



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:19 AM UTC

PDB ID : 6RFJ / pdb_00006rfj
Title : IRAK4 IN COMPLEX WITH inhibitor
Authors : Xue, Y.; Degorce, S.L.; Robb, G.R.; Ferguson, A.D.
Deposited on : 2019-04-15
Resolution : 2.61 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

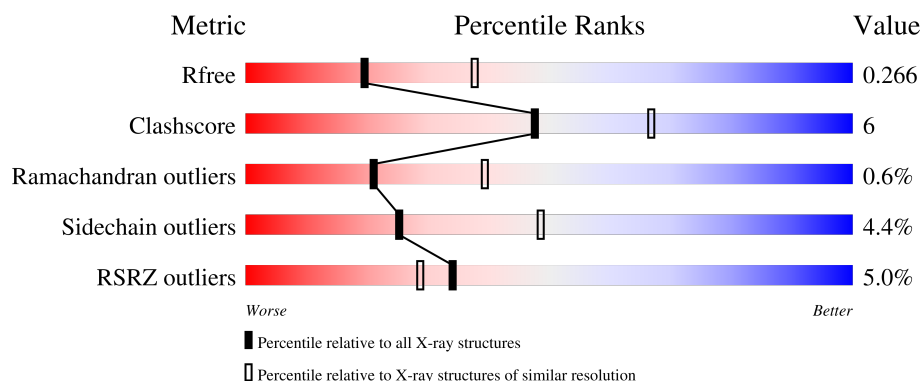
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	322	
1	B	322	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4450 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	268	Total	C	N	O	P	S	0	0	0
			2136	1346	359	415	2	14			
1	B	279	Total	C	N	O	P	S	0	0	0
			2211	1388	373	434	2	14			

There are 30 discrepancies between the modelled and reference sequences:

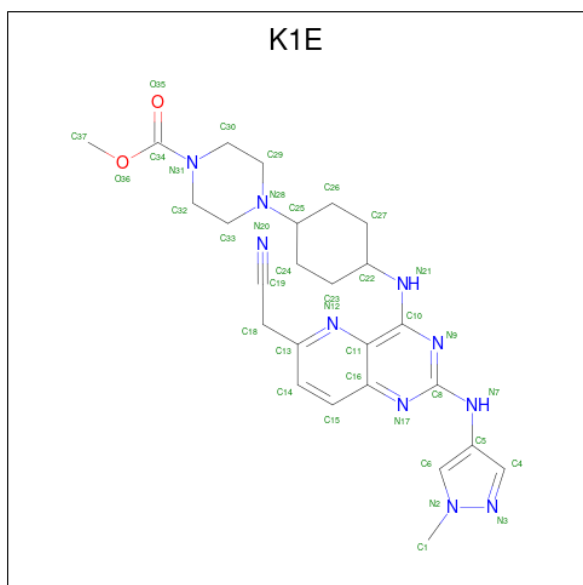
Chain	Residue	Modelled	Actual	Comment	Reference
A	139	MET	-	initiating methionine	UNP Q9NWZ3
A	140	HIS	-	expression tag	UNP Q9NWZ3
A	141	HIS	-	expression tag	UNP Q9NWZ3
A	142	HIS	-	expression tag	UNP Q9NWZ3
A	143	HIS	-	expression tag	UNP Q9NWZ3
A	144	HIS	-	expression tag	UNP Q9NWZ3
A	145	HIS	-	expression tag	UNP Q9NWZ3
A	146	HIS	-	expression tag	UNP Q9NWZ3
A	147	GLU	-	expression tag	UNP Q9NWZ3
A	148	ASN	-	expression tag	UNP Q9NWZ3
A	149	LEU	-	expression tag	UNP Q9NWZ3
A	150	TYR	-	expression tag	UNP Q9NWZ3
A	151	PHE	-	expression tag	UNP Q9NWZ3
A	152	GLN	-	expression tag	UNP Q9NWZ3
A	153	GLY	-	expression tag	UNP Q9NWZ3
B	139	MET	-	initiating methionine	UNP Q9NWZ3
B	140	HIS	-	expression tag	UNP Q9NWZ3
B	141	HIS	-	expression tag	UNP Q9NWZ3
B	142	HIS	-	expression tag	UNP Q9NWZ3
B	143	HIS	-	expression tag	UNP Q9NWZ3
B	144	HIS	-	expression tag	UNP Q9NWZ3
B	145	HIS	-	expression tag	UNP Q9NWZ3
B	146	HIS	-	expression tag	UNP Q9NWZ3
B	147	GLU	-	expression tag	UNP Q9NWZ3
B	148	ASN	-	expression tag	UNP Q9NWZ3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	149	LEU	-	expression tag	UNP Q9NWZ3
B	150	TYR	-	expression tag	UNP Q9NWZ3
B	151	PHE	-	expression tag	UNP Q9NWZ3
B	152	GLN	-	expression tag	UNP Q9NWZ3
B	153	GLY	-	expression tag	UNP Q9NWZ3

