

# Full wwPDB X-ray Structure Validation Report (i)

#### Dec 3, 2023 – 05:36 pm GMT

PDB ID	:	2CHX
Title	:	A pharmacological map of the PI3-K family defines a role for p110alpha in
		signaling: The structure of complex of phosphoinositide 3-kinase gamma with
		inhibitor PIK-90
Authors	:	Knight, Z.A.; Gonzalez, B.; Feldman, M.E.; Zunder, E.R.; Goldenberg, D.D.;
		Williams, O.; Loewith, R.; Stokoe, D.; Balla, A.; Toth, B.; Balla, T.; Weiss,
		W.A.; Williams, R.L.; Shokat, K.M.
Deposited on	:	2006-03-16
Resolution	:	2.50 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 (i) 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 (i)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as $541$ be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)

PERCENTILES INFOmissingINFO

Ideal geometry (DNA, RNA):Parkinson et al. (1996)Validation Pipeline (wwPDB-VP):2.36



#### $2\mathrm{CHX}$

# 1 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6863 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	А	843	Total 6837	C 4390	N 1170	0 1242	S 35	0	0	1

• Molecule 2 is N-(2,3-DIHYDRO-7,8-DIMETHOXYIMIDAZO[1,2-C] QUINAZOLIN-5-YL) NICOTINAMIDE (three-letter code: 090) (formula:  $C_{18}H_{16}N_5O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	Δ	1	Total	С	Ν	0	0	0
2	Π	T	26	18	5	3	0	0

SEQUENCE-PLOTS INFOmissingINFO



## 2 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	144.49Å 68.30Å 106.57Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $95.34^{\circ}$ $90.00^{\circ}$	Depositor
Resolution(A)	57.17 - 2.50	Depositor
Resolution (A)	54.29 - 2.50	EDS
% Data completeness	99.8 (57.17-2.50)	Depositor
(in resolution range)	99.8 (54.29-2.50)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.30 (at 2.51 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.230 , $0.280$	Depositor
$n, n_{free}$	0.257 , $0.303$	DCC
$R_{free}$ test set	1483 reflections $(4.12\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.3	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35 , $43.2$	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6863	wwPDB-VP
Average B, all atoms $(Å^2)$	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.25% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 3 Model quality (i)

## 3.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section:  $090\,$ 

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	Bo	nd lengths	Bond angles		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.81	7/6985~(0.1%)	0.81	4/9449~(0.0%)	

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	А	0	1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	1000	LYS	CE-NZ	11.39	1.77	1.49
1	А	411	ASN	CG-OD1	11.36	1.49	1.24
1	А	1001	LYS	CE-NZ	9.82	1.73	1.49
1	А	411	ASN	CG-ND2	8.81	1.54	1.32
1	А	366	ARG	C-N	7.93	1.47	1.33
1	А	1000	LYS	CD-CE	5.78	1.65	1.51
1	А	364	LYS	CE-NZ	5.76	1.63	1.49

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	1000	LYS	CD-CE-NZ	-7.11	95.36	111.70
1	А	823	LEU	CA-CB-CG	5.54	128.04	115.30
1	А	575	LEU	CA-CB-CG	5.40	127.73	115.30
1	А	412	VAL	CB-CA-C	-5.26	101.40	111.40

There are no chirality outliers.



All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	434	TYR	Peptide

### 3.2 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	А	6837	0	6879	191	0
2	А	26	0	16	2	0
All	All	6863	0	6895	192	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 14.

All (192) 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:1001:LYS:CE	1:A:1001:LYS:NZ	1.73	1.46
1:A:1000:LYS:CE	1:A:1000:LYS:NZ	1.77	1.43
1:A:629:GLN:HG2	1:A:1029:ILE:HG13	1.44	0.99
1:A:1039:MET:HB3	1:A:1040:PRO:HD2	1.49	0.94
1:A:949:ASN:H	1:A:1083:GLN:HE22	1.08	0.94
1:A:652:GLU:OE1	1:A:654:ASP:HB3	1.67	0.94
1:A:240:THR:HG22	1:A:242:GLY:H	1.35	0.92
1:A:724:CYS:HB2	1:A:728:MET:HE3	1.58	0.85
1:A:724:CYS:HB2	1:A:728:MET:CE	2.09	0.82
1:A:848:LEU:HD12	1:A:851:MET:HE1	1.62	0.80
1:A:380:THR:O	1:A:435:CYS:SG	2.42	0.77
1:A:874:ASP:O	1:A:875:LYS:HB2	1.83	0.76
1:A:550:GLN:O	1:A:554:GLN:HG3	1.87	0.75
1:A:561:THR:CG2	1:A:565:ASN:HB3	2.18	0.74
1:A:379:LEU:HD12	1:A:435:CYS:HB2	1.71	0.73
1:A:312:ASP:OD2	1:A:314:ALA:HB3	1.90	0.71
1:A:1000:LYS:NZ	1:A:1000:LYS:CD	2.53	0.70
1:A:949:ASN:H	1:A:1083:GLN:NE2	1.87	0.70
1:A:497:PHE:HD1	1:A:1041:GLN:HE21	1.37	0.70



