



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 11:38 PM UTC

PDB ID : 8SBC / pdb_00008sbc
Title : Co-structure of Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform and brain penetrant inhibitors
Authors : Knapp, M.S.; Elling, R.A.; Tang, J.
Deposited on : 2023-04-03
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

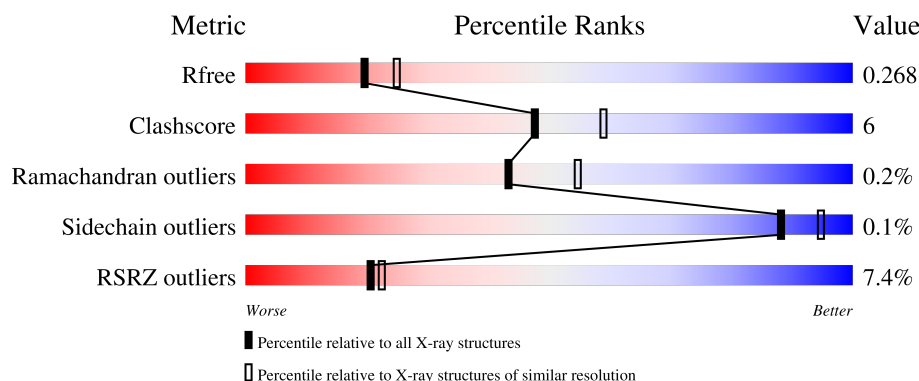
1 Overall quality at a glance

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	1074	7% 78% 12% 10%
2	B	293	7% 77% 13% 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9775 atoms, of which 26 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 Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	970	Total	C	N	O	S	0	3	0
			7580	4853	1285	1377	65			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	LYS	MET	engineered mutation	UNP P42336
A	233	LYS	LEU	engineered mutation	UNP P42336
A	780	LYS	TRP	engineered mutation	UNP P42336
A	800	MET	ILE	engineered mutation	UNP P42336
A	850	TRP	VAL	engineered mutation	UNP P42336
A	930	VAL	PHE	conflict	UNP P42336
A	1069	HIS	-	expression tag	UNP P42336
A	1070	HIS	-	expression tag	UNP P42336
A	1071	HIS	-	expression tag	UNP P42336
A	1072	HIS	-	expression tag	UNP P42336
A	1073	HIS	-	expression tag	UNP P42336
A	1074	HIS	-	expression tag	UNP P42336

- Molecule 2 is a protein called Phosphatidylinositol 3-kinase regulatory subunit alpha.

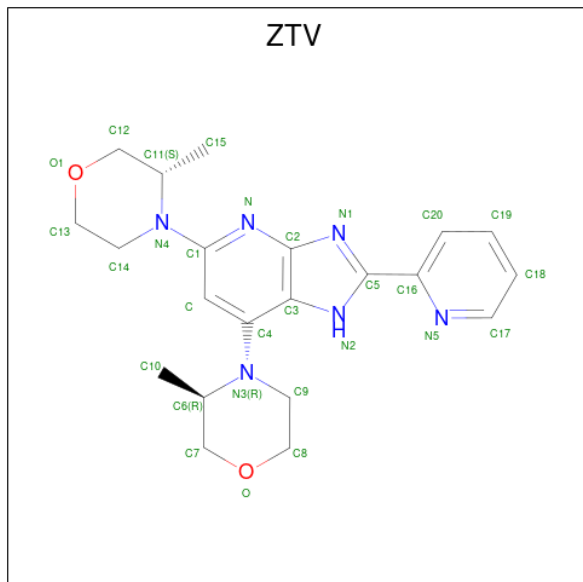
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	264	Total	C	N	O	S	0	0	0
			2101	1320	369	407	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	306	TYR	THR	engineered mutation	UNP P27986

