



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:51 PM UTC

PDB ID : 5TQ3 / pdb_00005tq3
Title : Design and Synthesis of a pan-JAK kinase inhibitor clinical candidate (PF-06263276) suitable for the treatment of inflammatory diseases of the lungs and skin
Authors : Chrencik, J.; Jones, P.
Deposited on : 2016-10-23
Resolution : 2.69 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

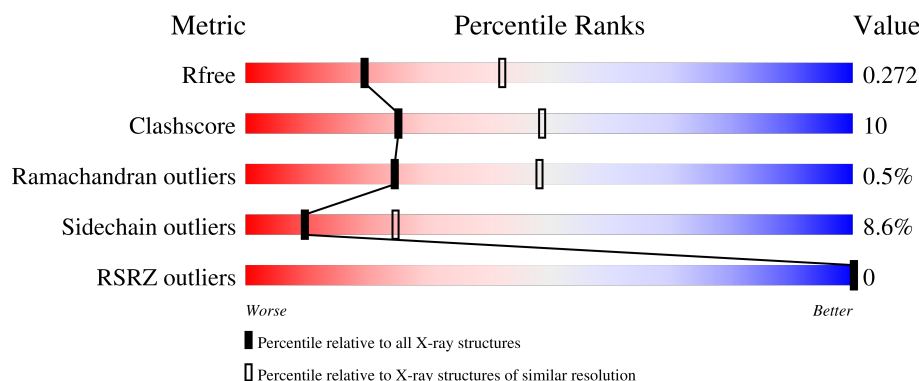
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	304	 70% 18% 5% 7%
1	B	304	 71% 17% 5% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4714 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.

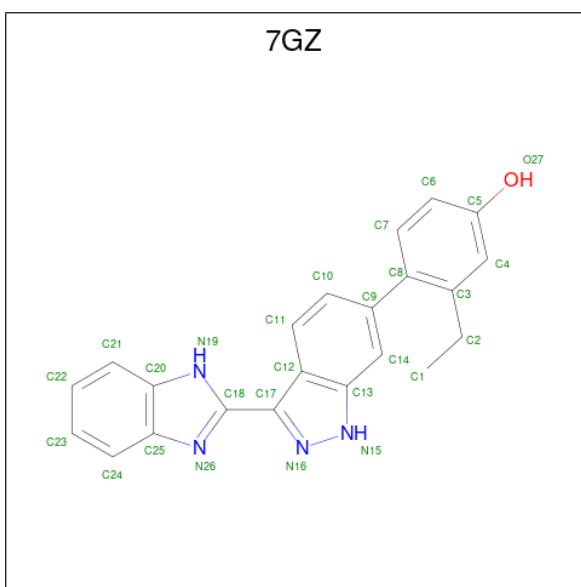
- Molecule 1 is a protein called Tyrosine-protein kinase JAK2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	P	S	0	1	0
			2296	1466	391	424	2	13			
1	B	287	Total	C	N	O	P	S	0	0	0
			2311	1472	391	433	2	13			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	829	MET	-	initiating methionine	UNP O60674
A	830	GLY	-	expression tag	UNP O60674
A	831	HIS	-	expression tag	UNP O60674
A	832	HIS	-	expression tag	UNP O60674
A	833	HIS	-	expression tag	UNP O60674
A	834	HIS	-	expression tag	UNP O60674
A	835	HIS	-	expression tag	UNP O60674
A	836	HIS	-	expression tag	UNP O60674
A	1073	SER	MET	engineered mutation	UNP O60674
A	1076	THR	PHE	engineered mutation	UNP O60674
A	1126	VAL	ILE	engineered mutation	UNP O60674
B	829	MET	-	initiating methionine	UNP O60674
B	830	GLY	-	expression tag	UNP O60674
B	831	HIS	-	expression tag	UNP O60674
B	832	HIS	-	expression tag	UNP O60674
B	833	HIS	-	expression tag	UNP O60674
B	834	HIS	-	expression tag	UNP O60674
B	835	HIS	-	expression tag	UNP O60674
B	836	HIS	-	expression tag	UNP O60674
B	1073	SER	MET	engineered mutation	UNP O60674
B	1076	THR	PHE	engineered mutation	UNP O60674
B	1126	VAL	ILE	engineered mutation	UNP O60674

