



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:13 AM UTC

PDB ID : 4XZ4 / pdb_00004xz4
Title : Structure of PI3K gamma in complex with an inhibitor
Authors : Collier, P.N.; Messersmith, D.; Le Tiran, A.; Bandarage, U.K.; Boucher, C.; Come, J.; Cottrell, K.M.; Damagnez, V.; Doran, J.D.; Griffith, J.P.; Khare-Pandit, S.; Krueger, E.B.; Ledebner, M.W.; Ledford, B.; Liao, Y.; Mahajan, S.; Moody, C.S.; Wang, T.; Xu, J.; Aronov, A.M.
Deposited on : 2015-02-03
Resolution : 2.60 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](#) ①) 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

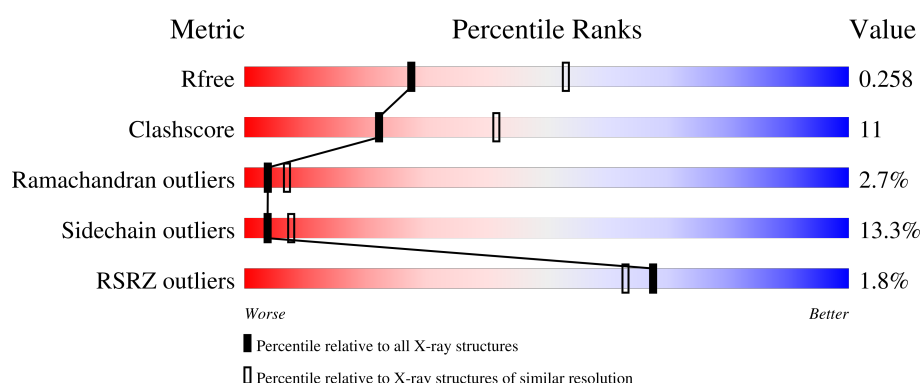
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	966	2% 57% 25% 5% • 13%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6871 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.

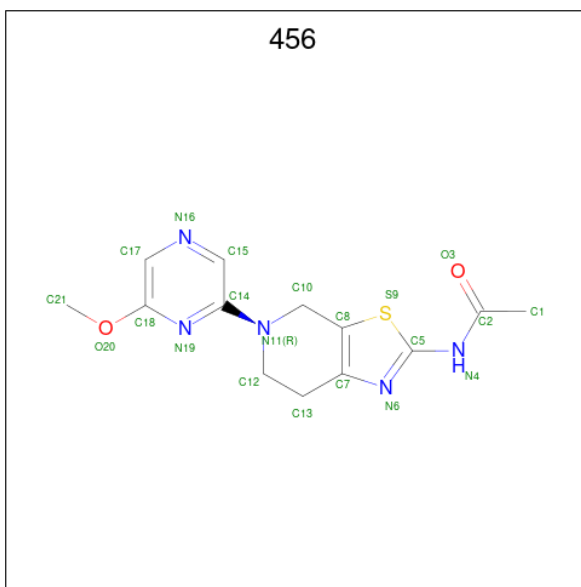
- Molecule 1 is a protein called Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	843	Total	C	N	O	S	0	0	0
			6844	4395	1170	1244	35			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	MET	-	initiating methionine	UNP P48736
A	459	ARG	GLN	conflict	UNP P48736
A	1103	HIS	-	expression tag	UNP P48736
A	1104	HIS	-	expression tag	UNP P48736
A	1105	HIS	-	expression tag	UNP P48736
A	1106	HIS	-	expression tag	UNP P48736
A	1107	HIS	-	expression tag	UNP P48736
A	1108	HIS	-	expression tag	UNP P48736

- Molecule 2 is N-[5-(6-methoxypyrazin-2-yl)-4,5,6,7-tetrahydro[1,3]thiazolo[5,4-c]pyridin-2-yl]acetamide (CCD ID: 456) (formula: C₁₃H₁₅N₅O₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			21	13	5	2	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		

HIS
HIS

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.70Å 67.18Å 106.34Å 90.00° 95.89° 90.00°	Depositor
Resolution (Å)	44.77 – 2.60 44.77 – 2.60	Depositor EDS
% Data completeness (in resolution range)	73.1 (44.77-2.60) 73.1 (44.77-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.199 , 0.262 0.200 , 0.258	Depositor DCC
R_{free} test set	1170 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	79.6	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 77.7	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	6871	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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: 456

