



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 09:41 PM UTC

PDB ID : 8UCC / pdb_00008ucc
Title : IRAK4 in complex with compound 20
Authors : Metrick, C.M.; Chodaparambil, J.V.
Deposited on : 2023-09-26
Resolution : 1.80 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

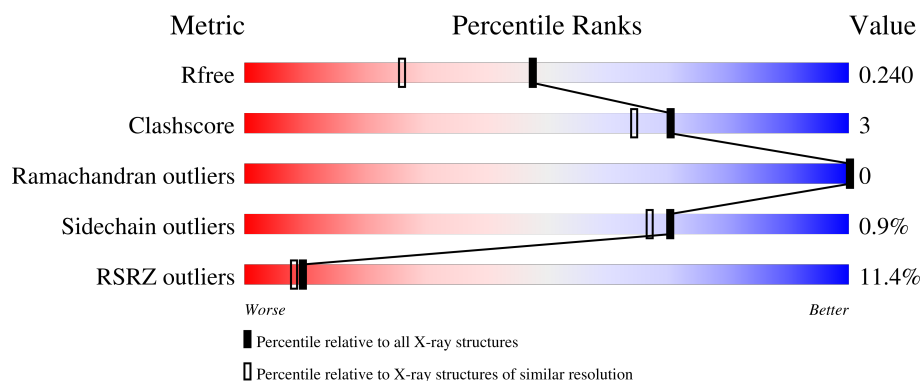
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	307	10% 88% 8% .
2	B	307	11% 86% 6% 7%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4648 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.

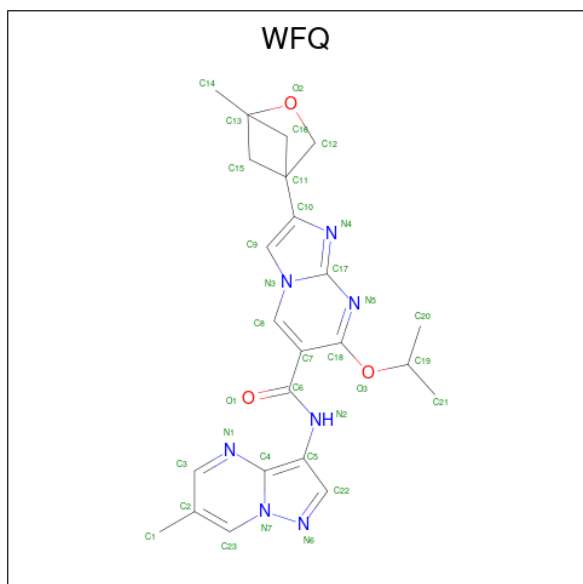
- Molecule 1 is a protein called Interleukin-1 receptor-associated kinase 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	P	S	0	0	0
			2251	1418	376	441	1	15			

- Molecule 2 is a protein called Interleukin-1 receptor-associated kinase 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	286	Total	C	N	O	P	S	0	0	0
			2145	1352	363	415	1	14			

- Molecule 3 is (4S)-2-[(1R,4s)-1-methyl-2-oxabicyclo[2.1.1]hexan-4-yl]-N-[(8S)-6-methylpyrazolo[1,5-a]pyrimidin-3-yl]-7-[(propan-2-yl)oxy]imidazo[1,2-a]pyrimidine-6-carboxamide (CCD ID: WFQ) (formula: C₂₃H₂₅N₇O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			33	23	7	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			33	23	7	3		

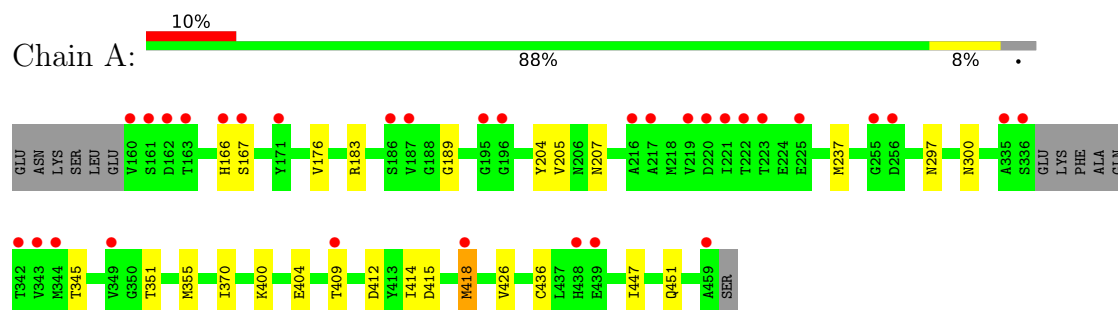
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	85	Total	O	0	0
			85	85		
4	B	101	Total	O	0	0
			101	101		

