL
1	A	493	ARG

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Mol	Chain	Res	Type
1	A	514	LEU
1	A	552	LEU
1	A	564	HIS
1	A	606	LEU
1	A	610	ILE
1	A	639	GLU
1	A	641	VAL
1	A	667	TRP
1	B	346	SER
1	B	355	LEU
1	B	402	MET
1	B	407	ARG
1	B	408	VAL
1	B	410	ARG
1	B	418	ARG
1	B	419	MET
1	B	453	ARG
1	B	510	THR
1	B	512	ARG
1	B	554	THR
1	B	600	GLN
1	B	606	LEU
1	B	618	ARG
1	B	623	SER
1	B	627	LEU
1	B	630	GLN
1	B	650	ARG
1	B	670	GLU

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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

7 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	K6Y	A	703	-	30,38,38	1.03	2 (6%)	35,59,59	1.74	10 (28%)
3	K6Y	B	704	-	30,38,38	1.14	2 (6%)	35,59,59	1.65	7 (20%)
2	SO4	B	701	-	4,4,4	0.24	0	6,6,6	0.37	0
2	SO4	A	701	-	4,4,4	0.38	0	6,6,6	0.37	0
2	SO4	A	702	-	4,4,4	0.25	0	6,6,6	0.28	0
2	SO4	B	703	-	4,4,4	0.38	0	6,6,6	0.41	0
2	SO4	B	702	-	4,4,4	0.30	0	6,6,6	0.25	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	K6Y	B	704	-	-	2/9/42/42	0/4/5/5
3	K6Y	A	703	-	-	3/9/42/42	0/4/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	703	K6Y	C3-C2	-3.72	1.34	1.39
3	B	704	K6Y	C3-C2	-3.67	1.34	1.39
3	B	704	K6Y	O34-C7	-3.15	1.40	1.43
3	A	703	K6Y	C21-C20	-2.32	1.50	1.53

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	703	K6Y	C21-C18-C14	-4.22	109.95	122.04
3	B	704	K6Y	C14-C18-C19	-3.88	110.92	122.04
3	B	704	K6Y	C25-C26-N22	-3.70	104.97	108.36
3	B	704	K6Y	C21-C18-C14	-3.70	111.45	122.04
3	A	703	K6Y	C25-C26-N22	-3.61	105.06	108.36
3	A	703	K6Y	C26-N22-C23	-3.38	105.83	108.73
3	A	703	K6Y	C14-C18-C19	-3.13	113.08	122.04
3	B	704	K6Y	C26-N22-C23	-2.98	106.17	108.73
3	B	704	K6Y	C25-C26-C27	2.94	136.69	131.27
3	A	703	K6Y	C13-C23-N24	-2.89	118.60	122.14
3	A	703	K6Y	C25-C26-C27	2.76	136.37	131.27
3	B	704	K6Y	O34-C7-C8	-2.61	99.88	107.26
3	A	703	K6Y	C16-C11-C10	2.47	126.20	120.75
3	B	704	K6Y	C13-C23-N24	-2.38	119.22	122.14
3	A	703	K6Y	C12-C13-C14	2.19	120.56	118.92
3	A	703	K6Y	C18-C21-C20	2.11	92.43	85.31
3	A	703	K6Y	C1-C2-C3	2.01	134.35	129.01

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	703	K6Y	C25-C26-C27-O28
3	B	704	K6Y	C9-C10-C11-C16
3	A	703	K6Y	C11-C10-C9-C7
3	B	704	K6Y	C9-C10-C11-C12
3	A	703	K6Y	C3-C4-C7-C8