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	0.81	0/6992	1.02	11/9457 (0.1%)

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	1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1085	ASN	N-CA-C	7.81	120.89	111.82
1	A	547	MET	N-CA-C	5.63	116.99	109.83
1	A	1012	ILE	CB-CA-C	-5.51	104.91	111.97
1	A	919	GLU	N-CA-C	-5.41	105.07	110.97
1	A	572	LYS	N-CA-C	5.32	117.08	111.28
1	A	1074	VAL	N-CA-C	-5.27	106.66	111.67
1	A	808	LYS	N-CA-C	-5.26	103.67	110.19
1	A	388	GLN	N-CA-C	5.14	117.96	109.85
1	A	381	VAL	N-CA-C	5.11	115.64	108.17
1	A	726	THR	N-CA-C	5.10	121.67	110.80
1	A	844	ILE	CB-CA-C	-5.07	105.48	111.97

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	201	TRP	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	6844	0	6886	146	0
2	A	21	0	15	1	0
3	A	6	0	0	0	0
All	All	6871	0	6901	146	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 11.

All (146) 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:893:GLN:HA	1:A:897:GLY:CA	1.88	1.03
1:A:893:GLN:HA	1:A:897:GLY:HA2	1.61	0.81
1:A:847:ILE:HG22	1:A:851:MET:HE2	1.64	0.79
1:A:804:MET:HE2	1:A:812:TRP:HB2	1.65	0.76
1:A:181:VAL:O	1:A:185:MET:HG3	1.87	0.74
1:A:947:ARG:NH2	1:A:963:ILE:O	2.20	0.74
1:A:834:HIS:HB2	1:A:876:ILE:HD12	1.70	0.71
1:A:475:LEU:HD21	1:A:522:ASN:HB2	1.74	0.70
1:A:995:MET:O	1:A:1003:SER:OG	2.10	0.70
1:A:893:GLN:HA	1:A:897:GLY:HA3	1.75	0.69
1:A:209:GLU:HB2	1:A:859:SER:HB3	1.76	0.67
1:A:625:GLY:O	1:A:629:GLN:HG3	1.94	0.67
1:A:925:VAL:O	1:A:929:VAL:HG23	1.95	0.66
1:A:1042:LEU:HD22	1:A:1042:LEU:O	1.96	0.66
1:A:640:VAL:O	1:A:643:ILE:HG12	1.96	0.65
1:A:395:CYS:CB	1:A:418:ILE:HD11	2.27	0.65
1:A:1011:ASP:OD1	1:A:1015:LYS:NZ	2.21	0.63
1:A:554:GLN:O	1:A:558:ILE:HD12	2.00	0.61
1:A:421:LYS:HE3	1:A:527:ILE:HD12	1.83	0.60
1:A:555:LEU:HD11	1:A:575:LEU:HD12	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:561:THR:CG2	1:A:565:ASN:HB3	2.31	0.60
1:A:923:ALA:O	1:A:926:GLU:HB3	2.02	0.60
1:A:395:CYS:HB2	1:A:418:ILE:HD11	1.85	0.59
1:A:1089:HIS:C	1:A:1091:VAL:N	2.61	0.58
1:A:561:THR:HG22	1:A:565:ASN:HB3	1.85	0.58
1:A:248:PHE:C	1:A:250:THR:N	2.62	0.57
1:A:632:ASP:C	1:A:632:ASP:OD1	2.47	0.57
1:A:378:ASP:N	1:A:378:ASP:OD1	2.38	0.57
1:A:988:THR:OG1	1:A:990:ASP:OD1	2.18	0.56
1:A:272:LEU:HB3	1:A:305:VAL:HG11	1.88	0.55
1:A:804:MET:HE1	1:A:831:ILE:HG12	1.89	0.55
1:A:359:ARG:HG3	1:A:360:LYS:O	2.08	0.54
1:A:1086:TRP:HE3	1:A:1087:PHE:HA	1.73	0.54
1:A:390:GLY:C	1:A:392:GLN:H	2.15	0.54