	A contraction of the contraction	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:165:VAL:HG12	1:A:165:VAL:O	1.91	0.70
1:A:225:HIS:CE1	1:A:304:HIS:HD2	2.09	0.70
1:A:1089:HIS:O	1:A:1092:LEU:N	2.24	0.70
1:A:848:LEU:HD12	1:A:851:MET:CE	2.21	0.69
1:A:184:ARG:O	1:A:188:VAL:HG23	1.94	0.68
1:A:823:LEU:HD12	1:A:823:LEU:H	1.58	0.67
1:A:225:HIS:HE1	1:A:304:HIS:HD2	1.42	0.67
1:A:1021:ARG:HE	1:A:1056:THR:CG2	2.07	0.66
1:A:848:LEU:HA	1:A:851:MET:HE2	1.76	0.66
1:A:935:TYR:O	1:A:939:THR:HB	1.96	0.65
1:A:1089:HIS:C	1:A:1091:VAL:H	2.00	0.65
1:A:652:GLU:OE1	1:A:654:ASP:CB	2.44	0.64
1:A:882:VAL:H	2:A:2093:090:HAA	1.44	0.64
1:A:981:GLU:HA	1:A:982:ARG:CZ	2.28	0.64
1:A:860:LEU:HD21	1:A:1015:LYS:HE2	1.79	0.64
1:A:1089:HIS:O	1:A:1091:VAL:N	2.32	0.63
1:A:387:ILE:HG13	1:A:418:ILE:CD1	2.28	0.63
1:A:807:LYS:HE3	1:A:807:LYS:H	1.64	0.63
1:A:834:HIS:CD2	1:A:834:HIS:C	2.72	0.63
1:A:834:HIS:CD2	1:A:835:GLY:N	2.67	0.63
1:A:743:GLN:O	1:A:747:LEU:HB2	1.99	0.62
1:A:1002:THR:HG23	1:A:1003:SER:N	2.16	0.60
1:A:1039:MET:HB3	1:A:1040:PRO:CD	2.29	0.60
1:A:608:TYR:CZ	1:A:639:ASN:ND2	2.70	0.60
1:A:371:PRO:HG2	1:A:511:GLU:O	2.02	0.59
1:A:410:TRP:HB3	1:A:412:VAL:CG2	2.32	0.59
1:A:767:LEU:HD12	1:A:803:VAL:HG23	1.84	0.59
1:A:178:ARG:HG3	1:A:178:ARG:NH1	2.17	0.59
1:A:675:SER:O	1:A:679:ARG:HG3	2.03	0.59
1:A:226:ARG:HD2	1:A:229:THR:HB	1.85	0.58
1:A:202:VAL:HG22	1:A:285:THR:HG21	1.85	0.58
1:A:1089:HIS:C	1:A:1091:VAL:N	2.57	0.57
1:A:1002:THR:CG2	1:A:1003:SER:N	2.67	0.57
1:A:1021:ARG:HE	1:A:1056:THR:HG23	1.66	0.57
1:A:395:CYS:HB3	1:A:418:ILE:HD11	1.87	0.57
1:A:939:THR:HG23	1:A:945:GLY:HA2	1.87	0.56
1:A:628:MET:HB2	1:A:1029:ILE:HG21	1.88	0.56
1:A:614:ARG:HG2	1:A:617:TRP:HB3	1.87	0.56
1:A:380:THR:O	1:A:435:CYS:CB	2.54	0.56
1:A:854:ILE:HG23	1:A:1023:HIS:CD2	2.41	0.56
1:A:927:ARG:HE	1:A:959:ASN:HD22	1.53	0.56