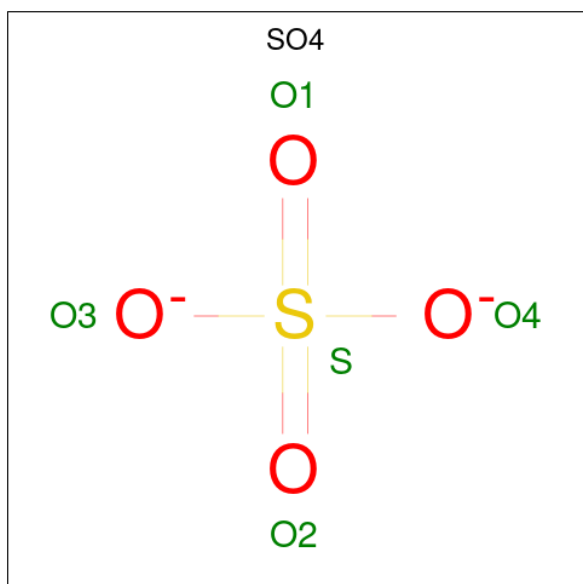
- Molecule 3 is (2M)-7-[(3R)-3-methylmorpholin-4-yl]-5-[(3S)-3-methylmorpholin-4-yl]-2-(py

ridin-2-yl)-1H-imidazo[4,5-b]pyridine (CCD ID: ZTV) (formula: $C_{21}H_{26}N_6O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			55	21	26	6	2		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

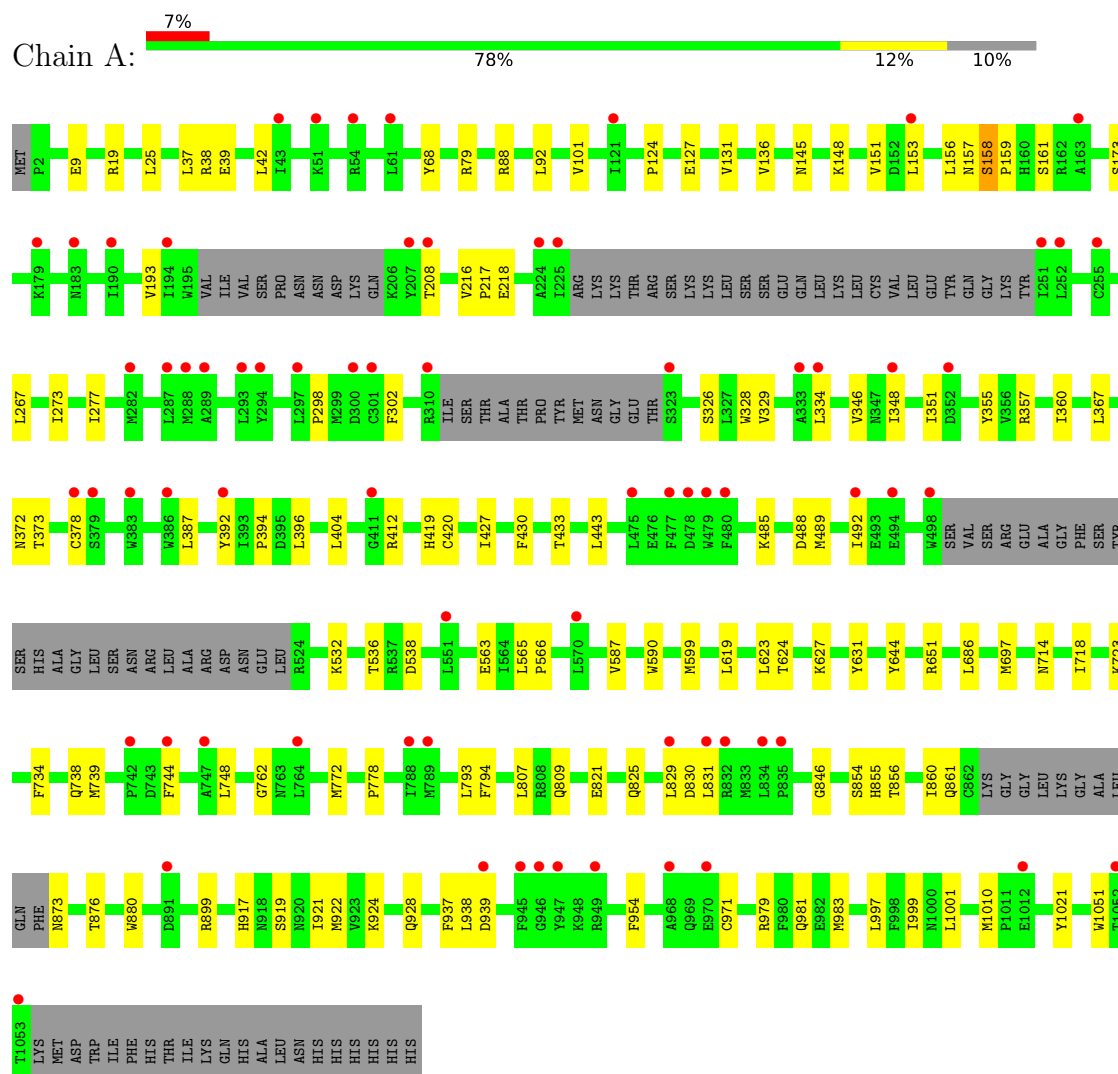
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	27	Total 27	O 27	0	0
5	B	7	Total 7	O 7	0	0