- Molecule 2 is 4-[3-(1H-benzimidazol-2-yl)-1H-indazol-6-yl]-3-ethylphenol (CCD ID: 7GZ) (formula: C₂₂H₁₈N₄O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			27	22	4	1		
2	B	1	Total	C	N	O	0	0
			27	22	4	1		

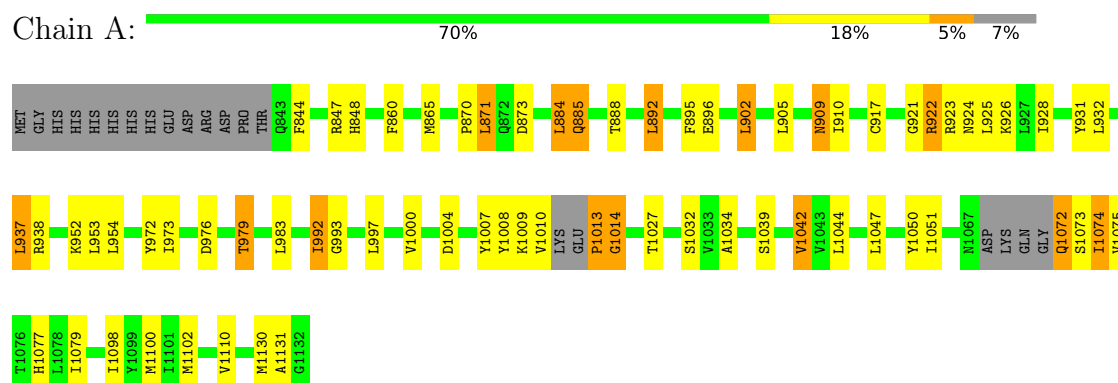
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	26	Total	O	0	0
			26	26		
3	B	27	Total	O	0	0
			27	27		

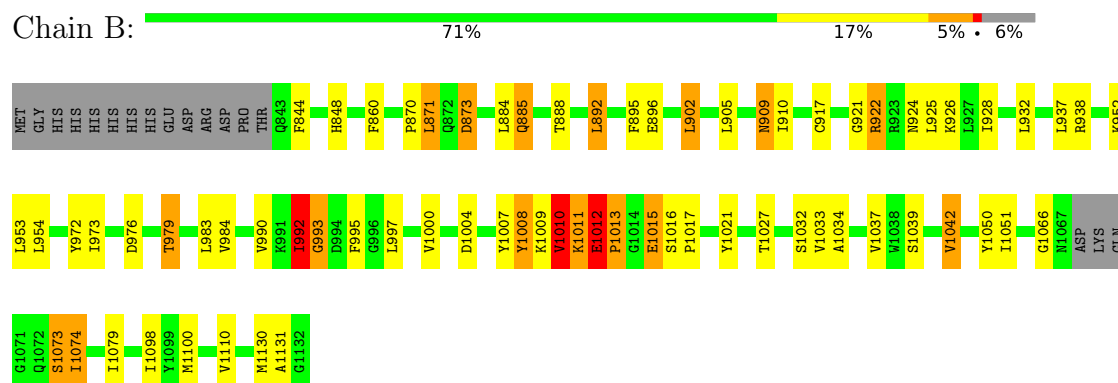
3 Residue-property plots [i](#)

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: Tyrosine-protein kinase JAK2



- Molecule 1: Tyrosine-protein kinase JAK2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	36.85Å 182.73Å 52.77Å 90.00° 110.41° 90.00°	Depositor
Resolution (Å)	34.54 – 2.69 34.54 – 2.69	Depositor EDS
% Data completeness (in resolution range)	90.9 (34.54-2.69) 91.4 (34.54-2.69)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.216 , 0.271 0.217 , 0.272	Depositor DCC
R_{free} test set	858 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	37.4	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 10.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.406 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4714	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.63% 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: 7GZ, PTR

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	0.63	2/2310 (0.1%)	0.96	9/3112 (0.3%)
1	B	0.68	3/2326 (0.1%)	0.98	12/3136 (0.4%)
All	All	0.65	5/4636 (0.1%)	0.97	21/6248 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
1	B	0	6
All	All	0	12

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1017	PRO	C-O	-5.98	1.16	1.24
1	B	1013	PRO	N-CD	5.36	1.55	1.47
1	B	1017	PRO	N-CD	5.31	1.55	1.47
1	A	1075	VAL	C-O	-5.30	1.18	1.24
1	A	1074	ILE	C-O	-5.21	1.18	1.23