1:A:395:CYS:HB3	1:A:418:ILE:HD11	1.90	0.54
1:A:233:ILE:HD12	1:A:233:ILE:N	2.23	0.53
1:A:726:THR:HA	1:A:729:LEU:HB2	1.91	0.53
1:A:1060:ASN:OD1	1:A:1062:GLU:HB2	2.09	0.52
1:A:811:LEU:O	1:A:831:ILE:HA	2.09	0.52
1:A:893:GLN:HA	1:A:897:GLY:N	2.25	0.52
1:A:952:ILE:HD11	1:A:986:VAL:HG21	1.92	0.52
1:A:652:GLU:HG3	1:A:654:ASP:HB3	1.92	0.52
1:A:204:SER:OG	1:A:652:GLU:OE2	2.14	0.51
1:A:1085:ASN:O	1:A:1086:TRP:C	2.54	0.51
1:A:461:LEU:HB3	1:A:462:TYR:CD1	2.46	0.51
1:A:364:LYS:HA	1:A:412:VAL:O	2.10	0.51
1:A:1035:LEU:HA	1:A:1039:MET:HG2	1.92	0.51
1:A:734:GLN:NE2	1:A:780:PRO:HB3	2.26	0.51
1:A:579:ARG:HB2	1:A:610:LEU:HD11	1.92	0.50
1:A:760:SER:OG	1:A:763:VAL:HG23	2.11	0.50
1:A:768:LYS:HE2	1:A:801:CYS:O	2.11	0.50
1:A:981:GLU:N	1:A:982:ARG:NH2	2.59	0.50
1:A:755:GLU:O	1:A:756:LYS:C	2.55	0.50
1:A:568:THR:HG22	1:A:570:GLU:H	1.77	0.50
1:A:467:LEU:HD13	1:A:672:TYR:CE1	2.47	0.49
1:A:580:TYR:CE1	1:A:610:LEU:HD23	2.48	0.49
1:A:726:THR:N	1:A:729:LEU:HD12	2.26	0.49
1:A:706:SER:O	1:A:710:GLN:HB3	2.12	0.49
1:A:802:LYS:HG3	1:A:812:TRP:HB3	1.93	0.49
1:A:949:ASN:H	1:A:1083:GLN:HE22	1.61	0.49
1:A:250:THR:HG22	1:A:250:THR:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:898:ASN:C	1:A:900:GLY:H	2.20	0.49
1:A:248:PHE:C	1:A:250:THR:H	2.20	0.48
1:A:434:TYR:HA	1:A:459:ARG:O	2.12	0.48
1:A:955:THR:OG1	1:A:957:THR:HG22	2.13	0.48
1:A:174:GLU:O	1:A:178:ARG:HG2	2.13	0.48
1:A:743:GLN:NE2	1:A:872:THR:OG1	2.46	0.48
1:A:1056:THR:O	1:A:1056:THR:HG23	2.14	0.48
1:A:848:LEU:HA	1:A:851:MET:HE3	1.94	0.47
1:A:1086:TRP:CE3	1:A:1087:PHE:HA	2.49	0.47
1:A:589:TYR:O	1:A:593:PHE:CD2	2.68	0.47
1:A:894:SER:OG	1:A:895:THR:N	2.43	0.47
1:A:878:MET:C	1:A:879:ILE:HG13	2.40	0.47
1:A:1035:LEU:HB3	1:A:1042:LEU:HG	1.95	0.47
1:A:872:THR:OG1	1:A:877:GLY:HA2	2.14	0.47
1:A:935:TYR:O	1:A:939:THR:HB	2.15	0.47
1:A:629:GLN:HG2	1:A:1029:ILE:HG13	1.97	0.47
1:A:802:LYS:CG	1:A:812:TRP:HB3	2.45	0.47
1:A:743:GLN:O	1:A:747:LEU:HD12	2.15	0.47
1:A:887:THR:CG2	1:A:950:ASP:HA	2.46	0.46
1:A:1089:HIS:O	1:A:1090:LEU:C	2.58	0.46
1:A:764:ILE:O	1:A:765:SER:C	2.59	0.46
1:A:411:ASN:O	1:A:411:ASN:CG	2.56	0.46
1:A:1086:TRP:CE3	1:A:1087:PHE:CD2	3.04	0.45
1:A:741:MET:SD	1:A:779:LEU:HD12	2.57	0.45
1:A:879:ILE:HG21	2:A:1201:456:H6	1.98	0.45
1:A:741:MET:HE1	1:A:779:LEU:N	2.31	0.45
1:A:271:VAL:HG23	1:A:282:VAL:CG1	2.46	0.45
1:A:568:THR:HG22	1:A:570:GLU:N	2.31	0.45
1:A:1026:LEU:HD22	1:A:1030:LEU:HG	1.99	0.45
1:A:1089:HIS:O	1:A:1091:VAL:N	2.49	0.45
1:A:273:ARG:O	1:A:305:VAL:HG13	2.17	0.45