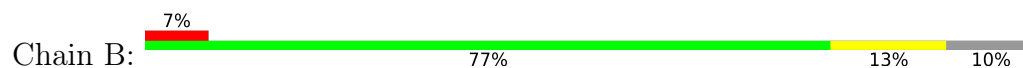
3 Residue-property plots [i](#)

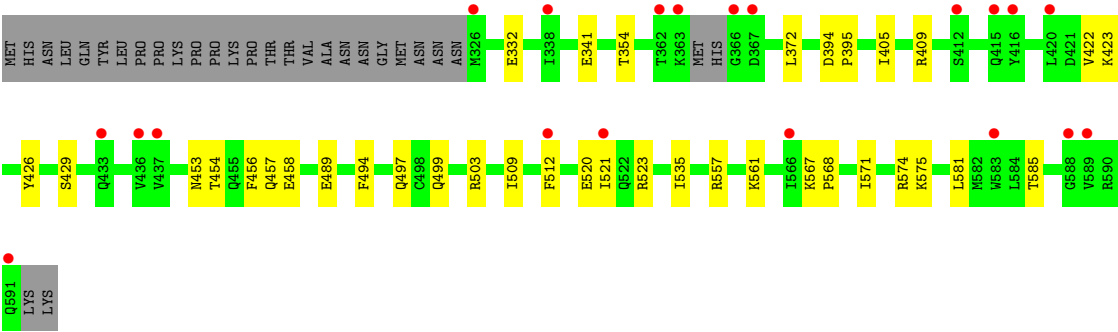
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform



- Molecule 2: Phosphatidylinositol 3-kinase regulatory subunit alpha





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	100.08Å 107.85Å 133.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	83.95 – 2.30 83.95 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.4 (83.95-2.30) 99.4 (83.95-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.241 , 0.271 0.239 , 0.268	Depositor DCC
R_{free} test set	3190 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	60.8	Xtriage
Anisotropy	0.536	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 53.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9775	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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: SO4, ZTV

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	0.07	0/7757	0.21	0/10546
2	B	0.06	0/2137	0.18	0/2885
All	All	0.07	0/9894	0.20	0/13431