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	923	ARG	N-CA-C	-13.50	96.81	113.28
1	A	1013	PRO	CB-CA-C	-13.38	84.69	110.10
1	B	922	ARG	N-CA-CB	-10.21	95.05	110.16
1	A	1013	PRO	N-CA-C	10.07	137.27	112.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1074	ILE	N-CA-C	-8.87	90.89	109.34
1	B	1131	ALA	N-CA-C	8.16	122.52	112.23
1	B	922	ARG	N-CA-C	7.60	119.64	111.36
1	B	992	ILE	N-CA-C	-7.30	100.16	109.58
1	B	993	GLY	N-CA-C	7.13	120.93	110.38
1	B	1013	PRO	N-CA-C	6.80	126.47	112.47
1	B	873	ASP	N-CA-C	-6.71	97.79	108.73
1	A	1131	ALA	N-CA-C	6.29	117.93	111.14
1	B	1013	PRO	CA-N-CD	-5.96	103.66	112.00
1	B	1131	ALA	CB-CA-C	-5.86	98.42	110.38
1	A	1014	GLY	N-CA-C	-5.79	96.52	113.30
1	A	1013	PRO	CA-N-CD	-5.75	103.94	112.00
1	A	1013	PRO	N-CA-CB	-5.47	96.98	103.00
1	A	1072	GLN	CA-C-N	5.20	131.07	121.70
1	A	1072	GLN	C-N-CA	5.20	131.07	121.70
1	B	1073	SER	CA-C-N	-5.01	112.94	121.97
1	B	1073	SER	C-N-CA	-5.01	112.94	121.97

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	GLY	Peptide
1	A	1072	GLN	Peptide
1	A	873	ASP	Peptide
1	A	921	GLY	Peptide
1	A	922	ARG	Peptide
1	A	992	ILE	Peptide
1	B	1010	VAL	Mainchain
1	B	1066	GLY	Peptide
1	B	1073	SER	Peptide
1	B	873	ASP	Peptide
1	B	921	GLY	Peptide
1	B	992	ILE	Peptide