1:A:363:VAL:HG13	1:A:363:VAL:O	2.15	0.45
1:A:272:LEU:HD22	1:A:305:VAL:HG11	1.99	0.44
1:A:375:ARG:NH1	1:A:377:THR:OG1	2.44	0.44
1:A:576:TRP:O	1:A:577:HIS:C	2.58	0.44
1:A:806:SER:O	1:A:808:LYS:O	2.36	0.44
1:A:575:LEU:HD23	1:A:595:SER:OG	2.17	0.44
1:A:741:MET:HE1	1:A:779:LEU:HA	2.00	0.44
1:A:767:LEU:O	1:A:771:LEU:HG	2.18	0.44
1:A:568:THR:O	1:A:571:ASP:HB2	2.18	0.44
1:A:766:GLN:HE21	1:A:766:GLN:HB2	1.68	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1034:MET:HG2	1:A:1039:MET:HE3	2.00	0.44
1:A:564:LEU:O	1:A:1052:ARG:NH2	2.50	0.44
1:A:565:ASN:C	1:A:565:ASN:ND2	2.76	0.44
1:A:954:ILE:HA	1:A:960:LEU:HA	2.00	0.43
1:A:144:SER:O	1:A:148:GLN:NE2	2.51	0.43
1:A:470:ASP:OD1	1:A:470:ASP:C	2.61	0.43
1:A:861:ASP:C	1:A:862:LEU:HD22	2.43	0.43
1:A:955:THR:HG1	1:A:959:ASN:H	1.63	0.43
1:A:526:PRO:O	1:A:527:ILE:HG22	2.18	0.43
1:A:217:ASN:ND2	1:A:219:CYS:SG	2.92	0.43
1:A:248:PHE:O	1:A:251:LYS:N	2.49	0.43
1:A:702:GLU:HA	1:A:702:GLU:OE1	2.18	0.43
1:A:756:LYS:O	1:A:758:ASP:N	2.52	0.43
1:A:720:TYR:OH	1:A:728:MET:HE3	2.18	0.43
1:A:1008:LYS:O	1:A:1012:ILE:HG13	2.19	0.42
1:A:660:LEU:O	1:A:664:VAL:HG23	2.19	0.42
1:A:1012:ILE:O	1:A:1013:CYS:C	2.62	0.42
1:A:381:VAL:HG21	1:A:404:PHE:CG	2.54	0.42
1:A:225:HIS:CE1	1:A:304:HIS:CD2	3.08	0.42
1:A:702:GLU:OE1	1:A:839:ARG:NH1	2.52	0.42
1:A:525:HIS:CB	1:A:526:PRO:HD3	2.50	0.42
1:A:561:THR:HB	1:A:591:LYS:HE3	2.02	0.42
1:A:463:TYR:CE2	1:A:501:LYS:HA	2.55	0.41
1:A:919:GLU:O	1:A:920:LYS:C	2.63	0.41
1:A:937:VAL:O	1:A:941:VAL:HG23	2.20	0.41
1:A:837:ASP:HB3	1:A:840:GLN:NE2	2.35	0.41
1:A:207:LEU:HD21	1:A:294:ARG:HG2	2.02	0.41
1:A:863:CYS:SG	1:A:927:ARG:NH1	2.94	0.41
1:A:579:ARG:HD2	1:A:610:LEU:HG	2.02	0.41
1:A:782:SER:O	1:A:783:PHE:HB3	2.21	0.41
1:A:812:TRP:C	1:A:813:LEU:HD23	2.45	0.41
1:A:677:LEU:O	1:A:678:ALA:C	2.61	0.41
1:A:860:LEU:HD22	1:A:862:LEU:HD21	2.02	0.41
1:A:1026:LEU:O	1:A:1030:LEU:HG	2.21	0.41
1:A:149:ALA:O	1:A:150:PHE:C	2.64	0.41
1:A:806:SER:HB2	1:A:810:PRO:HD3	2.03	0.41
1:A:997:THR:HG23	1:A:1001:LYS:HG3	2.03	0.40
1:A:655:ASP:O	1:A:656:VAL:C	2.62	0.40
1:A:764:ILE:O	1:A:768:LYS:HG2	2.21	0.40
1:A:312:ASP:HA	1:A:313:PRO:HD3	1.93	0.40
1:A:507:ASN:HA	1:A:508:PRO:HD2	1.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:682:LEU:HD22	1:A:686:LEU:HD11	2.02	0.40
1:A:391:GLN:OE1	1:A:633:CYS:HB2	2.21	0.40
1:A:500:ASP:HB3	1:A:708:HIS:CD2	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	827/966 (86%)	744 (90%)	61 (7%)	22 (3%)	4 7