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	7580	0	7206	83	0
2	B	2101	0	1940	25	0
3	A	29	26	0	0	0
4	A	5	0	0	0	0
5	A	27	0	0	0	0
5	B	7	0	0	0	0
All	All	9749	26	9146	105	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 (105) 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:809:GLN:HG2	1:A:1010:MET:HE3	1.66	0.77
1:A:158:SER:CB	1:A:159:PRO:HD3	2.22	0.69
1:A:619:LEU:HD22	1:A:623:LEU:HD22	1.76	0.68
1:A:158:SER:CB	1:A:159:PRO:CD	2.73	0.67
1:A:346:VAL:HG21	1:A:351:ILE:HG13	1.75	0.66
1:A:357[B]:ARG:HG2	1:A:372:ASN:OD1	2.00	0.62
1:A:216:VAL:HG12	1:A:218:GLU:H	1.64	0.62
2:B:512:PHE:HB2	2:B:521:ILE:HD11	1.82	0.62
2:B:372:LEU:HD21	2:B:422:VAL:CG1	2.30	0.61
1:A:298:PRO:HB2	1:A:697:MET:HE3	1.82	0.60
1:A:216:VAL:HG13	1:A:217:PRO:HD2	1.84	0.60
1:A:124:PRO:HG2	1:A:127:GLU:HG3	1.84	0.58
1:A:193:VAL:HG22	1:A:208:THR:HG22	1.85	0.58
1:A:145:ASN:HA	1:A:148:LYS:HZ2	1.68	0.57
1:A:744:PHE:CE1	1:A:748:LEU:HD22	2.39	0.57
2:B:557:ARG:O	2:B:561:LYS:HG3	2.05	0.57
1:A:326:SER:HB3	1:A:329:VAL:HG23	1.86	0.56
1:A:937:PHE:HD1	1:A:938:LEU:HG	1.70	0.56
1:A:856:THR:HG22	1:A:922:MET:HG2	1.88	0.56
2:B:332:GLU:HB2	2:B:429:SER:HB2	1.88	0.56
1:A:19:ARG:HG2	1:A:37:LEU:HD23	1.88	0.56
1:A:328:TRP:HA	1:A:394:PRO:HB3	1.90	0.54
1:A:355:TYR:OH	1:A:419:HIS:ND1	2.30	0.54
1:A:79:ARG:HD2	2:B:489:GLU:OE2	2.07	0.53
1:A:355:TYR:HE2	1:A:357[B]:ARG:HG3	1.74	0.53
1:A:355:TYR:CE2	1:A:357[B]:ARG:HG3	2.44	0.52
2:B:509:ILE:HG23	2:B:521:ILE:HD12	1.92	0.52
1:A:351:ILE:C	1:A:412:ARG:HH22	2.18	0.51
1:A:136:VAL:HG13	1:A:686:LEU:HD11	1.93	0.51
1:A:9:GLU:OE2	1:A:38:ARG:NH2	2.36	0.51
2:B:456:PHE:CE1	2:B:574:ARG:HB2	2.45	0.51
1:A:793:LEU:HG	1:A:794:PHE:HD1	1.75	0.51
2:B:354:THR:HA	2:B:426:TYR:O	2.11	0.51
1:A:772:MET:HB2	1:A:778:PRO:HG2	1.92	0.50
1:A:599:MET:HE1	1:A:631:TYR:CD2	2.47	0.50
2:B:422:VAL:HG22	2:B:423:LYS:N	2.27	0.50
2:B:567:LYS:O	2:B:571:ILE:HG12	2.12	0.50
1:A:39:GLU:HB2	1:A:88:ARG:HH11	1.77	0.50
1:A:489:MET:HA	1:A:492:ILE:HG12	1.94	0.50
2:B:581:LEU:O	2:B:585:THR:HG23	2.13	0.49
2:B:499:GLN:O	2:B:503:ARG:HG3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:VAL:HG11	1:A:136:VAL:HG21	1.95	0.49
1:A:538:ASP:HB2	1:A:999:ILE:HD12	1.95	0.49
1:A:25:LEU:HD13	2:B:497:GLN:HG3	1.95	0.49
1:A:917:HIS:CE1	1:A:919:SER:HB2	2.48	0.48
1:A:153:LEU:HA	1:A:156:LEU:HD23	1.95	0.48
1:A:829:LEU:HB3	1:A:831:LEU:HD13	1.96	0.47
1:A:151:VAL:HG21	1:A:302:PHE:HB2	1.97	0.47
1:A:430:PHE:O	1:A:644:TYR:OH	2.26	0.47
1:A:939:ASP:HB3	1:A:1021:TYR:CD1	2.49	0.47
1:A:145:ASN:OD1	1:A:651:ARG:NH2	2.47	0.47
1:A:427:ILE:HD11	1:A:443:LEU:HD22	1.97	0.46