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	2296	0	2224	39	0
1	B	2311	0	2234	49	0
2	A	27	0	0	1	0
2	B	27	0	0	1	0
3	A	26	0	0	0	0
3	B	27	0	0	0	0
All	All	4714	0	4458	88	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 (88) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1010:VAL:HA	1:B:1011:LYS:CB	1.77	1.13
1:B:1011:LYS:H	1:B:1012:GLU:HG2	1.18	1.07
1:B:1015:GLU:N	1:B:1015:GLU:OE2	1.87	1.06
1:B:1010:VAL:HA	1:B:1011:LYS:HB3	1.38	1.05
1:B:1011:LYS:HA	1:B:1012:GLU:HB2	1.55	0.86
1:A:848:HIS:ND1	1:A:870:PRO:HA	1.92	0.84
1:B:1010:VAL:HA	1:B:1011:LYS:HB2	1.56	0.84
1:B:848:HIS:ND1	1:B:870:PRO:HA	1.93	0.83
1:B:954:LEU:HD21	1:B:1098:ILE:HD11	1.68	0.75
1:A:954:LEU:HD21	1:A:1098:ILE:HD11	1.70	0.73
1:B:1010:VAL:CA	1:B:1011:LYS:CB	2.60	0.71
1:A:847:ARG:NH1	1:A:848:HIS:HE2	1.92	0.68
1:B:938:ARG:HB2	1:B:979:THR:HG23	1.77	0.67
1:A:892:LEU:HD23	1:A:922:ARG:CZ	2.25	0.66
1:A:938:ARG:HB2	1:A:979:THR:HG23	1.77	0.66
1:B:1011:LYS:H	1:B:1012:GLU:CG	2.01	0.66
1:B:892:LEU:HD23	1:B:922:ARG:CZ	2.26	0.66
1:B:1008:PTR:HD1	1:B:1010:VAL:HG12	1.79	0.64
1:A:932:LEU:HD12	1:A:983:LEU:HB3	1.80	0.63
1:B:1016:SER:HB3	1:B:1021:TYR:CE2	2.34	0.62
1:B:932:LEU:HD12	1:B:983:LEU:HB3	1.81	0.62
1:B:1011:LYS:CA	1:B:1012:GLU:HB2	2.26	0.60
1:A:902:LEU:HD21	2:A:4000:7GZ:O27	2.02	0.60
1:A:1073:SER:O	1:A:1077:HIS:HD2	1.84	0.60
1:A:871:LEU:H	1:A:871:LEU:HD12	1.67	0.60
1:A:1034:ALA:CB	1:A:1110:VAL:HG13	2.34	0.57
1:B:871:LEU:HD12	1:B:871:LEU:H	1.70	0.56
1:B:902:LEU:HD21	2:B:4001:7GZ:O27	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1051:ILE:HG22	1:B:1051:ILE:O	2.05	0.56
1:B:1016:SER:HB3	1:B:1021:TYR:CZ	2.40	0.55
1:A:860:PHE:O	1:A:885:GLN:N	2.32	0.55
1:B:954:LEU:HD21	1:B:1098:ILE:CD1	2.36	0.54
1:A:847:ARG:HG3	1:A:848:HIS:CD2	2.43	0.54
1:B:1039:SER:O	1:B:1042:VAL:HG13	2.07	0.54
1:B:1034:ALA:CB	1:B:1110:VAL:HG13	2.37	0.54
1:A:954:LEU:HD21	1:A:1098:ILE:CD1	2.37	0.53
1:A:1051:ILE:HG22	1:A:1051:ILE:O	2.09	0.53
1:B:992:ILE:HG22	1:B:993:GLY:HA2	1.89	0.52
1:B:1011:LYS:CA	1:B:1012:GLU:CB	2.86	0.52
1:A:1039:SER:O	1:A:1042:VAL:HG13	2.09	0.52
1:B:993:GLY:HA3	1:B:995:PHE:CE1	2.45	0.52
1:B:884:LEU:HD13	1:B:895:PHE:CD2	2.45	0.51
1:A:932:LEU:HD12	1:A:983:LEU:CB	2.41	0.51
1:A:992:ILE:HG22	1:A:993:GLY:HA2	1.92	0.51
1:B:909:ASN:N	1:B:909:ASN:HD22	2.10	0.50
1:A:871:LEU:HD12	1:A:871:LEU:N	2.27	0.49
1:B:860:PHE:O	1:B:885:GLN:N	2.36	0.49
1:A:884:LEU:HD13	1:A:895:PHE:CD2	2.47	0.49
1:B:1011:LYS:HA	1:B:1012:GLU:CB	2.33	0.49
1:B:1010:VAL:CA	1:B:1011:LYS:HB3	2.24	0.49
1:B:932:LEU:HD12	1:B:983:LEU:CB	2.43	0.48
1:B:1010:VAL:CA	1:B:1011:LYS:HB2	2.33	0.48
1:A:1010:VAL:HG13	1:A:1010:VAL:O	2.13	0.48
1:A:909:ASN:HD22	1:A:909:ASN:N	2.13	0.47
1:A:973:ILE:HD12	1:A:1032:SER:C	2.38	0.47
1:A:1010:VAL:O	1:A:1010:VAL:CG1	2.62	0.47
1:B:871:LEU:HD12	1:B:871:LEU:N	2.30	0.47
1:A:1027:THR:HG22	1:A:1079:ILE:HD13	1.97	0.47
1:B:938:ARG:CB	1:B:979:THR:HG23	2.45	0.47
1:B:1027:THR:HG22	1:B:1079:ILE:HD13	1.97	0.47
1:A:938:ARG:CB	1:A:979:THR:HG23	2.45	0.46
1:A:1073:SER:O	1:A:1077:HIS:CD2	2.69	0.45
1:B:973:ILE:HD12	1:B:1032:SER:C	2.40	0.45
1:A:953:LEU:HD11	1:A:1050:TYR:CZ	2.52	0.45
1:B:1011:LYS:N	1:B:1012:GLU:HG2	2.04	0.45
1:B:972:TYR:CE1	1:B:1000:VAL:HG22	2.52	0.44
1:B:1033:VAL:O	1:B:1037:VAL:HG23	2.18	0.44
1:A:847:ARG:CG	1:A:848:HIS:CD2	3.01	0.43
1:A:865:MET:HE3	1:A:931:TYR:CE2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:972:TYR:CE1	1:A:1000:VAL:HG22	2.53	0.43
1:A:844:PHE:CG	1:A:928:ILE:HD12	2.54	0.43
1:A:905:LEU:HD13	1:A:910:ILE:HG21	2.01	0.42
1:A:884:LEU:CD1	1:A:895:PHE:CD2	3.03	0.42
1:B:909:ASN:N	1:B:909:ASN:ND2	2.67	0.42
1:A:937:LEU:HD13	1:A:1047:LEU:HD21	2.02	0.42
1:B:917:CYS:HB3	1:B:926:LYS:HB2	2.02	0.41
1:B:984:VAL:HG22	1:B:990:VAL:HG12	2.02	0.41
1:B:884:LEU:CD1	1:B:895:PHE:CD2	3.04	0.41
1:A:976:ASP:HB2	1:A:997:LEU:HD12	2.03	0.41
1:B:844:PHE:CG	1:B:928:ILE:HD12	2.56	0.41
1:B:848:HIS:CD2	1:B:848:HIS:N	2.88	0.41
1:B:976:ASP:HB2	1:B:997:LEU:HD12	2.03	0.41
1:A:848:HIS:CD2	1:A:848:HIS:N	2.89	0.41
1:B:953:LEU:HD11	1:B:1050:TYR:CZ	2.56	0.41
1:A:917:CYS:HB3	1:A:926:LYS:HB2	2.03	0.40
1:B:905:LEU:HD13	1:B:910:ILE:HG21	2.03	0.40
1:A:909:ASN:N	1:A:909:ASN:ND2	2.68	0.40
1:A:1044:LEU:HD23	1:A:1102:MET:HG3	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	277/304 (91%)	264 (95%)	13 (5%)	0	100	100
1	B	281/304 (92%)	262 (93%)	16 (6%)	3 (1%)	11	29
All	All	558/608 (92%)	526 (94%)	29 (5%)	3 (0%)	24	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1011	LYS
1	B	1012	GLU
1	B	1013	PRO