- Molecule 2 is methyl 4-[4-[[6-(cyanomethyl)-2-[(1-methylpyrazol-4-yl)amino]pyrido[3,2-d]pyrimidin-4-yl]amino]cyclohexyl]piperazine-1-carboxylate (CCD ID: K1E) (formula: $C_{25}H_{32}N_{10}O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			37	25	10	2		
2	B	1	Total	C	N	O	0	0
			37	25	10	2		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).

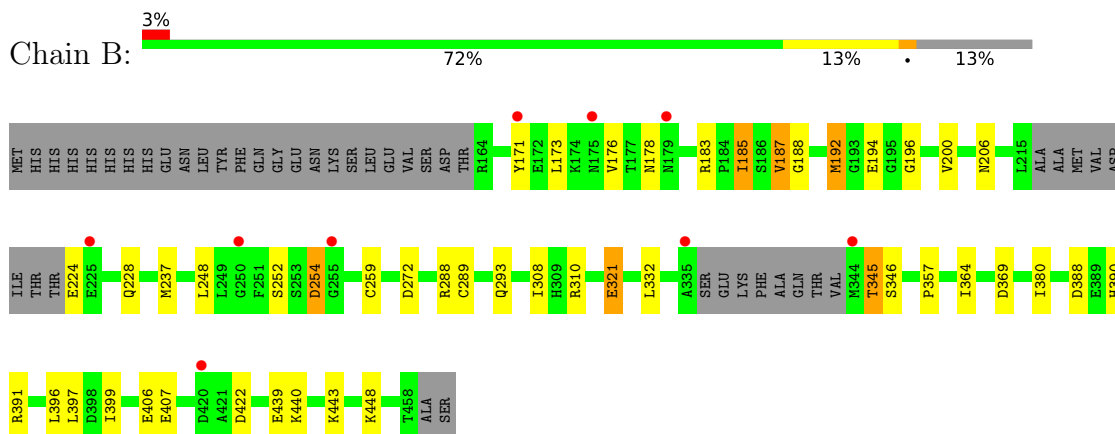
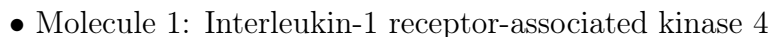


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		
4	B	16	Total	O	0	0
			16	16		

- Molecule 1: 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	87.61Å 118.92Å 140.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.34 – 2.61 28.34 – 2.61	Depositor EDS
% Data completeness (in resolution range)	97.0 (28.34-2.61) 97.4 (28.34-2.61)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.61Å)	Xtriage
Refinement program	BUSTER 2.11.6 PACIOREK	Depositor
R, R_{free}	0.245 , 0.254 0.256 , 0.266	Depositor DCC
R_{free} test set	1084 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	57.0	Xtriage
Anisotropy	0.709	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 86.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4450	wwPDB-VP
Average B, all atoms (Å ²)	92.0	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 23.15 % 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 4.9323e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SO4, TPO, SEP, K1E