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	527	ILE
1	A	561	THR
1	A	726	THR
1	A	776	ASN
1	A	1040	PRO
1	A	378	ASP
1	A	756	LYS
1	A	777	SER
1	A	899	THR
1	A	999	GLY
1	A	1000	LYS
1	A	1090	LEU
1	A	317	GLU
1	A	391	GLN
1	A	526	PRO
1	A	754	ALA
1	A	867	TYR
1	A	898	ASN

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Mol	Chain	Res	Type
1	A	1044	SER
1	A	374	PRO
1	A	1084	PHE
1	A	1079	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	757/864 (88%)	656 (87%)	101 (13%)	4 8

All (101) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	145	GLU
1	A	168	VAL
1	A	182	THR
1	A	204	SER
1	A	214	LYS
1	A	219	CYS
1	A	229	THR
1	A	232	THR
1	A	235	VAL
1	A	240	THR
1	A	247	SER
1	A	252	MET
1	A	268	GLN
1	A	269	ASP
1	A	271	VAL
1	A	277	ARG
1	A	281	LEU
1	A	285	THR
1	A	287	ILE
1	A	291	GLN
1	A	309	THR
1	A	320	LYS

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Mol	Chain	Res	Type
1	A	357	CYS
1	A	358	ASP
1	A	372	VAL
1	A	375	ARG
1	A	376	ASN
1	A	377	THR
1	A	378	ASP
1	A	379	LEU
1	A	381	VAL
1	A	391	GLN
1	A	406	GLU
1	A	418	ILE
1	A	487	ILE
1	A	502	LEU
1	A	520	LEU
1	A	525	HIS
1	A	550	GLN
1	A	558	ILE
1	A	565	ASN
1	A	574	LEU
1	A	575	LEU
1	A	583	LEU
1	A	601	GLN
1	A	610	LEU
1	A	613	ARG
1	A	616	VAL
1	A	626	LEU
1	A	646	GLN
1	A	662	GLN
1	A	682	LEU
1	A	688	ASN
1	A	701	SER
1	A	705	GLN
1	A	706	SER
1	A	717	LEU
1	A	739	ILE
1	A	749	ILE
1	A	753	SER
1	A	756	LYS
1	A	764	ILE
1	A	767	LEU
1	A	776	ASN

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Mol	Chain	Res	Type
1	A	777	SER
1	A	799	GLU
1	A	807	LYS
1	A	811	LEU
1	A	825	ASN
1	A	838	LEU
1	A	843	LEU
1	A	845	LEU
1	A	862	LEU
1	A	865	LEU
1	A	875	LYS
1	A	886	THR
1	A	896	VAL
1	A	912	LYS
1	A	913	GLU
1	A	917	THR
1	A	918	GLU
1	A	939	THR
1	A	967	HIS
1	A	982	ARG
1	A	988	THR
1	A	997	THR
1	A	1001	LYS
1	A	1002	THR
1	A	1011	ASP
1	A	1013	CYS
1	A	1026	LEU
1	A	1029	ILE
1	A	1032	SER
1	A	1042	LEU
1	A	1044	SER
1	A	1052	ARG
1	A	1056	THR
1	A	1083	GLN
1	A	1084	PHE
1	A	1089	HIS
1	A	1092	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	GLN

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Mol	Chain	Res	Type
1	A	153	GLN
1	A	217	ASN
1	A	225	HIS
1	A	268	GLN
1	A	291	GLN
1	A	304	HIS
1	A	389	HIS
1	A	549	ASN
1	A	565	ASN
1	A	634	ASN
1	A	646	GLN
1	A	734	GLN
1	A	743	GLN
1	A	766	GLN
1	A	773	ASN
1	A	893	GLN
1	A	962	HIS
1	A	1005	HIS
1	A	1007	GLN
1	A	1023	HIS
1	A	1083	GLN