5.3.2 Protein sidechains [i](#)

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	238/275 (86%)	218 (92%)	20 (8%)	10	26
1	B	242/275 (88%)	221 (91%)	21 (9%)	9	24
All	All	480/550 (87%)	439 (92%)	41 (8%)	10	25

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	871	LEU
1	A	884	LEU
1	A	885	GLN
1	A	888	THR
1	A	892	LEU
1	A	896	GLU
1	A	902	LEU
1	A	909	ASN
1	A	924	ASN
1	A	925	LEU
1	A	937	LEU
1	A	952	LYS
1	A	979	THR
1	A	1004	ASP
1	A	1009	LYS
1	A	1013	PRO
1	A	1042	VAL
1	A	1074	ILE
1	A	1100	MET
1	A	1130	MET
1	B	871	LEU

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Mol	Chain	Res	Type
1	B	885	GLN
1	B	888	THR
1	B	892	LEU
1	B	896	GLU
1	B	902	LEU
1	B	909	ASN
1	B	924	ASN
1	B	925	LEU
1	B	937	LEU
1	B	952	LYS
1	B	979	THR
1	B	1004	ASP
1	B	1009	LYS
1	B	1010	VAL
1	B	1012	GLU
1	B	1015	GLU
1	B	1042	VAL
1	B	1074	ILE
1	B	1100	MET
1	B	1130	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	853	GLN
1	A	885	GLN
1	A	891	HIS
1	A	988	ASN
1	A	1077	HIS
1	A	1112	GLN
1	B	853	GLN
1	B	885	GLN
1	B	891	HIS
1	B	924	ASN
1	B	1077	HIS
1	B	1108	ASN
1	B	1112	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	PTR	A	1007	1	15,16,17	2.03	1 (6%)	17,22,24	0.70	1 (5%)
1	PTR	A	1008	1	15,16,17	1.93	1 (6%)	17,22,24	0.73	0
1	PTR	B	1008	1	15,16,17	2.01	1 (6%)	17,22,24	0.75	0
1	PTR	B	1007	1	15,16,17	2.07	1 (6%)	17,22,24	0.55	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
1	PTR	A	1007	1	-	0/10/11/13	0/1/1/1
1	PTR	A	1008	1	-	1/10/11/13	0/1/1/1
1	PTR	B	1008	1	-	0/10/11/13	0/1/1/1
1	PTR	B	1007	1	-	0/10/11/13	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1007	PTR	OH-CZ	-7.50	1.23	1.40
1	A	1007	PTR	OH-CZ	-7.30	1.24	1.40
1	B	1008	PTR	OH-CZ	-7.26	1.24	1.40
1	A	1008	PTR	OH-CZ	-7.20	1.24	1.40

