



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:28 AM UTC

PDB ID : 7QG5 / pdb_00007qg5
Title : IRAK4 in complex with inhibitor
Authors : Xue, Y.; Aagaard, A.; Robb, G.R.; Degorce, S.L.
Deposited on : 2021-12-07
Resolution : 2.30 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

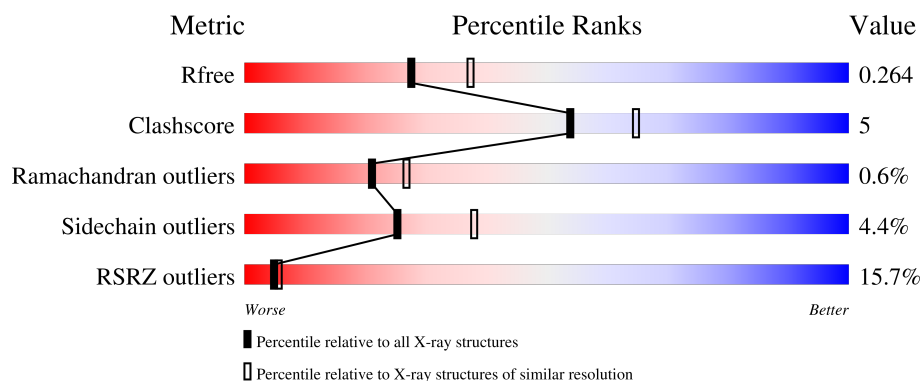
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	308	12% 76% 10% 12%
1	B	308	16% 74% 17% 9%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4643 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.

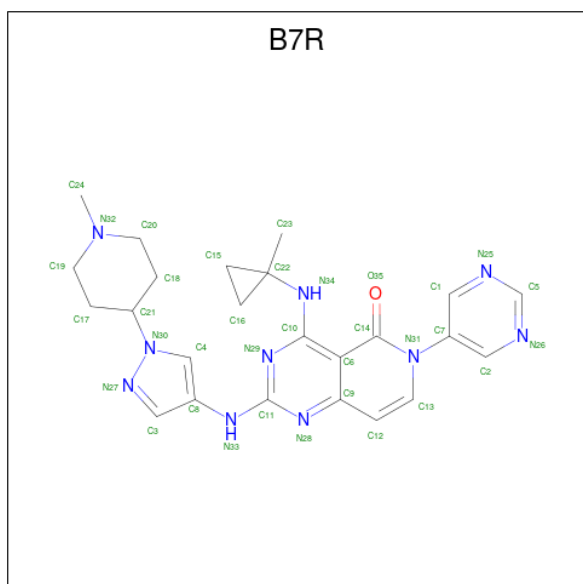
- Molecule 1 is a protein called Interleukin-1 receptor-associated kinase 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	270	Total	C	N	O	P	S	0	1	0
			2156	1360	361	418	2	15			
1	B	281	Total	C	N	O	P	S	0	0	0
			2225	1397	375	437	2	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	GLY	-	expression tag	UNP Q9NWZ3
B	153	GLY	-	expression tag	UNP Q9NWZ3

- Molecule 2 is 4-[(1-methylcyclopropyl)amino]-2-[[1-(1-methylpiperidin-4-yl)pyrazol-4-yl]amino]-6-pyrimidin-5-yl-pyrido[4,3-d]pyrimidin-5-one (CCD ID: B7R) (formula: C₂₄H₂₈N₁₀O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			35	24	10	1		
2	B	1	Total	C	N	O	0	0
			35	24	10	1		

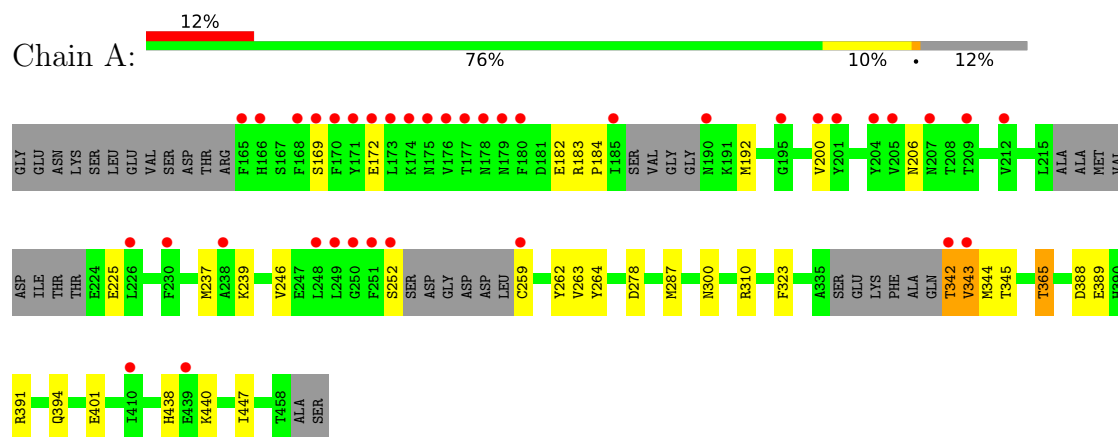
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	102	Total	O	0	0
			102	102		
3	B	90	Total	O	0	0
			90	90		