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	0.77	0/2149	1.27	5/2890 (0.2%)
1	B	0.83	1/2226 (0.0%)	1.26	6/2996 (0.2%)
All	All	0.80	1/4375 (0.0%)	1.27	11/5886 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	192	MET	SD-CE	-9.36	1.56	1.79

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	185	ILE	CA-C-N	7.00	129.97	120.38
1	B	185	ILE	C-N-CA	7.00	129.97	120.38
1	B	254	ASP	CA-CB-CG	6.79	119.39	112.60
1	B	369	ASP	CA-CB-CG	6.07	118.67	112.60
1	A	405	ASP	CA-C-N	5.87	132.76	121.54
1	A	405	ASP	C-N-CA	5.87	132.76	121.54
1	A	446	ASP	CA-CB-CG	5.81	118.41	112.60
1	B	192	MET	N-CA-C	-5.70	106.46	113.41
1	B	272	ASP	CA-CB-CG	5.29	117.89	112.60
1	A	182	GLU	N-CA-C	5.24	119.30	113.01
1	A	225	GLU	N-CA-C	-5.23	106.05	112.90

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	2136	0	2106	32	0
1	B	2211	0	2174	19	0
2	A	37	0	0	0	0
2	B	37	0	0	0	0
3	B	5	0	0	0	0
4	A	8	0	0	0	0
4	B	16	0	0	0	0
All	All	4450	0	4280	49	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 6.

All (49) 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:237:MET:HE1	1:A:246:VAL:HG23	1.44	1.00
1:A:176:VAL:HG11	1:A:205:VAL:HG13	1.56	0.88
1:A:176:VAL:HG11	1:A:205:VAL:CG1	2.10	0.81
1:A:169:SER:HB3	1:A:172:GLU:HG3	1.73	0.71
1:B:187:VAL:HG23	1:B:188:GLY:H	1.56	0.71
1:A:396:LEU:O	1:A:399:ILE:HG12	1.94	0.68
1:A:438:HIS:CD2	1:A:440:LYS:HB2	2.30	0.67
1:B:192:MET:HE3	1:B:200:VAL:HG12	1.78	0.66
1:B:252:SER:HB3	1:B:259:CYS:HB2	1.79	0.65
1:A:438:HIS:HD2	1:A:440:LYS:HB2	1.64	0.63
1:A:408:LYS:HG2	1:A:413:TYR:HE2	1.64	0.60
1:B:173:LEU:HA	1:B:176:VAL:HG22	1.83	0.60
1:A:438:HIS:HD2	1:A:440:LYS:H	1.49	0.59
1:A:381:ILE:HG21	1:A:410:ILE:HD11	1.85	0.58
1:A:205:VAL:O	1:A:208:THR:HB	2.04	0.58
1:B:321:GLU:H	1:B:321:GLU:CD	2.11	0.58
1:A:237:MET:CE	1:A:246:VAL:HG23	2.29	0.55
1:B:310:ARG:HD3	1:B:332:LEU:O	2.08	0.54
1:A:408:LYS:HG2	1:A:413:TYR:CE2	2.42	0.54
1:A:206:ASN:C	1:A:208:THR:H	2.16	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:MET:SD	1:A:264:TYR:HE1	2.34	0.51
1:B:288:ARG:HB3	1:B:380:ILE:HG23	1.91	0.51
1:B:357:PRO:HG3	1:B:439:GLU:OE2	2.10	0.51
1:B:187:VAL:HG23	1:B:188:GLY:N	2.24	0.50
1:A:202:LYS:HE2	1:A:209:THR:HG21	1.94	0.50
1:A:438:HIS:CD2	1:A:440:LYS:H	2.29	0.50
1:B:345:TPO:HG21	1:B:364:ILE:HD11	1.93	0.49
1:A:284:SER:O	1:A:288:ARG:HG3	2.13	0.48
1:A:205:VAL:O	1:A:206:ASN:HB2	2.14	0.48
1:A:388:ASP:HB3	1:A:391:ARG:HB3	1.95	0.48
1:A:390:HIS:O	1:B:391:ARG:HA	2.14	0.48
1:A:391:ARG:HA	1:B:390:HIS:O	2.14	0.47
1:A:191:LYS:HE3	1:A:199:VAL:CG1	2.45	0.47
1:A:400:LYS:O	1:A:404:GLU:HB2	2.15	0.46
1:A:191:LYS:HE3	1:A:199:VAL:HG11	1.99	0.45
1:B:388:ASP:HB3	1:B:391:ARG:HB3	1.99	0.45
1:A:206:ASN:C	1:A:208:THR:N	2.75	0.44
1:A:178:ASN:O	1:A:181:ASP:HB2	2.17	0.44
1:A:247:GLU:HB3	1:A:263:VAL:HG12	1.99	0.44
1:A:345:TPO:CG2	1:A:364:ILE:HD11	2.48	0.44
1:B:396:LEU:O	1:B:399:ILE:HG12	2.17	0.44
1:B:308:ILE:HG22	1:B:310:ARG:HG3	2.01	0.43
1:B:289:CYS:O	1:B:293:GLN:HG3	2.18	0.43
1:A:264:TYR:CE2	1:A:266:PRO:HA	2.54	0.42
1:A:173:LEU:HA	1:A:176:VAL:HG22	2.01	0.42
1:B:183:ARG:HH11	1:B:188:GLY:HA3	1.85	0.41
1:B:440:LYS:HB2	1:B:443:LYS:HG3	2.02	0.41
1:B:237:MET:HE3	1:B:248:LEU:HB2	2.04	0.40
1:A:239:LYS:HD3	1:A:239:LYS:HA	1.93	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	256/322 (80%)	248 (97%)	7 (3%)	1 (0%)	30	49
1	B	271/322 (84%)	261 (96%)	8 (3%)	2 (1%)	18	35
All	All	527/644 (82%)	509 (97%)	15 (3%)	3 (1%)	21	39