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1007	PTR	O3P-P-OH	2.10	111.52	105.32

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1008	PTR	CZ-OH-P-O1P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	1008	PTR	1	0

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	7GZ	B	4001	-	31,31,31	0.26	0	44,45,45	1.01	2 (4%)
2	7GZ	A	4000	-	31,31,31	0.26	0	44,45,45	1.01	2 (4%)

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	7GZ	B	4001	-	-	1/9/18/18	0/5/5/5
2	7GZ	A	4000	-	-	1/9/18/18	0/5/5/5

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	4000	7GZ	C12-C17-N16	-5.01	107.22	111.17
2	B	4001	7GZ	C12-C17-N16	-4.99	107.23	111.17
2	A	4000	7GZ	C17-N16-N15	3.33	108.50	106.07
2	B	4001	7GZ	C17-N16-N15	3.29	108.47	106.07

There are no chirality outliers.

All (2) torsion outliers are listed below:

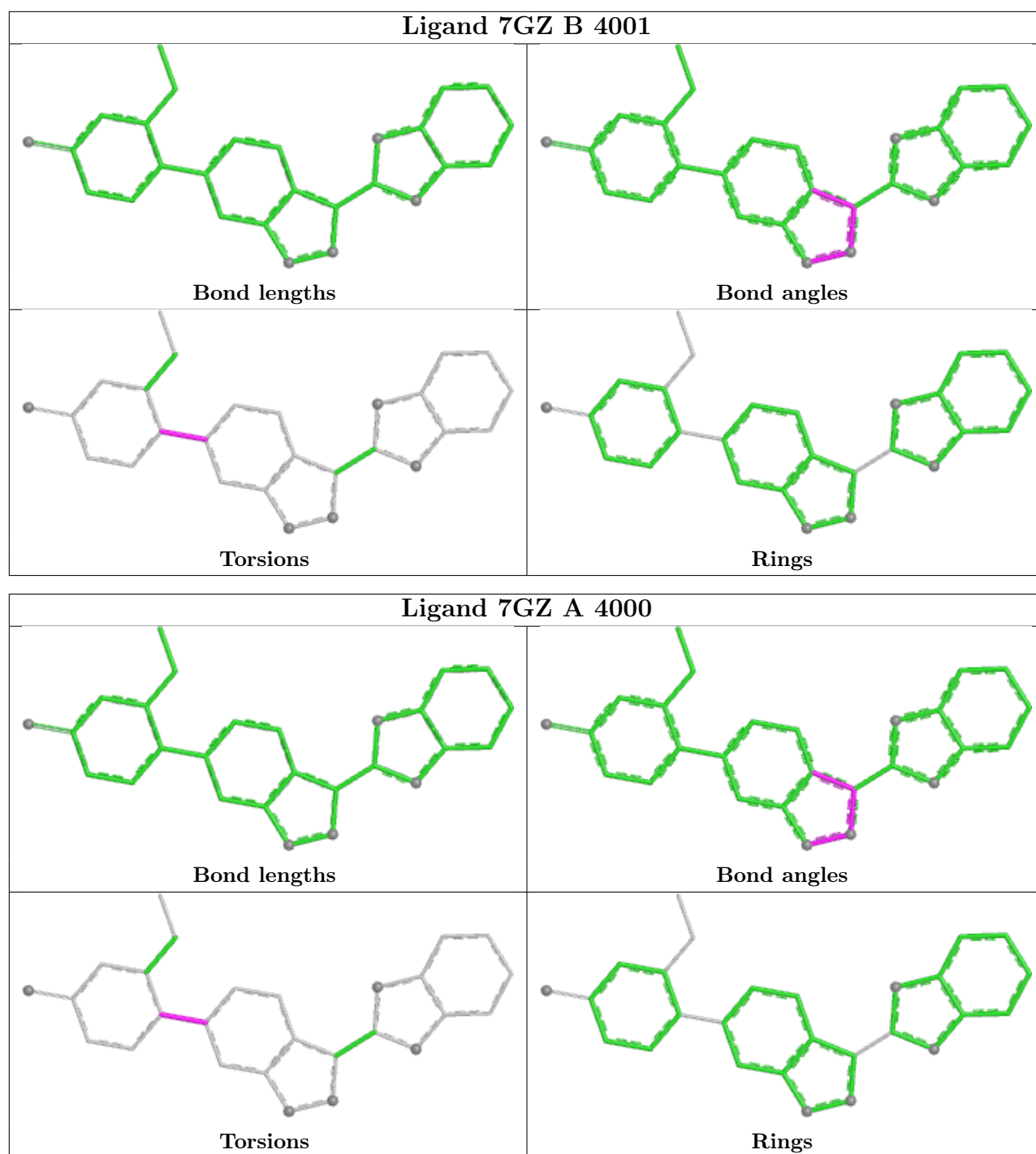
Mol	Chain	Res	Type	Atoms
2	B	4001	7GZ	C3-C8-C9-C14
2	A	4000	7GZ	C3-C8-C9-C14