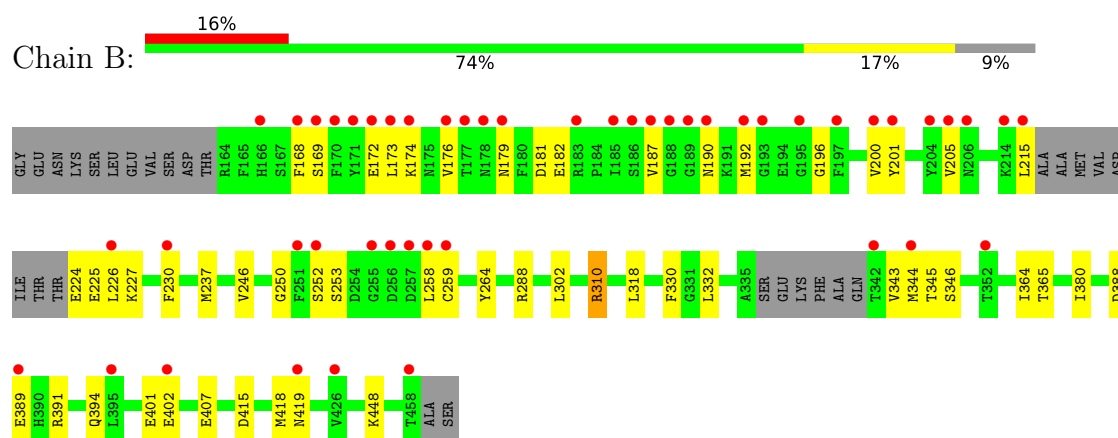
3 Residue-property plots [i](#)

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 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	87.40Å 110.38Å 142.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	68.52 – 2.30 68.52 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.0 (68.52-2.30) 98.0 (68.52-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.247 , 0.275 0.239 , 0.264	Depositor DCC
R_{free} test set	1472 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	47.5	Xtriage
Anisotropy	0.525	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 66.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4643	wwPDB-VP
Average B, all atoms (Å ²)	69.0	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 36.25 % 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 5.1454e-04. 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: B7R, TPO, SEP

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	0.70	0/2172	1.03	4/2921 (0.1%)
1	B	0.73	0/2240	1.08	2/3016 (0.1%)
All	All	0.72	0/4412	1.06	6/5937 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	342	THR	CA-C-N	6.76	134.14	121.97
1	A	342	THR	C-N-CA	6.76	134.14	121.97
1	A	310	ARG	CD-NE-CZ	6.23	133.12	124.40
1	B	187	VAL	N-CA-CB	-5.61	106.04	112.21
1	A	310	ARG	CG-CD-NE	-5.22	100.51	112.00
1	B	310	ARG	CD-NE-CZ	5.09	131.52	124.40

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	2156	0	2133	13	0
1	B	2225	0	2190	29	0
2	A	35	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	35	0	0	1	0
3	A	102	0	0	1	0
3	B	90	0	0	0	0
All	All	4643	0	4323	43	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 5.