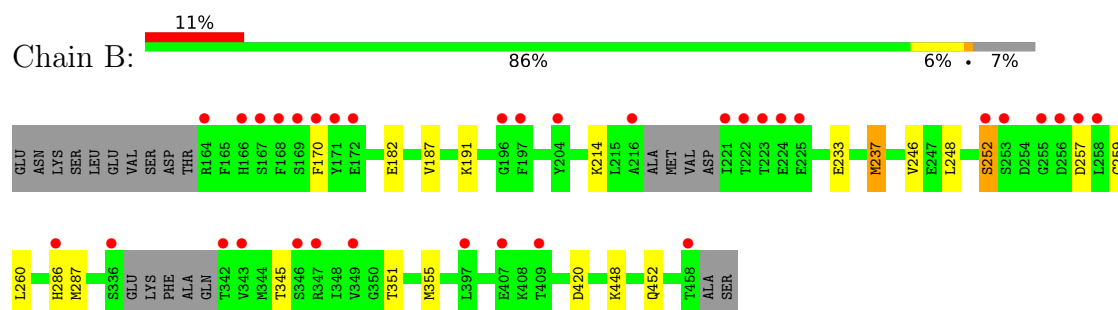
3 Residue-property plots [i](#)

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: Interleukin-1 receptor-associated kinase 4



- Molecule 2: Interleukin-1 receptor-associated kinase 4



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	88.63Å 118.03Å 140.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.99 – 1.80 31.99 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (31.99-1.80) 99.8 (31.99-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.208 , 0.240 0.208 , 0.240	Depositor DCC
R_{free} test set	3373 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.453	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 38.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4648	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.84% 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: TPO, SEP, WFQ

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	0.59	0/2272	0.71	0/3073
2	B	0.66	0/2169	0.74	0/2939
All	All	0.63	0/4441	0.73	0/6012

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	A	2251	0	2164	17	0
2	B	2145	0	2034	11	0
3	A	33	0	0	1	0
3	B	33	0	0	0	0
4	A	85	0	0	0	0
4	B	101	0	0	0	0
All	All	4648	0	4198	29	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 3.

All (29) 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:400:LYS:O	1:A:404:GLU:HG3	2.01	0.61
2:B:252:SER:HB2	2:B:259:CYS:HB2	1.83	0.60
2:B:448:LYS:O	2:B:452:GLN:HG3	2.05	0.56
2:B:237:MET:HE2	2:B:248:LEU:H	1.74	0.53
1:A:237:MET:HA	1:A:237:MET:HE2	1.91	0.52
1:A:414:ILE:HD11	1:A:426:VAL:HG11	1.92	0.51
1:A:176:VAL:HG21	1:A:205:VAL:HG13	1.94	0.50
2:B:351:THR:O	2:B:355:MET:HG3	2.12	0.50
2:B:170:PHE:C	2:B:170:PHE:CD1	2.92	0.48
1:A:414:ILE:CD1	1:A:426:VAL:HG11	2.44	0.48
2:B:233:GLU:HG2	2:B:260:LEU:HD13	1.96	0.48
1:A:300:ASN:HA	1:A:447:ILE:HG21	1.96	0.47
1:A:409:THR:HG22	1:A:412:ASP:OD2	2.13	0.47
2:B:182:GLU:O	2:B:191:LYS:HE3	2.14	0.47
1:A:204:TYR:CE2	1:A:207:ASN:HA	2.50	0.47
2:B:237:MET:HE1	2:B:246:VAL:O	2.14	0.46
2:B:286:HIS:ND1	2:B:420:ASP:OD2	2.50	0.45
2:B:214:LYS:NZ	2:B:257:ASP:OD2	2.46	0.44
1:A:415:ASP:HB3	1:A:418:MET:HE2	2.00	0.44
1:A:297:ASN:HA	1:A:451:GLN:HE21	1.83	0.43
1:A:183:ARG:HB2	1:A:189:GLY:HA3	2.00	0.43
2:B:287:MET:HE2	2:B:287:MET:HA	2.01	0.43
1:A:351:THR:O	1:A:355:MET:HG3	2.19	0.43
1:A:176:VAL:HG21	1:A:205:VAL:CG1	2.49	0.42
1:A:166:HIS:CD2	1:A:167:SER:N	2.87	0.42
3:A:501:WFQ:O3	3:A:501:WFQ:N2	2.51	0.41
1:A:418:MET:HE2	1:A:418:MET:HB2	1.93	0.41
1:A:409:THR:HG23	1:A:412:ASP:H	1.86	0.41
1:A:370:ILE:O	1:A:436:CYS:HB3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	289/307 (94%)	280 (97%)	9 (3%)	0	100	100
2	B	279/307 (91%)	270 (97%)	9 (3%)	0	100	100
All	All	568/614 (92%)	550 (97%)	18 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	237/266 (89%)	236 (100%)	1 (0%)	84	83
2	B	221/267 (83%)	218 (99%)	3 (1%)	59	52
All	All	458/533 (86%)	454 (99%)	4 (1%)	70	67