1:A:360:ILE:HG22	1:A:367:LEU:HD12	1.97	0.46
1:A:42:LEU:HD21	1:A:92:LEU:HD11	1.98	0.46
2:B:571:ILE:HG22	2:B:575:LYS:HE2	1.97	0.46
1:A:273:ILE:O	1:A:277:ILE:HG13	2.15	0.46
1:A:488:ASP:O	1:A:492:ILE:HG23	2.16	0.46
1:A:373:THR:HG22	1:A:387:LEU:HD11	1.97	0.46
1:A:937:PHE:CD1	1:A:938:LEU:HG	2.51	0.45
1:A:433:THR:O	1:A:485:LYS:NZ	2.49	0.45
2:B:454:THR:O	2:B:458:GLU:HG2	2.16	0.45
2:B:372:LEU:HD21	2:B:422:VAL:HG11	1.97	0.45
1:A:348:ILE:HG22	1:A:378:CYS:SG	2.57	0.45
1:A:420[B]:CYS:SG	2:B:568:PRO:HB3	2.57	0.45
1:A:563:GLU:H	1:A:563:GLU:CD	2.24	0.45
1:A:861:GLN:HA	1:A:876:THR:HG21	1.99	0.44
1:A:981:GLN:OE1	1:A:1051:TRP:HA	2.16	0.44
1:A:937:PHE:O	1:A:938:LEU:HB2	2.18	0.44
1:A:624:THR:HG23	1:A:627:LYS:H	1.83	0.44
1:A:855:HIS:HB2	1:A:860:ILE:HD11	1.99	0.43
2:B:394:ASP:HA	2:B:395:PRO:C	2.42	0.43
2:B:405:ILE:O	2:B:409:ARG:HG3	2.18	0.43
1:A:587:VAL:HA	1:A:590:TRP:HB2	2.01	0.43
1:A:860:ILE:HD12	1:A:880:TRP:CE2	2.54	0.43
1:A:937:PHE:HZ	1:A:1010:MET:HE1	1.83	0.43
1:A:734:PHE:O	1:A:738:GLN:HG2	2.18	0.43
1:A:921:ILE:HD13	1:A:954:PHE:HE1	1.84	0.42
1:A:357[B]:ARG:O	1:A:404:LEU:HA	2.19	0.42
1:A:157:ASN:CB	1:A:161:SER:HB3	2.50	0.42
1:A:830:ASP:O	1:A:899:ARG:HD3	2.20	0.42
1:A:357[A]:ARG:O	1:A:404:LEU:HA	2.20	0.42
1:A:854:SER:HB2	1:A:922:MET:HE3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:821:GLU:O	1:A:825:GLN:HG2	2.19	0.42
2:B:453:ASN:O	2:B:457:GLN:HG2	2.19	0.42
2:B:567:LYS:N	2:B:568:PRO:HD2	2.34	0.42
1:A:772:MET:HA	1:A:772:MET:HE2	2.02	0.41
2:B:422:VAL:HG22	2:B:423:LYS:H	1.85	0.41
1:A:714:ASN:O	1:A:718:ILE:HG13	2.19	0.41
1:A:979:ARG:O	1:A:983:MET:HG3	2.20	0.41
1:A:807:LEU:HD12	1:A:846:GLY:HA3	2.02	0.41
1:A:873:ASN:HB3	1:A:876:THR:OG1	2.21	0.41
1:A:924:LYS:HD3	1:A:928:GLN:HB3	2.02	0.41
1:A:532:LYS:O	1:A:536:THR:HG23	2.20	0.41
1:A:173:SER:OG	1:A:624:THR:HG21	2.20	0.41
1:A:334:LEU:HD22	1:A:396:LEU:HD11	2.02	0.41
1:A:997:LEU:O	1:A:1001:LEU:HG	2.21	0.41
2:B:341:GLU:OE1	2:B:341:GLU:N	2.49	0.41
2:B:494:PHE:HB3	2:B:535:ILE:HG12	2.01	0.41
2:B:520:GLU:OE2	2:B:523:ARG:NH1	2.54	0.41
1:A:392:TYR:CD2	1:A:394:PRO:HD2	2.55	0.40
1:A:565:LEU:HB3	1:A:566:PRO:HD3	2.03	0.40
1:A:267:LEU:HG	1:A:273:ILE:HG13	2.01	0.40
1:A:68:TYR:HB3	1:A:101:VAL:HG13	2.03	0.40
1:A:723:LYS:HE3	1:A:734:PHE:CD1	2.57	0.40
1:A:739:MET:HA	1:A:744:PHE:CD1	2.57	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	961/1074 (90%)	928 (97%)	31 (3%)	2 (0%)	43	55
2	B	260/293 (89%)	254 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1221/1367 (89%)	1182 (97%)	37 (3%)	2 (0%)	43	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	158	SER
1	A	762	GLY