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](#)

1 ligand is 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	456	A	1201	-	22,23,23	1.39	4 (18%)	27,32,32	3.03	15 (55%)

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	456	A	1201	-	-	4/10/19/19	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	456	C10-C8	2.65	1.52	1.50
2	A	1201	456	O20-C18	2.30	1.38	1.35
2	A	1201	456	C14-N11	2.23	1.42	1.37
2	A	1201	456	C18-N19	2.11	1.36	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	456	S9-C5-N6	-6.32	110.13	115.78
2	A	1201	456	C17-C18-N19	-5.68	119.03	122.99
2	A	1201	456	C14-N19-C18	5.67	121.46	117.52
2	A	1201	456	C5-N6-C7	5.24	117.59	110.09
2	A	1201	456	C10-C8-S9	3.85	125.39	121.91
2	A	1201	456	C10-N11-C14	-3.61	110.22	117.27
2	A	1201	456	C21-O20-C18	3.57	122.64	117.33
2	A	1201	456	N19-C14-N11	3.52	121.01	116.56
2	A	1201	456	C15-C14-N19	-3.28	117.07	121.22
2	A	1201	456	C1-C2-N4	2.85	119.87	115.27
2	A	1201	456	C12-N11-C14	-2.74	113.12	120.41
2	A	1201	456	C8-C10-N11	2.70	111.80	109.22
2	A	1201	456	C8-S9-C5	2.63	90.07	88.76
2	A	1201	456	N4-C5-N6	2.24	125.04	121.18
2	A	1201	456	O3-C2-C1	-2.15	118.23	122.05

There are no chirality outliers.

All (4) torsion outliers are listed below:

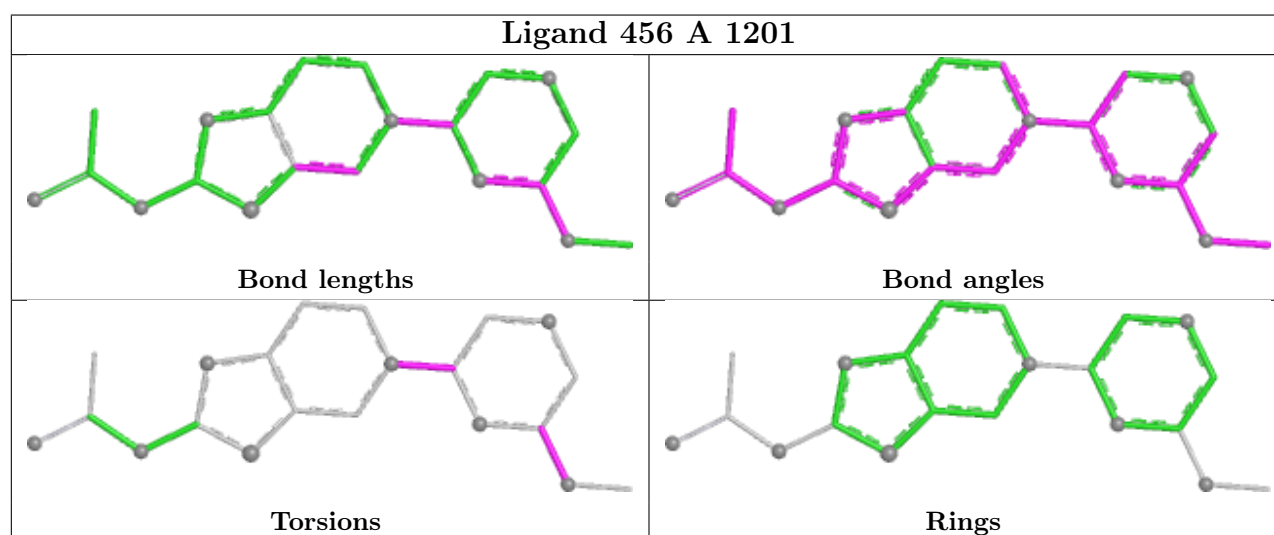
Mol	Chain	Res	Type	Atoms
2	A	1201	456	C17-C18-O20-C21
2	A	1201	456	N19-C18-O20-C21
2	A	1201	456	N19-C14-N11-C12
2	A	1201	456	C15-C14-N11-C12

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	456	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