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	418	MET
2	B	187	VAL
2	B	237	MET
2	B	252	SER

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	166	HIS
1	A	229	GLN
1	A	451	GLN
1	A	452	GLN
2	B	229	GLN
2	B	232	GLN

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Mol	Chain	Res	Type
2	B	394	GLN
2	B	442	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues 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
1	SEP	A	346	1	3,4,10	0.76	0	2,4,14	0.85	0
1	TPO	A	345	1	8,10,11	1.76	1 (12%)	10,14,16	1.62	2 (20%)
2	TPO	B	345	2	8,10,11	1.98	3 (37%)	10,14,16	1.75	2 (20%)

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
1	SEP	A	346	1	-	0/1/2/10	-
1	TPO	A	345	1	-	3/9/11/13	-
2	TPO	B	345	2	-	3/9/11/13	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	345	TPO	P-O1P	3.57	1.61	1.50
2	B	345	TPO	P-O1P	3.46	1.61	1.50
2	B	345	TPO	CB-CA	2.70	1.59	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	345	TPO	P-OG1	2.15	1.63	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	345	TPO	P-OG1-CB	-4.70	110.55	123.33
1	A	345	TPO	P-OG1-CB	-3.39	114.11	123.33
1	A	345	TPO	CG2-CB-CA	-2.64	108.11	113.26
2	B	345	TPO	CG2-CB-CA	-2.09	109.18	113.26

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	345	TPO	N-CA-CB-OG1
1	A	345	TPO	O-C-CA-CB
2	B	345	TPO	N-CA-CB-OG1
2	B	345	TPO	CB-OG1-P-O1P
1	A	345	TPO	CA-CB-OG1-P
2	B	345	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	WFQ	A	501	-	35,38,38	1.08	2 (5%)	32,60,60	1.33	5 (15%)
3	WFQ	B	501	-	35,38,38	1.29	2 (5%)	32,60,60	1.33	6 (18%)

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	WFQ	A	501	-	-	1/11/37/37	0/7/6/6
3	WFQ	B	501	-	-	1/11/37/37	0/7/6/6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	WFQ	C11-C10	-5.14	1.48	1.51
3	B	501	WFQ	O2-C13	-3.76	1.41	1.45
3	A	501	WFQ	O2-C13	-3.56	1.41	1.45
3	A	501	WFQ	C11-C10	-3.06	1.49	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	WFQ	C2-C23-N7	-3.39	116.13	121.32
3	B	501	WFQ	C2-C23-N7	-3.08	116.59	121.32
3	A	501	WFQ	C9-N3-C8	2.80	132.73	130.04
3	B	501	WFQ	N7-C4-N1	2.70	125.22	121.96
3	B	501	WFQ	C5-C4-N7	2.68	107.16	104.30
3	A	501	WFQ	N7-C4-N1	2.48	124.95	121.96
3	A	501	WFQ	N3-C17-N4	-2.34	108.91	111.95
3	B	501	WFQ	N3-C17-N4	-2.31	108.94	111.95
3	B	501	WFQ	C14-C13-C16	2.16	123.72	116.07
3	A	501	WFQ	C5-C4-N7	2.14	106.58	104.30
3	B	501	WFQ	C9-N3-C8	2.04	132.00	130.04

There are no chirality outliers.