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	792/980 (81%)	791 (100%)	1 (0%)	88	95
2	B	207/272 (76%)	207 (100%)	0	100	100
All	All	999/1252 (80%)	998 (100%)	1 (0%)	88	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	971	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	HIS
1	A	362	HIS
1	A	661	GLN
1	A	875	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

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	$\# Z > 2$
4	SO4	A	1102	-	4,4,4	0.23	0	6,6,6	0.07	0
3	ZTV	A	1101	-	32,33,33	0.75	1 (3%)	38,47,47	0.97	2 (5%)

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	ZTV	A	1101	-	-	7/12/34/34	0/5/5/5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1101	ZTV	C3-C4	-2.44	1.36	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1101	ZTV	C13-O1-C12	-2.48	106.56	110.02
3	A	1101	ZTV	C14-N4-C11	2.38	118.75	114.63

There are no chirality outliers.

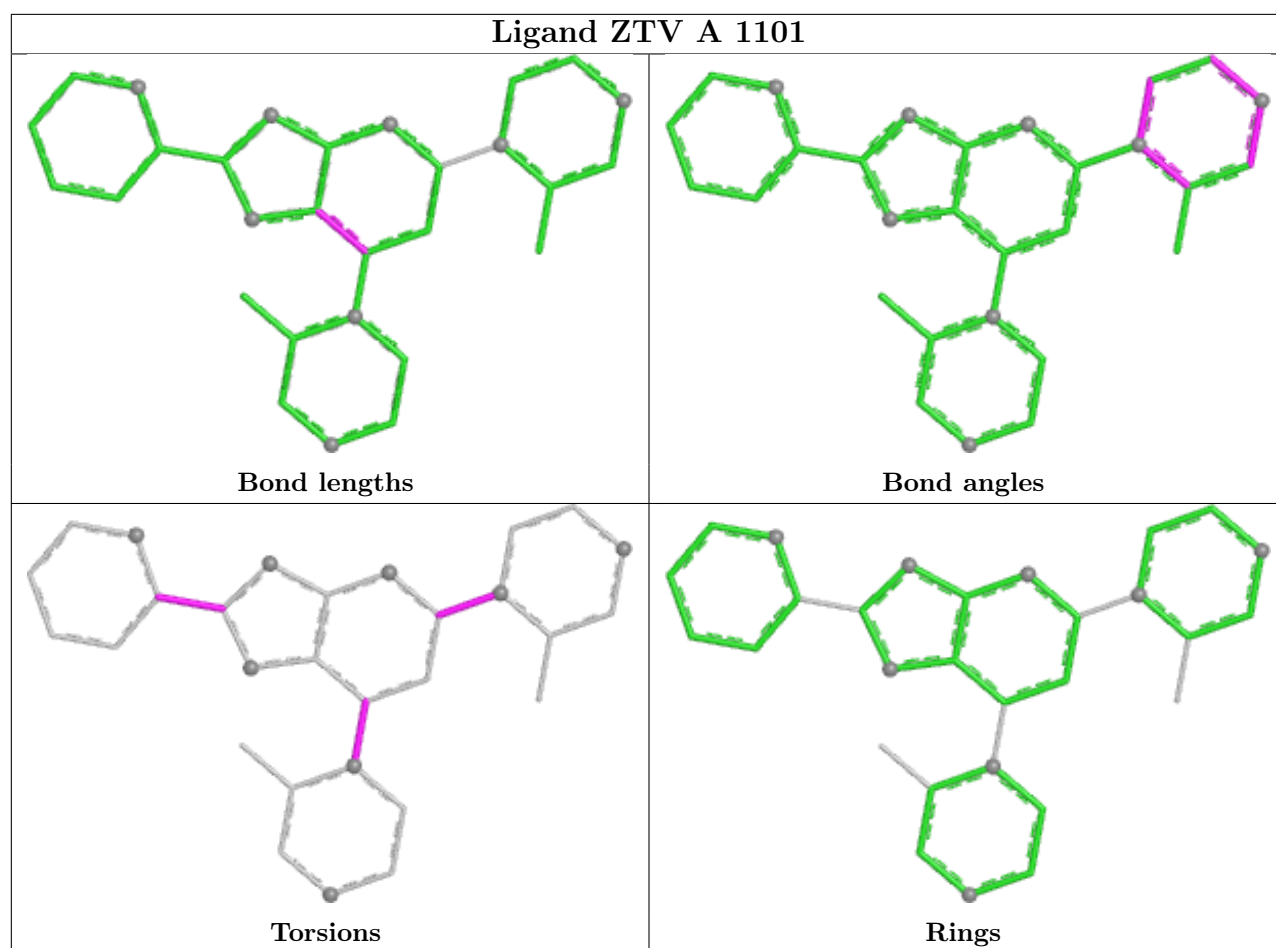
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1101	ZTV	C20-C16-C5-N1
3	A	1101	ZTV	N5-C16-C5-N1
3	A	1101	ZTV	N5-C16-C5-N2
3	A	1101	ZTV	C20-C16-C5-N2
3	A	1101	ZTV	C-C4-N3-C9
3	A	1101	ZTV	N-C1-N4-C14
3	A	1101	ZTV	C-C1-N4-C11