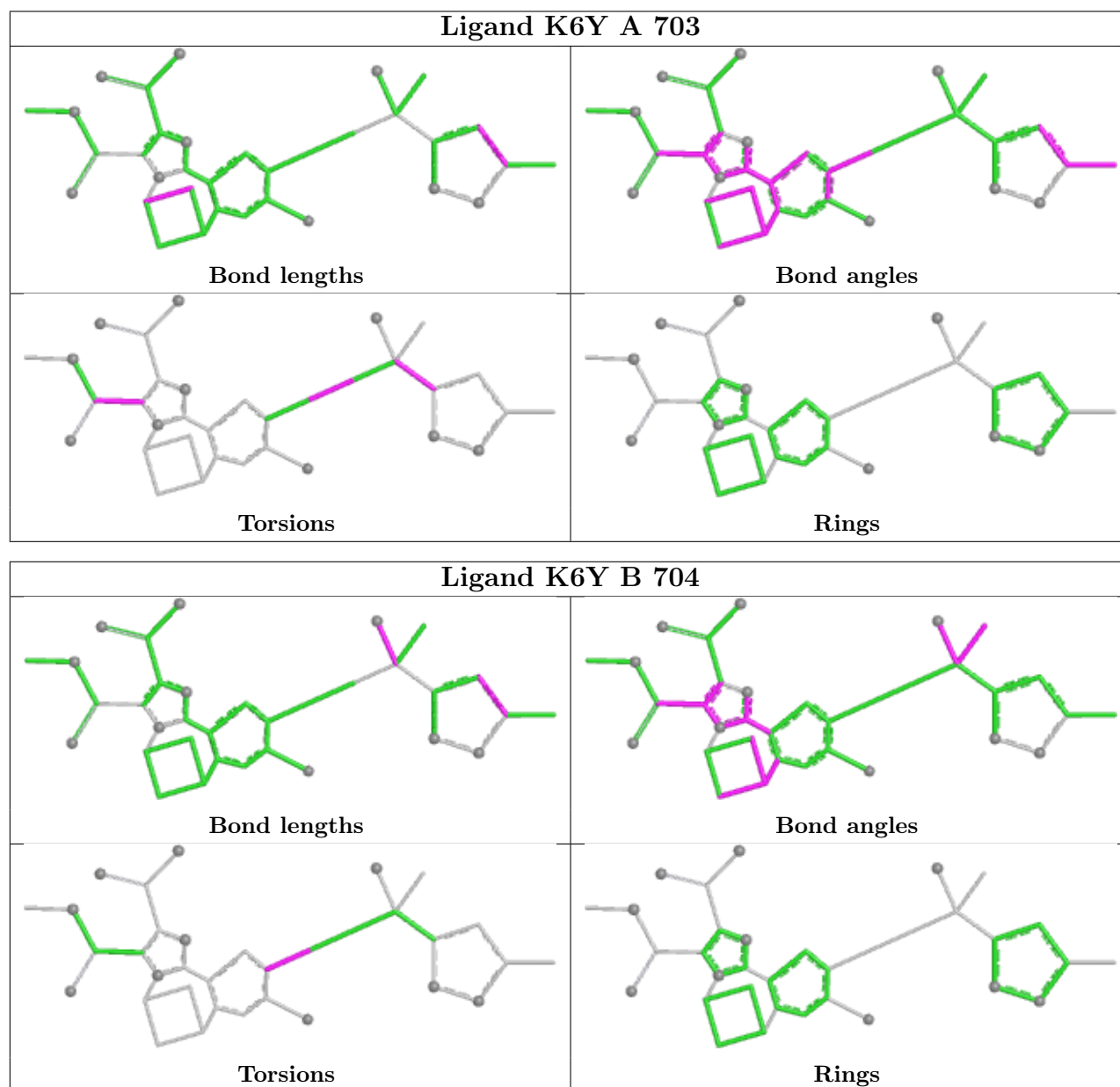
There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	703	K6Y	3	0
3	B	704	K6Y	1	0
2	A	701	SO4	1	0
2	B	702	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 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 ⓘ