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	4001	7GZ	1	0
2	A	4000	7GZ	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 [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	282/304 (92%)	-1.35	0 100 100	16, 34, 63, 91	1 (0%)
1	B	285/304 (93%)	-1.43	0 100 100	22, 34, 64, 90	0
All	All	567/608 (93%)	-1.39	0 100 100	16, 34, 64, 91	1 (0%)

There are no RSRZ outliers to report.

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	PTR	A	1007	16/17	0.99	0.04	43,55,62,65	0
1	PTR	A	1008	16/17	0.99	0.04	39,49,59,68	0
1	PTR	B	1007	16/17	0.99	0.04	42,55,64,68	0
1	PTR	B	1008	16/17	0.99	0.04	39,49,57,64	0

6.3 Carbohydrates [i](#)

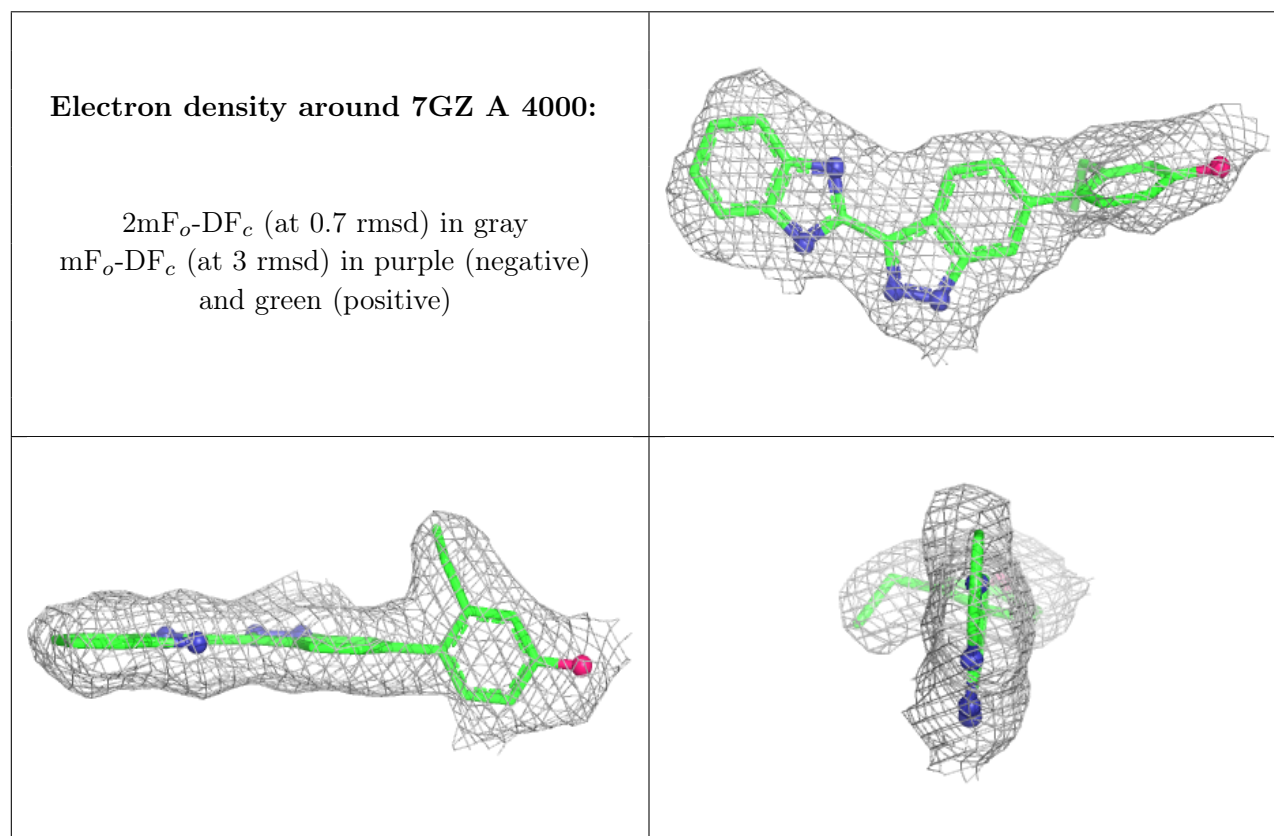
There are no oligosaccharides in this entry.