All (43) 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	1.51	0.92
1:B:310:ARG:HD3	1:B:332:LEU:O	1.72	0.89
1:B:224:GLU:HA	1:B:227:LYS:NZ	2.12	0.65
1:B:181:ASP:HB3	1:B:190:ASN:HB2	1.79	0.64
1:B:237:MET:HE1	1:B:246:VAL:HG23	1.80	0.63
1:A:192:MET:HE3	1:A:200:VAL:HG12	1.81	0.63
1:A:192:MET:SD	1:A:264:TYR:HE1	2.26	0.59
1:A:169:SER:OG	1:A:172:GLU:HG3	2.03	0.58
1:A:278:ASP:O	1:B:419:ASN:HB2	2.06	0.55
1:B:169:SER:HB3	1:B:172:GLU:HG3	1.89	0.54
1:B:343:VAL:HG13	1:B:364:ILE:HB	1.90	0.54
1:B:224:GLU:HA	1:B:227:LYS:HZ2	1.73	0.53
1:B:168:PHE:HE1	1:B:250:GLY:HA3	1.72	0.53
1:A:438:HIS:HD2	1:A:440:LYS:H	1.57	0.53
1:B:174:LYS:CG	1:B:179:ASN:HA	2.40	0.51
1:B:192:MET:HE2	1:B:201:TYR:C	2.37	0.50
1:A:287[B]:MET:HE2	1:A:323:PHE:HB2	1.93	0.50
1:B:174:LYS:HG2	1:B:179:ASN:HA	1.94	0.48
1:B:173:LEU:HA	1:B:176:VAL:HG22	1.95	0.48
1:B:215:LEU:HD12	1:B:258:LEU:HB2	1.94	0.48
2:B:501:B7R:C3	2:B:501:B7R:N29	2.72	0.48
1:B:176:VAL:HG11	1:B:205:VAL:HG22	1.95	0.48
1:B:310:ARG:CD	1:B:332:LEU:O	2.55	0.47
1:B:224:GLU:N	1:B:227:LYS:HZ1	2.13	0.46
1:B:192:MET:SD	1:B:264:TYR:CE2	3.09	0.45
1:A:237:MET:HE3	1:A:262:TYR:HE2	1.83	0.44
1:B:224:GLU:CA	1:B:227:LYS:NZ	2.80	0.44
2:A:501:B7R:C3	2:A:501:B7R:N29	2.81	0.44
1:B:224:GLU:CA	1:B:227:LYS:HZ1	2.30	0.43
1:B:388:ASP:HB3	1:B:391:ARG:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:252:SER:HB3	1:B:259:CYS:HB2	2.00	0.43
1:B:215:LEU:HB3	1:B:226:LEU:HD21	2.01	0.42
1:A:252:SER:HB2	1:A:259:CYS:HB2	2.01	0.42
1:A:388:ASP:HB3	1:A:391:ARG:HB3	2.01	0.42
1:A:172:GLU:HA	3:A:615:HOH:O	2.18	0.42
1:B:246:VAL:HG11	1:B:318:LEU:HD12	2.00	0.42
1:A:342:THR:N	1:A:365:THR:HB	2.34	0.42
1:B:302:LEU:HD11	1:B:330:PHE:HE1	1.84	0.42
1:B:230:PHE:CZ	1:B:253:SER:HB3	2.56	0.41
1:A:300:ASN:HA	1:A:447:ILE:HG21	2.03	0.40
1:B:415:ASP:HB3	1:B:418:MET:HE2	2.04	0.40
1:B:288:ARG:HB3	1:B:380:ILE:HG23	2.04	0.40
1:B:402:GLU:OE2	1:B:407:GLU:OE1	2.39	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	259/308 (84%)	250 (96%)	7 (3%)	2 (1%)	16	20
1	B	273/308 (89%)	263 (96%)	9 (3%)	1 (0%)	30	38
All	All	532/616 (86%)	513 (96%)	16 (3%)	3 (1%)	21	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	343	VAL
1	A	184	PRO
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	237/266 (89%)	225 (95%)	12 (5%)	21	32
1	B	244/266 (92%)	235 (96%)	9 (4%)	30	45
All	All	481/532 (90%)	460 (96%)	21 (4%)	25	38

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

Mol	Chain	Res	Type
1	A	182	GLU
1	A	183	ARG
1	A	206	ASN
1	A	225	GLU
1	A	239	LYS
1	A	263	VAL
1	A	343	VAL
1	A	344	MET
1	A	365	THR
1	A	389	GLU
1	A	394	GLN
1	A	401	GLU
1	B	182	GLU
1	B	200	VAL
1	B	225	GLU
1	B	344	MET
1	B	365	THR
1	B	389	GLU
1	B	394	GLN
1	B	401	GLU
1	B	448	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	179	ASN