All (2) torsion outliers are listed below:

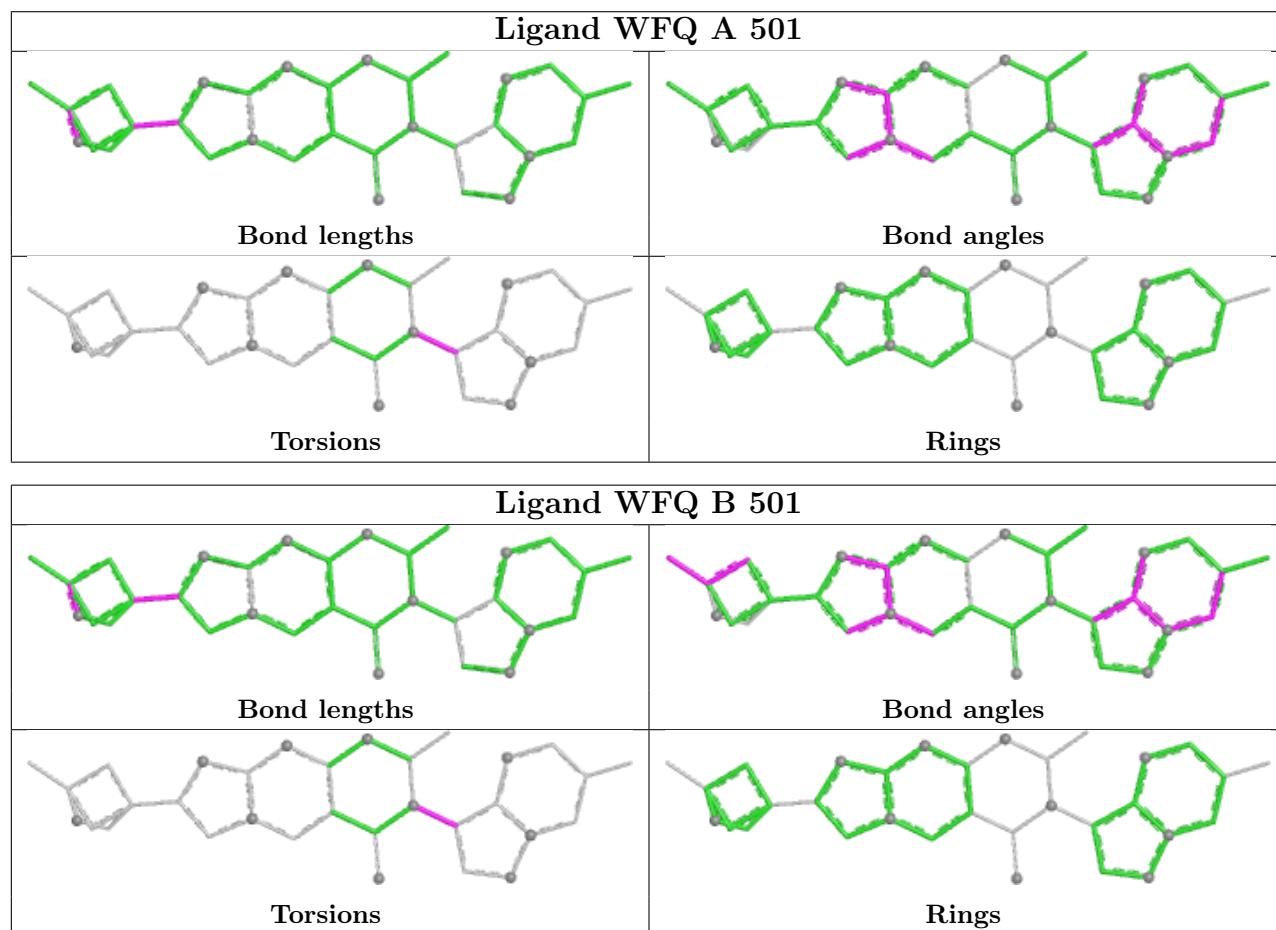
Mol	Chain	Res	Type	Atoms
3	B	501	WFQ	C4-C5-N2-C6
3	A	501	WFQ	C4-C5-N2-C6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	WFQ	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 [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	293/307 (95%)	0.65	32 (10%) 10 9	24, 42, 73, 109	0
2	B	285/307 (92%)	0.58	34 (11%) 9 7	23, 37, 66, 98	0
All	All	578/614 (94%)	0.62	66 (11%) 10 8	23, 40, 72, 109	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	222	THR	6.2
2	B	221	ILE	5.5
1	A	342	THR	5.3
1	A	221	ILE	5.1
2	B	342	THR	5.0
2	B	343	VAL	4.8
1	A	160	VAL	4.7
2	B	164	ARG	4.5
2	B	172	GLU	4.4
2	B	170	PHE	4.2
1	A	220	ASP	4.1
1	A	343	VAL	3.9
2	B	171	TYR	3.8
1	A	219	VAL	3.8
1	A	161	SER	3.7
2	B	255	GLY	3.6
1	A	438	HIS	3.5
2	B	225	GLU	3.4
2	B	204	TYR	3.3
2	B	458	THR	3.1
2	B	168	PHE	3.0
1	A	187	VAL	3.0
1	A	163	THR	3.0
1	A	217	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	171	TYR	2.9
2	B	407	GLU	2.9
1	A	256	ASP	2.9
1	A	409	THR	2.9
2	B	224	GLU	2.8
1	A	459	ALA	2.8
2	B	397	LEU	2.8
1	A	439	GLU	2.8
2	B	253	SER	2.8
2	B	258	LEU	2.8
1	A	162	ASP	2.7
2	B	169	SER	2.7
1	A	216	ALA	2.5
1	A	344	MET	2.5
1	A	166	HIS	2.5
1	A	349	VAL	2.5
1	A	186	SER	2.4
1	A	195	GLY	2.4
2	B	166	HIS	2.4
2	B	197	PHE	2.4
1	A	223	THR	2.4
2	B	409	THR	2.4
2	B	346	SER	2.4
1	A	255	GLY	2.4
2	B	223	THR	2.3
2	B	257	ASP	2.3
1	A	335	ALA	2.3
1	A	196	GLY	2.3
2	B	216	ALA	2.3
2	B	252	SER	2.3
1	A	222	THR	2.3
2	B	336	SER	2.2
2	B	286	HIS	2.2
1	A	418	MET	2.2
2	B	349	VAL	2.2
2	B	256	ASP	2.1
1	A	336	SER	2.1
2	B	167	SER	2.1
1	A	167	SER	2.1
2	B	347	ARG	2.1
1	A	225	GLU	2.0
2	B	196	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SEP	A	346	5/11	0.66	0.15	49,49,60,63	0
2	TPO	B	345	11/12	0.90	0.10	45,52,61,80	0
1	TPO	A	345	11/12	0.91	0.09	39,50,66,69	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