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 [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	843/966 (87%)	-0.09	15 (1%) 67 63	40, 95, 166, 218	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	248	PHE	4.2
1	A	674	ASP	3.5
1	A	898	ASN	3.4
1	A	934	GLY	2.9
1	A	1044	SER	2.8
1	A	987	LEU	2.6
1	A	900	GLY	2.5
1	A	1086	TRP	2.5
1	A	901	ALA	2.4
1	A	468	LEU	2.3
1	A	1088	LEU	2.3
1	A	1091	VAL	2.2
1	A	527	ILE	2.2
1	A	936	CYS	2.2
1	A	212	TRP	2.1

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

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

6.3 Carbohydrates [i](#)

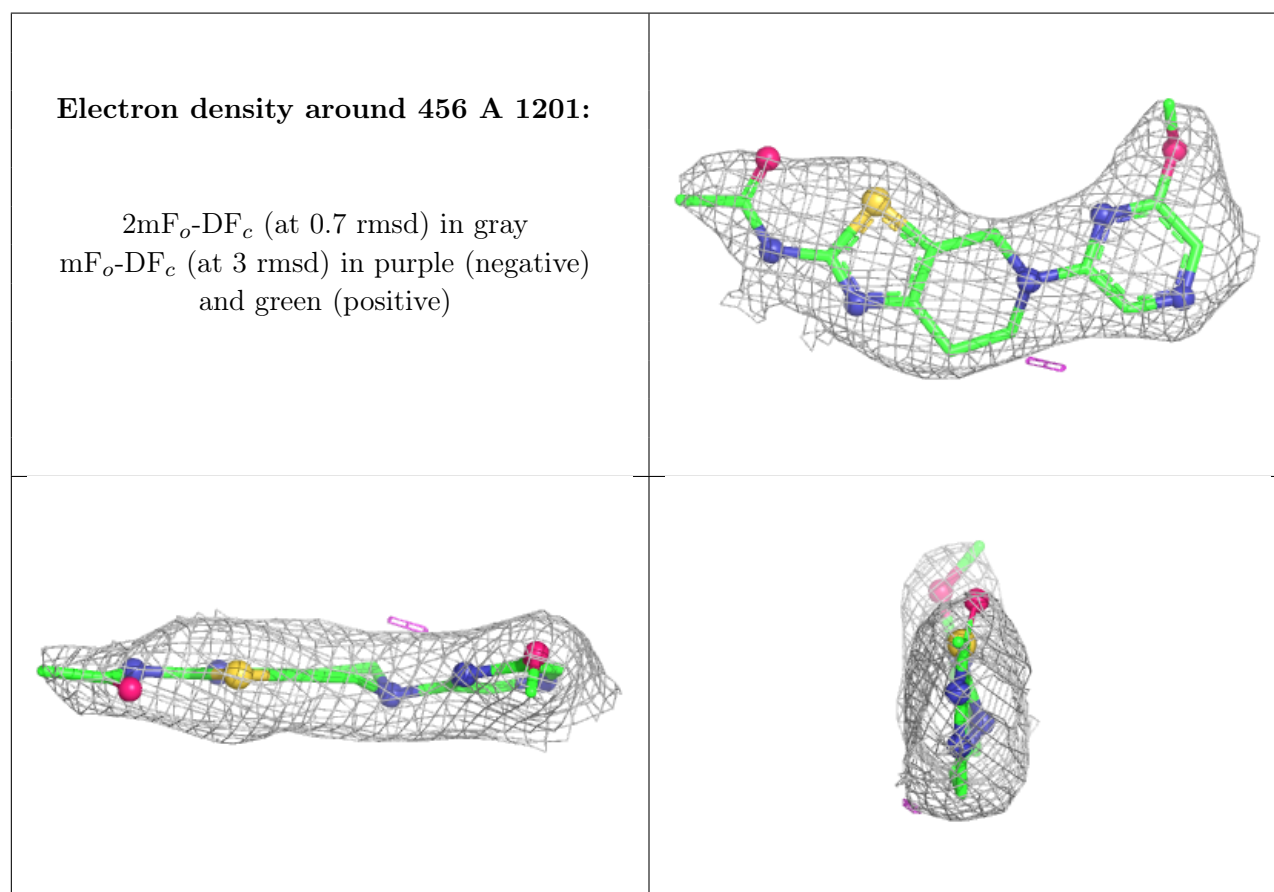
There are no oligosaccharides in this entry.

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	456	A	1201	21/21	0.93	0.07	59,79,91,98	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.