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Mol	Chain	Res	Type
1	A	306	HIS
1	A	455	GLN
1	B	206	ASN
1	B	438	HIS
1	B	455	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	SEP	B	346	1	8,9,10	0.93	0	7,12,14	1.09	1 (14%)
1	TPO	A	345	1	8,10,11	1.65	2 (25%)	10,14,16	1.38	2 (20%)
1	SEP	A	346	1	8,9,10	0.92	0	7,12,14	1.01	0
1	TPO	B	345	1	8,10,11	1.45	2 (25%)	10,14,16	1.37	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	B	346	1	-	0/6/8/10	-
1	TPO	A	345	1	-	3/9/11/13	-
1	SEP	A	346	1	-	0/6/8/10	-
1	TPO	B	345	1	-	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	CB-CA	2.99	1.60	1.53
1	A	345	TPO	P-OG1	-2.80	1.54	1.59
1	B	345	TPO	P-OG1	-2.68	1.54	1.59
1	B	345	TPO	CB-CA	2.43	1.59	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	345	TPO	O2P-P-OG1	2.63	116.12	105.85
1	B	345	TPO	P-OG1-CB	-2.59	116.28	123.33
1	A	345	TPO	P-OG1-CB	-2.57	116.34	123.33
1	A	345	TPO	O2P-P-OG1	2.55	115.79	105.85
1	B	346	SEP	OG-P-O1P	2.10	112.12	106.44

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	B	345	TPO	N-CA-CB-OG1
1	A	345	TPO	CB-OG1-P-O1P
1	B	345	TPO	CB-OG1-P-O1P
1	A	345	TPO	O-C-CA-CB
1	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	$\# Z > 2$
2	B7R	A	501	-	37,40,40	0.86	0	40,59,59	1.88	9 (22%)
2	B7R	B	501	-	37,40,40	0.95	1 (2%)	40,59,59	1.63	10 (25%)

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	B7R	A	501	-	-	3/16/31/31	0/6/6/6
2	B7R	B	501	-	-	2/16/31/31	0/6/6/6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	B7R	C23-C22	-2.53	1.49	1.53

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	B7R	C17-C21-N30	6.09	119.29	110.95
2	A	501	B7R	C18-C21-N30	3.99	116.41	110.95
2	B	501	B7R	C7-N31-C14	-3.93	115.36	119.13
2	A	501	B7R	C15-C22-N34	3.72	120.64	115.60
2	A	501	B7R	C4-N30-N27	3.30	114.67	112.45
2	A	501	B7R	C21-N30-N27	-3.03	116.26	120.41
2	B	501	B7R	C17-C21-N30	3.03	115.11	110.95
2	B	501	B7R	C15-C22-N34	3.03	119.71	115.60
2	B	501	B7R	C7-N31-C13	2.67	121.26	118.15
2	B	501	B7R	C24-N32-C20	-2.64	105.59	110.63
2	B	501	B7R	C19-C17-C21	-2.53	106.14	110.78
2	B	501	B7R	C24-N32-C19	-2.43	106.00	110.63
2	A	501	B7R	C20-N32-C19	2.37	113.31	109.54
2	B	501	B7R	O35-C14-C6	-2.27	119.49	124.19
2	B	501	B7R	C4-N30-N27	2.26	113.97	112.45
2	A	501	B7R	O35-C14-C6	-2.22	119.59	124.19
2	A	501	B7R	C3-N27-N30	-2.13	103.04	104.14
2	B	501	B7R	C2-C7-N31	2.02	122.43	120.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	B7R	C1-N25-C5	-2.00	113.44	115.80

There are no chirality outliers.

All (5) torsion outliers are listed below:

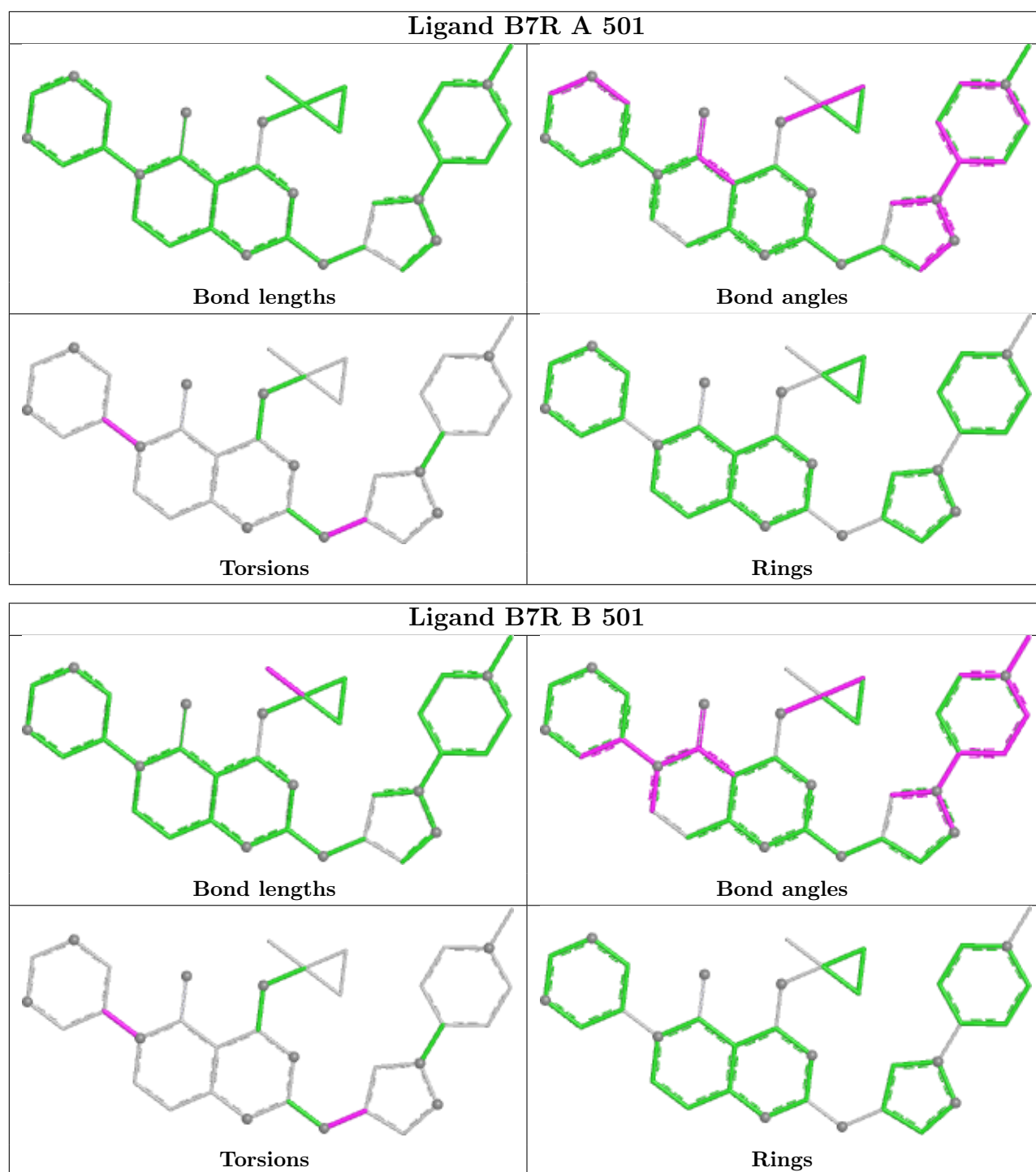
Mol	Chain	Res	Type	Atoms
2	A	501	B7R	C1-C7-N31-C13
2	A	501	B7R	C2-C7-N31-C13
2	A	501	B7R	C4-C8-N33-C11
2	B	501	B7R	C4-C8-N33-C11
2	B	501	B7R	C2-C7-N31-C13

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	B7R	1	0
2	B	501	B7R	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	268/308 (87%)	0.85	38 (14%) 6 7	23, 63, 154, 164	1 (0%)
1	B	279/308 (90%)	0.90	48 (17%) 4 4	36, 65, 95, 103	0
All	All	547/616 (88%)	0.87	86 (15%) 5 6	23, 64, 108, 164	1 (0%)