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	406	GLU
1	B	187	VAL
1	B	196	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	234/280 (84%)	227 (97%)	7 (3%)	36	62
1	B	242/280 (86%)	228 (94%)	14 (6%)	18	37
All	All	476/560 (85%)	455 (96%)	21 (4%)	25	48

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	182	GLU
1	A	213	LYS
1	A	227	LYS
1	A	243	GLU
1	A	329	ASP
1	A	408	LYS
1	A	410	ILE
1	B	171	TYR
1	B	178	ASN
1	B	185	ILE
1	B	194	GLU
1	B	206	ASN
1	B	224	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	228	GLN
1	B	254	ASP
1	B	321	GLU
1	B	397	LEU
1	B	406	GLU
1	B	407	GLU
1	B	422	ASP
1	B	448	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	190	ASN
1	A	306	HIS
1	A	307	HIS
1	A	435	GLN
1	A	438	HIS
1	B	175	ASN
1	B	179	ASN
1	B	229	GLN
1	B	267	ASN
1	B	435	GLN
1	B	438	HIS
1	B	442	ASN
1	B	451	GLN
1	B	452	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	TPO	B	345	1	8,10,11	1.52	2 (25%)	10,14,16	1.65	5 (50%)
1	TPO	A	345	1	8,10,11	0.99	0	10,14,16	1.62	2 (20%)
1	SEP	B	346	1	8,9,10	0.91	0	7,12,14	1.79	2 (28%)
1	SEP	A	346	1	8,9,10	0.67	0	7,12,14	2.17	3 (42%)