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	A	322/347 (92%)	-0.15	6 (1%) 66 73	31, 48, 83, 112	0
1	B	328/347 (94%)	-0.04	11 (3%) 45 50	31, 53, 89, 103	0
All	All	650/694 (93%)	-0.09	17 (2%) 56 63	31, 50, 88, 112	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	602	PHE	3.6
1	B	672	LYS	3.6
1	B	405	GLN	3.5
1	A	544	GLN	3.4
1	B	602	PHE	3.4
1	B	608	LEU	3.2
1	A	405	GLN	3.1
1	B	404	HIS	3.1
1	A	601	TYR	2.7
1	B	601	TYR	2.6
1	B	402	MET	2.5
1	B	407	ARG	2.5
1	B	675	ARG	2.2
1	A	675	ARG	2.2
1	B	671	TYR	2.1
1	A	603	ARG	2.1
1	B	406	PRO	2.1

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](#)

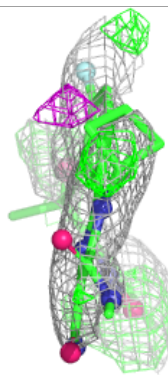
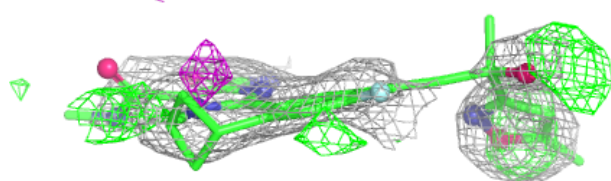
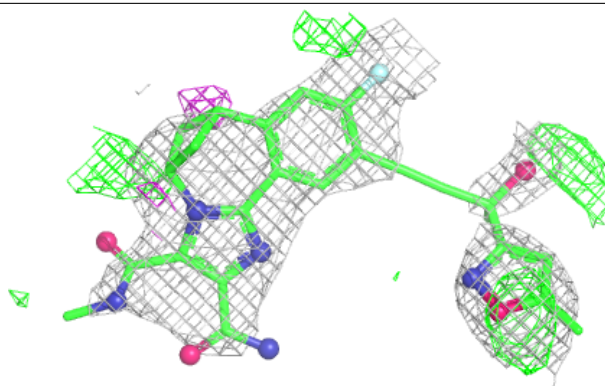
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	B	702	5/5	0.82	0.26	97,100,129,134	0
3	K6Y	A	703	34/34	0.87	0.31	34,48,58,68	34
3	K6Y	B	704	34/34	0.89	0.27	34,50,59,69	34
2	SO4	A	702	5/5	0.95	0.10	66,78,89,90	0
2	SO4	B	701	5/5	0.96	0.11	74,74,87,95	0
2	SO4	B	703	5/5	0.96	0.17	62,67,73,93	0
2	SO4	A	701	5/5	0.97	0.10	67,71,90,97	0

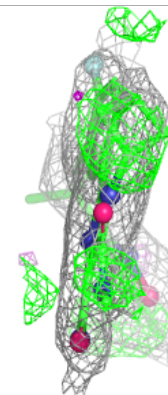
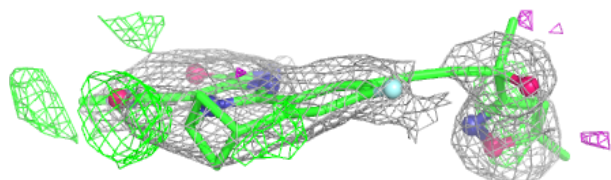
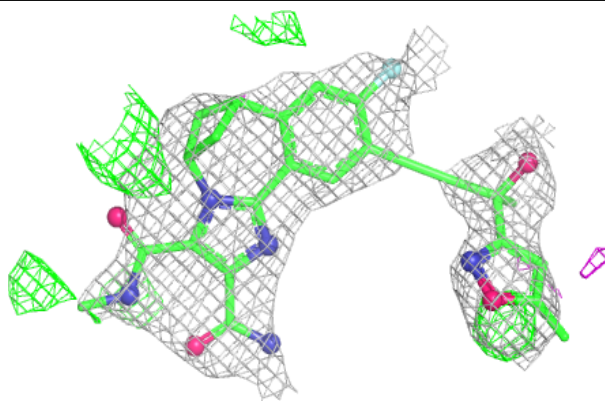
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around K6Y A 703:

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

**Electron density around K6Y B 704:**

$2mF_o-DF_c$ (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.