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	185	ILE	7.1
1	A	342	THR	5.3
1	B	170	PHE	5.3
1	A	173	LEU	4.8
1	A	170	PHE	4.7
1	B	176	VAL	4.5
1	A	238	ALA	4.4
1	A	171	TYR	4.3
1	A	165	PHE	4.2
1	B	258	LEU	4.2
1	A	176	VAL	4.2
1	A	205	VAL	3.8
1	A	168	PHE	3.7
1	A	252	SER	3.6
1	B	257	ASP	3.6
1	A	180	PHE	3.6
1	B	226	LEU	3.6
1	A	439	GLU	3.4
1	B	168	PHE	3.3
1	B	259	CYS	3.2
1	A	251	PHE	3.1
1	A	204	TYR	3.0
1	B	201	TYR	3.0
1	B	230	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	192	MET	3.0
1	B	173	LEU	3.0
1	B	179	ASN	2.9
1	B	344	MET	2.9
1	B	188	GLY	2.9
1	A	177	THR	2.9
1	B	190	ASN	2.9
1	B	177	THR	2.8
1	B	171	TYR	2.8
1	B	205	VAL	2.8
1	A	175	ASN	2.8
1	A	179	ASN	2.8
1	B	252	SER	2.8
1	B	195	GLY	2.7
1	A	226	LEU	2.7
1	B	256	ASP	2.7
1	B	183	ARG	2.7
1	A	248	LEU	2.7
1	A	174	LYS	2.6
1	B	200	VAL	2.6
1	B	251	PHE	2.6
1	B	255	GLY	2.5
1	A	250	GLY	2.5
1	B	215	LEU	2.5
1	B	458	THR	2.4
1	A	410	ILE	2.4
1	B	342	THR	2.4
1	A	343	VAL	2.4
1	B	197	PHE	2.4
1	A	178	ASN	2.4
1	B	178	ASN	2.3
1	A	195	GLY	2.3
1	B	169	SER	2.3
1	A	200	VAL	2.3
1	B	389	GLU	2.3
1	B	402	GLU	2.3
1	B	189	GLY	2.3
1	B	193	GLY	2.3
1	B	174	LYS	2.3
1	A	172	GLU	2.2
1	A	201	TYR	2.2
1	A	166	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	169	SER	2.2
1	B	204	TYR	2.2
1	B	185	ILE	2.2
1	A	212	VAL	2.1
1	A	230	PHE	2.1
1	B	166	HIS	2.1
1	A	209	THR	2.1
1	A	249	LEU	2.1
1	A	190	ASN	2.1
1	B	186	SER	2.1
1	B	214	LYS	2.1
1	B	172	GLU	2.1
1	B	206	ASN	2.1
1	B	187	VAL	2.1
1	A	207	ASN	2.1
1	B	419	ASN	2.1
1	B	426	VAL	2.1
1	B	352	THR	2.0
1	A	259	CYS	2.0
1	B	395	LEU	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	10/11	0.62	0.15	86,89,126,129	0
1	SEP	B	346	10/11	0.75	0.11	86,89,115,125	0
1	TPO	B	345	11/12	0.91	0.09	82,88,99,100	0
1	TPO	A	345	11/12	0.94	0.09	79,83,86,88	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

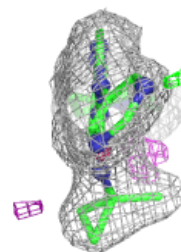
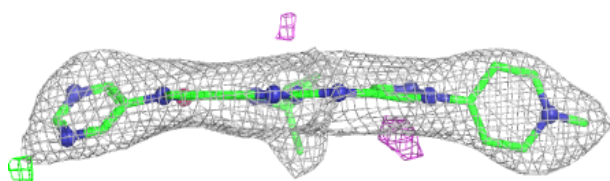
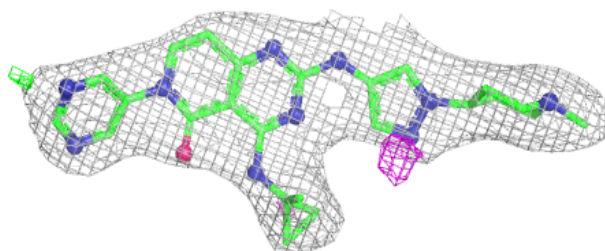
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	B7R	A	501	35/35	0.91	0.10	48,50,52,52	0
2	B7R	B	501	35/35	0.94	0.09	39,43,52,53	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.

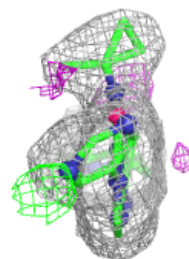
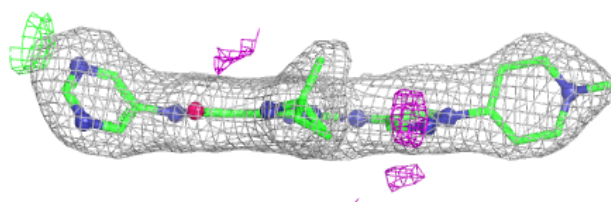
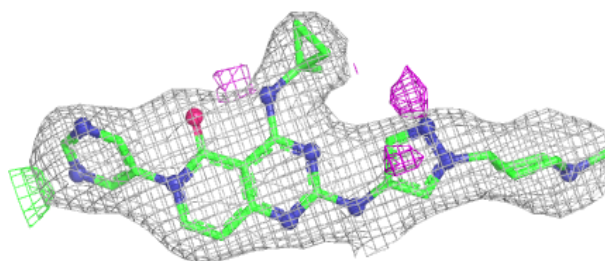
Electron density around B7R A 501:

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 B7R 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.