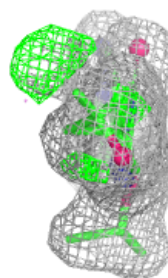
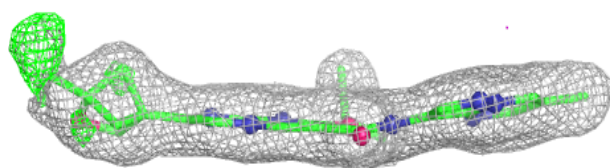
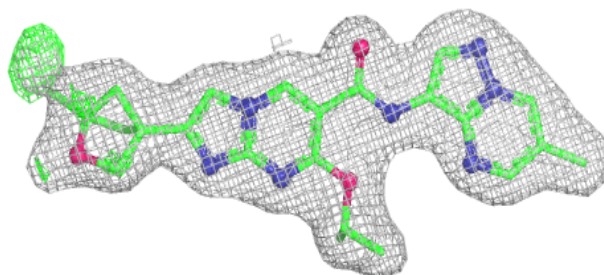
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	WFQ	A	501	33/33	0.95	0.08	27,32,50,63	0
3	WFQ	B	501	33/33	0.95	0.07	23,29,42,60	0

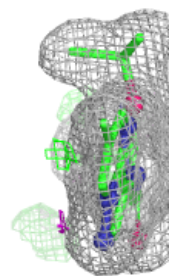
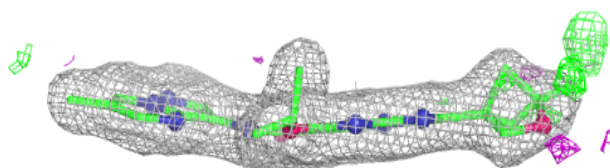
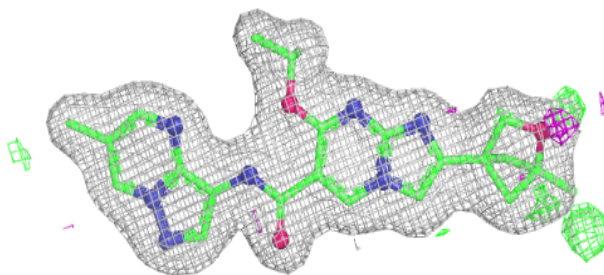
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around WFQ A 501:

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

**Electron density around WFQ B 501:**

$2mF_o-DF_c$ (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.