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 [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	970/1074 (90%)	0.68	71 (7%) 21 23	39, 86, 140, 178	3 (0%)
2	B	264/293 (90%)	0.69	20 (7%) 20 21	51, 86, 138, 164	0
All	All	1234/1367 (90%)	0.68	91 (7%) 20 22	39, 86, 140, 178	3 (0%)

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1053	THR	4.5
1	A	225	ILE	4.4
1	A	832	ARG	4.2
1	A	411	GLY	4.1
1	A	498	TRP	3.9
1	A	747	ALA	3.9
1	A	310	ARG	3.6
1	A	834	LEU	3.5
2	B	591	GLN	3.5
1	A	945	PHE	3.4
1	A	835	PRO	3.3
1	A	970	GLU	3.2
1	A	300	ASP	3.1
1	A	551	LEU	3.0
2	B	436	VAL	3.0
1	A	494	GLU	3.0
1	A	891	ASP	3.0
2	B	433	GLN	2.9
2	B	566	ILE	2.9
1	A	252	LEU	2.9
1	A	477	PHE	2.9
1	A	492	ILE	2.8
1	A	207	TYR	2.8
1	A	323	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	742	PRO	2.7
1	A	378	CYS	2.7
2	B	416	TYR	2.6
2	B	362	THR	2.6
2	B	437	VAL	2.6
1	A	333	ALA	2.6
1	A	968	ALA	2.6
2	B	521	ILE	2.6
2	B	363	LYS	2.6
1	A	831	LEU	2.5
1	A	383	TRP	2.5
1	A	480	PHE	2.5
2	B	589	VAL	2.4
2	B	326	MET	2.4
1	A	301	CYS	2.4
1	A	764	LEU	2.4
1	A	251	ILE	2.4
2	B	512	PHE	2.4
1	A	293	LEU	2.4
1	A	334	LEU	2.4
1	A	386	TRP	2.4
2	B	415	GLN	2.4
1	A	190	ILE	2.4
2	B	420	LEU	2.4
1	A	153	LEU	2.3
1	A	1052	THR	2.3
1	A	1012	GLU	2.3
2	B	583	TRP	2.3
1	A	194	ILE	2.3
1	A	744	PHE	2.3
1	A	829	LEU	2.3
1	A	183	ASN	2.3
2	B	366	GLY	2.3
1	A	949	ARG	2.3
1	A	392	TYR	2.2
2	B	412	SER	2.2
1	A	348	ILE	2.2
1	A	352	ASP	2.2
2	B	367	ASP	2.2
1	A	789	MET	2.2
1	A	163	ALA	2.2
1	A	289	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	61	LEU	2.2
1	A	478	ASP	2.2
1	A	179	LYS	2.2
1	A	282	MET	2.2
1	A	379	SER	2.2
1	A	287	LEU	2.1
1	A	255	CYS	2.1
1	A	54	ARG	2.1
1	A	43	ILE	2.1
1	A	121	ILE	2.1
1	A	297	LEU	2.1
2	B	338	ILE	2.1
1	A	224	ALA	2.1
1	A	51	LYS	2.1
1	A	475	LEU	2.1
1	A	570	LEU	2.1
1	A	939	ASP	2.1
1	A	294	TYR	2.1
1	A	947	TYR	2.1
1	A	946	GLY	2.1
1	A	208	THR	2.0
2	B	588	GLY	2.0
1	A	479	TRP	2.0
1	A	288	MET	2.0
1	A	788	ILE	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