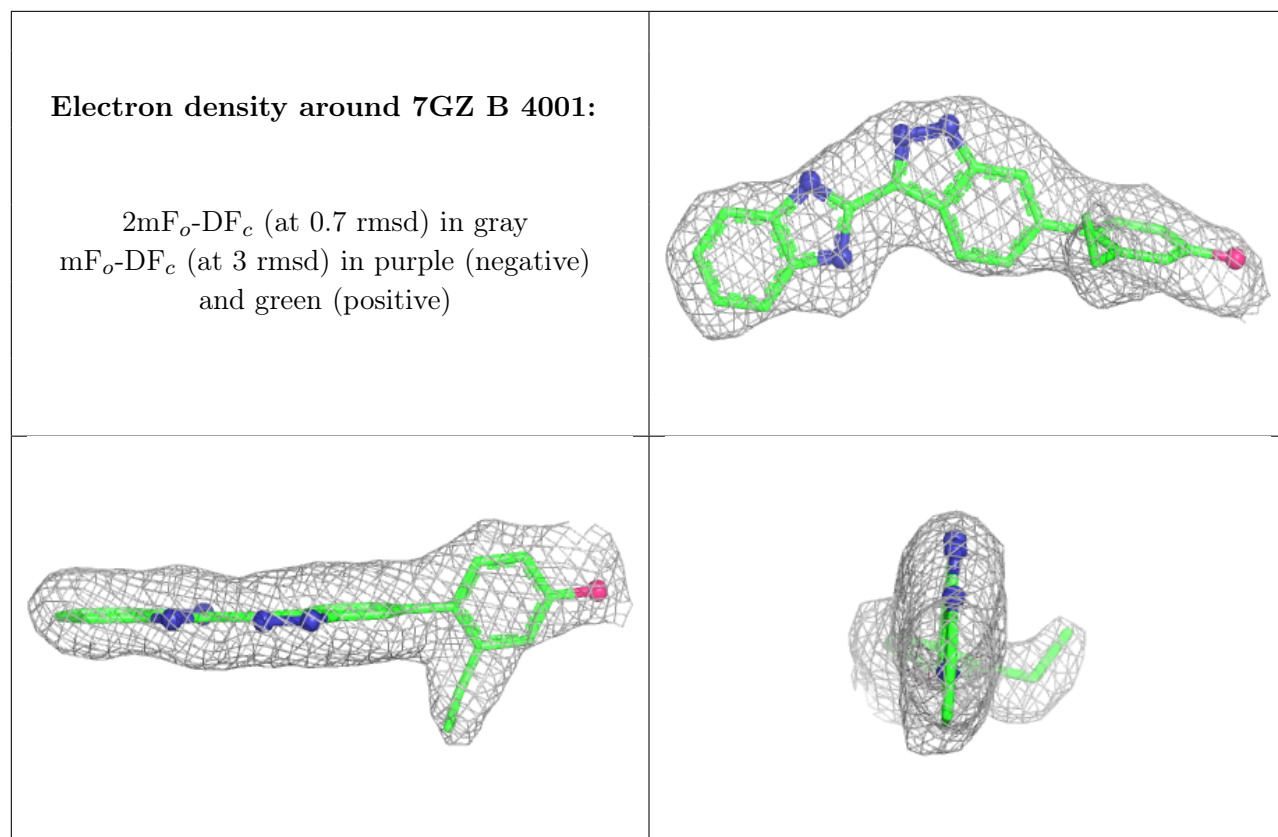
6.4 Ligands [i](#)

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
2	7GZ	A	4000	27/27	0.99	0.02	20,23,28,29	0
2	7GZ	B	4001	27/27	0.99	0.03	21,24,29,32	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.