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	TPO	B	345	1	-	3/9/11/13	-
1	TPO	A	345	1	-	4/9/11/13	-
1	SEP	B	346	1	-	0/6/8/10	-
1	SEP	A	346	1	-	0/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	345	TPO	CB-CA	2.85	1.59	1.53
1	B	345	TPO	P-OG1	-2.02	1.56	1.59

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	346	SEP	OG-CB-CA	4.38	112.41	108.14
1	A	345	TPO	CG2-CB-CA	4.24	121.51	113.26
1	B	346	SEP	OG-CB-CA	3.57	111.62	108.14
1	B	345	TPO	OG1-P-O1P	2.81	119.34	109.33
1	A	346	SEP	O3P-P-OG	2.48	113.13	106.67
1	B	346	SEP	OG-P-O1P	2.33	112.73	106.44
1	A	346	SEP	OG-P-O1P	2.30	112.64	106.44
1	B	345	TPO	P-OG1-CB	-2.17	117.42	123.33
1	B	345	TPO	O3P-P-O1P	-2.14	102.49	110.83
1	A	345	TPO	O2P-P-OG1	2.06	113.87	105.85
1	B	345	TPO	O2P-P-OG1	2.03	113.78	105.85
1	B	345	TPO	CG2-CB-CA	2.01	117.17	113.26

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	345	TPO	N-CA-CB-OG1
1	A	345	TPO	CA-CB-OG1-P
1	B	345	TPO	N-CA-CB-OG1
1	A	345	TPO	CB-OG1-P-O1P
1	B	345	TPO	CB-OG1-P-O2P
1	A	345	TPO	O-C-CA-CB
1	B	345	TPO	O-C-CA-CB

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	345	TPO	1	0
1	A	345	TPO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	K1E	A	501	-	38,41,41	0.48	0	50,57,57	0.94	2 (4%)
3	SO4	B	501	-	4,4,4	0.29	0	6,6,6	0.16	0
2	K1E	B	502	-	38,41,41	0.66	1 (2%)	50,57,57	0.87	1 (2%)

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	K1E	A	501	-	-	3/21/41/41	0/5/5/5
2	K1E	B	502	-	-	6/21/41/41	0/5/5/5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	K1E	N2-N3	3.30	1.39	1.35

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	K1E	C13-C18-C19	-3.55	109.42	113.56
2	B	502	K1E	C10-N21-C22	-2.51	119.66	124.06
2	A	501	K1E	C23-C22-N21	2.41	114.65	110.77

There are no chirality outliers.

All (9) torsion outliers are listed below:

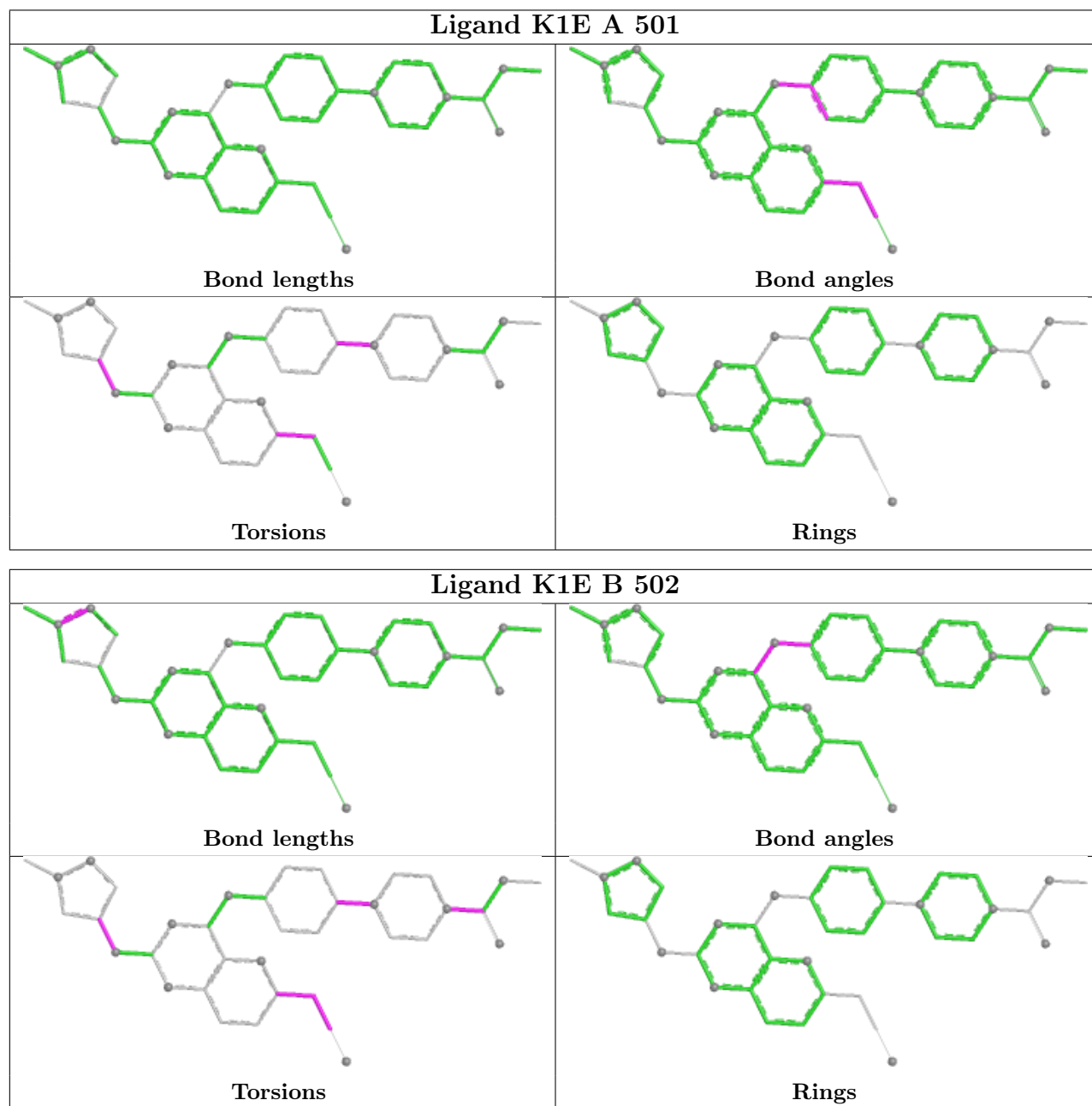
Mol	Chain	Res	Type	Atoms
2	A	501	K1E	C6-C5-N7-C8
2	B	502	K1E	C13-C18-C19-N20
2	B	502	K1E	C6-C5-N7-C8
2	B	502	K1E	O36-C34-N31-C32
2	B	502	K1E	O35-C34-N31-C32
2	A	501	K1E	C24-C25-N28-C33
2	A	501	K1E	N12-C13-C18-C19
2	B	502	K1E	N12-C13-C18-C19
2	B	502	K1E	C24-C25-N28-C33

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.



5.7 Other polymers ⓘ

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

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	266/322 (82%)	0.62	18 (6%)	23 19	45, 95, 137, 159	1 (0%)
1	B	277/322 (86%)	0.45	9 (3%)	50 45	41, 82, 131, 160	0
All	All	543/644 (84%)	0.53	27 (4%)	34 29	41, 88, 136, 160	1 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	250	GLY	3.9
1	A	287	MET	3.8
1	A	458	THR	3.7
1	B	335	ALA	3.7
1	A	343	VAL	3.6
1	B	179	ASN	3.5
1	B	175	ASN	3.3
1	A	192	MET	3.1
1	B	171	TYR	3.0
1	A	335	ALA	3.0
1	B	420	ASP	2.9
1	B	255	GLY	2.7
1	A	348	ILE	2.7
1	A	165	PHE	2.6
1	A	344	MET	2.6
1	B	344	MET	2.6
1	A	208	THR	2.5
1	A	226	LEU	2.5
1	A	225	GLU	2.5
1	A	215	LEU	2.4
1	A	204	TYR	2.4
1	B	225	GLU	2.3
1	A	209	THR	2.2
1	A	409	THR	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	259	CYS	2.1
1	A	178	ASN	2.1
1	A	413	TYR	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(Å ²)	Q<0.9
1	SEP	A	346	10/11	0.43	0.12	136,144,152,156	0
1	SEP	B	346	10/11	0.68	0.15	131,141,155,156	0
1	TPO	A	345	11/12	0.83	0.13	127,135,140,140	0
1	TPO	B	345	11/12	0.92	0.10	117,126,130,130	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