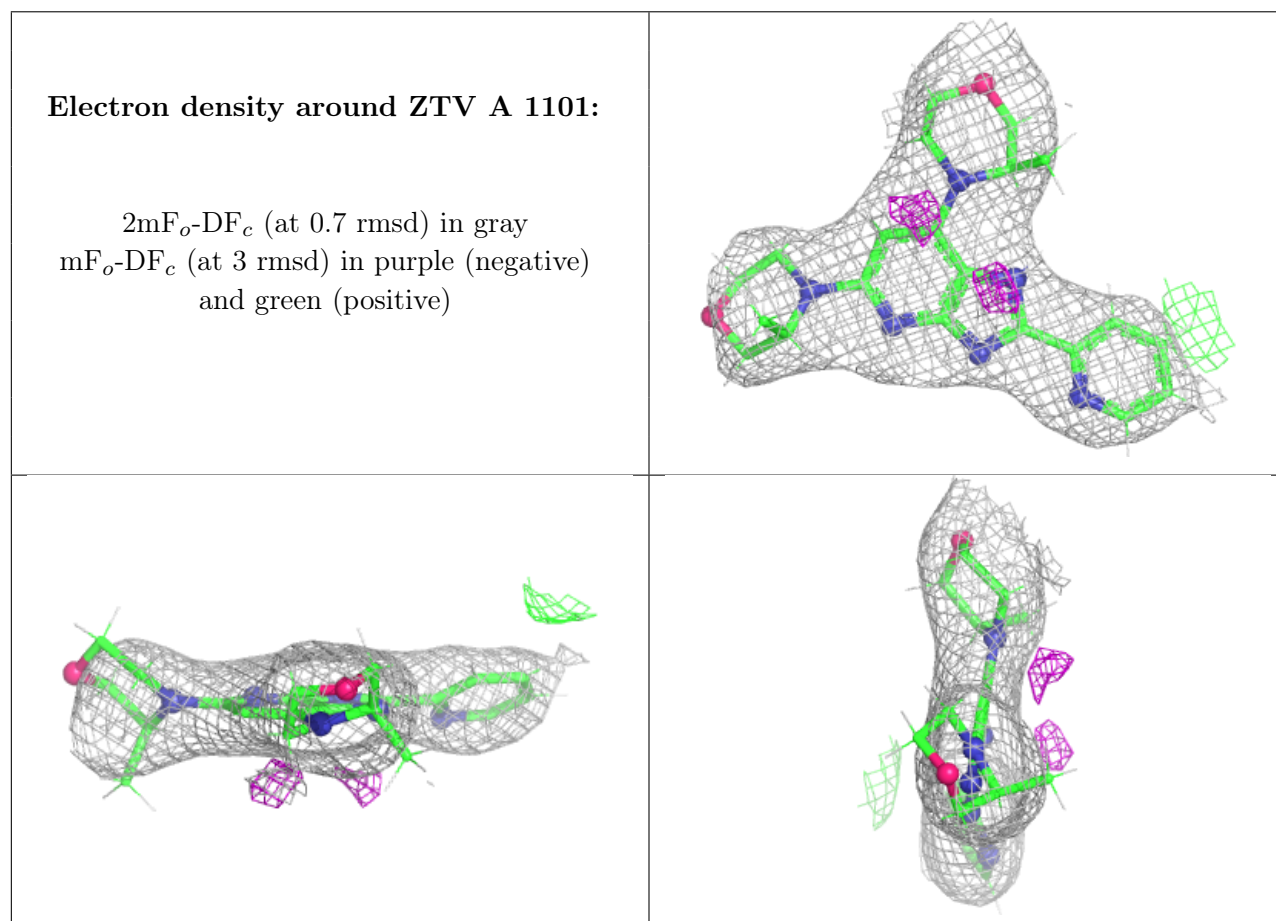
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
4	SO4	A	1102	5/5	0.76	0.14	80,94,100,166	0
3	ZTV	A	1101	29/29	0.88	0.11	83,102,124,140	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 ⓘ

There are no such residues in this entry.