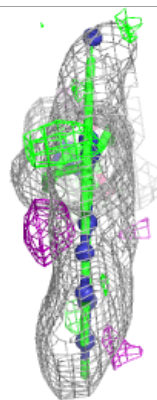
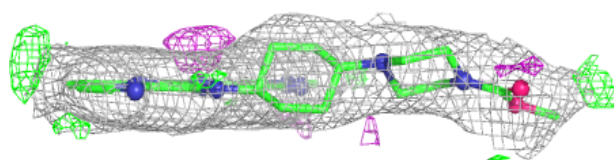
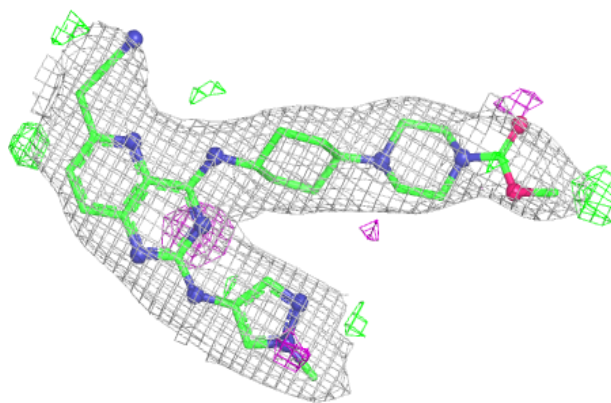
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	B	501	5/5	0.63	0.13	138,139,139,140	0
2	K1E	B	502	37/37	0.89	0.12	39,50,80,81	0
2	K1E	A	501	37/37	0.91	0.11	44,56,72,83	0

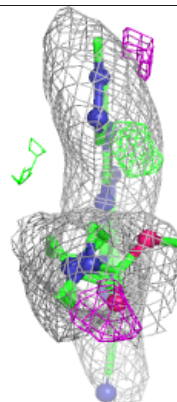
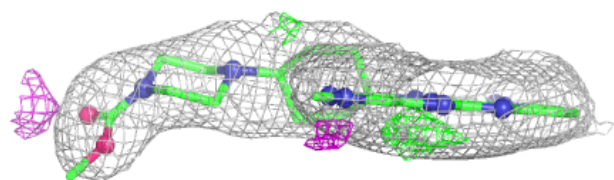
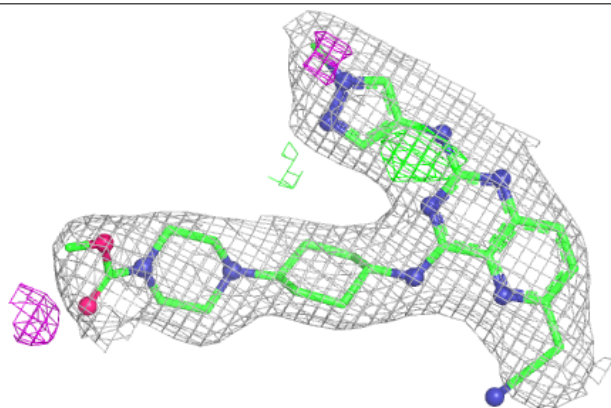
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around K1E B 502:

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

**Electron density around K1E 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.