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:526:PRO:O	1:A:527:ILE:HG13	2.05	0.56
1:A:473:PHE:O	1:A:527:ILE:HD12	2.06	0.55
1:A:478:GLY:N	1:A:520:LEU:O	2.29	0.55
1:A:893:GLN:HA	1:A:897:GLY:CA	2.37	0.55
1:A:271:VAL:HG21	1:A:282:VAL:HG11	1.89	0.55
1:A:271:VAL:HG22	1:A:282:VAL:CG1	2.37	0.55
1:A:922:GLN:HA	1:A:922:GLN:OE1	2.06	0.54
1:A:178:ARG:HG3	1:A:178:ARG:HH11	1.71	0.54
1:A:428:LEU:HD22	1:A:465:ASN:HB3	1.90	0.54
1:A:145:GLU:HA	1:A:148:GLN:HE21	1.72	0.54
1:A:745:VAL:C	1:A:747:LEU:N	2.61	0.53
1:A:561:THR:HG23	1:A:565:ASN:HB3	1.87	0.53
1:A:1042:LEU:HD22	1:A:1042:LEU:O	2.08	0.53
1:A:806:SER:O	1:A:808:LYS:O	2.27	0.53
1:A:836:ASP:O	1:A:875:LYS:HA	2.08	0.53
1:A:1035:LEU:HB3	1:A:1042:LEU:HG	1.89	0.53
1:A:651:LEU:HD22	1:A:655:ASP:HB3	1.91	0.53
1:A:804:MET:HE1	1:A:810:PRO:HB2	1.91	0.53
1:A:733:THR:O	1:A:737:GLN:HG3	2.08	0.52
1:A:745:VAL:O	1:A:747:LEU:N	2.42	0.52
1:A:1055:LEU:O	1:A:1056:THR:HG22	2.09	0.52
1:A:851:MET:HE1	1:A:938:ALA:HB1	1.91	0.52
1:A:887:THR:HG22	1:A:890:LYS:H	1.74	0.52
1:A:834:HIS:CG	1:A:835:GLY:N	2.77	0.51
1:A:214:LYS:NZ	1:A:300:GLY:HA2	2.25	0.51
1:A:225:HIS:HE1	1:A:304:HIS:CD2	2.24	0.51
1:A:527:ILE:HG22	1:A:528:ALA:N	2.25	0.51
1:A:368:ILE:HG21	1:A:433:ILE:HD11	1.92	0.51
1:A:357:CYS:N	1:A:421:LYS:HD3	2.26	0.51
1:A:824:SER:C	1:A:825:ASN:HD22	2.14	0.51
1:A:939:THR:HG23	1:A:945:GLY:CA	2.40	0.51
1:A:272:LEU:HD22	1:A:305:VAL:CG1	2.41	0.50
1:A:965:PHE:O	1:A:967:HIS:N	2.45	0.50
1:A:825:ASN:HD22	1:A:825:ASN:N	2.10	0.50
1:A:898:ASN:N	1:A:898:ASN:HD22	2.08	0.50
1:A:927:ARG:NE	1:A:959:ASN:HD22	2.09	0.50
1:A:387:ILE:HG13	1:A:418:ILE:HD13	1.94	0.49
1:A:747:LEU:HB3	1:A:748:ASP:OD1	2.11	0.49
1:A:165:VAL:O	1:A:165:VAL:CG1	2.58	0.49
1:A:844:ILE:HD13	1:A:1034:MET:SD	2.52	0.49
1:A:378:ASP:O	1:A:379:LEU:C	2.51	0.49



		Interatomic	Clash
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)
1:A:764:ILE:HG22	1:A:764:ILE:O	2.12	0.49
1:A:564:LEU:HD11	1:A:1048:ILE:HG22	1.95	0.49
1:A:874:ASP:O	1:A:875:LYS:CB	2.58	0.49
1:A:1008:LYS:O	1:A:1012:ILE:HG13	2.12	0.49
1:A:285:THR:HG22	1:A:289:ASN:HB2	1.95	0.49
1:A:898:ASN:N	1:A:898:ASN:ND2	2.60	0.49
1:A:903:LYS:HB2	1:A:906:VAL:HG23	1.94	0.49
1:A:948:HIS:HD2	1:A:950:ASP:HB2	1.78	0.49
1:A:302:GLU:OE1	1:A:304:HIS:HE1	1.95	0.48
1:A:210:TYR:O	1:A:213:LYS:HD2	2.13	0.48
1:A:620:SER:O	1:A:647:LYS:NZ	2.43	0.48
1:A:807:LYS:HZ2	1:A:808:LYS:H	1.61	0.48
1:A:274:VAL:HG21	1:A:292:TRP:CD1	2.48	0.48
1:A:583:LEU:HD22	1:A:610:LEU:HD22	1.95	0.48
1:A:271:VAL:CG2	1:A:282:VAL:CG1	2.91	0.48
1:A:178:ARG:HH11	1:A:178:ARG:CG	2.26	0.48
1:A:387:ILE:HG13	1:A:418:ILE:HD11	1.96	0.48
1:A:421:LYS:HA	1:A:421:LYS:HD2	1.59	0.48
1:A:925:VAL:O	1:A:929:VAL:HG23	2.14	0.48
1:A:1045:LYS:O	1:A:1046:GLU:HG3	2.14	0.48
1:A:1035:LEU:HD12	1:A:1048:ILE:HD13	1.96	0.47
1:A:840:GLN:HG2	1:A:1039:MET:HE2	1.96	0.47
1:A:823:LEU:H	1:A:823:LEU:CD1	2.26	0.47
1:A:1001:LYS:NZ	1:A:1001:LYS:CD	2.70	0.47
1:A:743:GLN:HG2	1:A:876:ILE:HD11	1.96	0.47
1:A:231:GLN:HE21	1:A:232:THR:H	1.62	0.47
1:A:1043:THR:HB	1:A:1046:GLU:HB2	1.97	0.47
1:A:804:MET:HE1	1:A:831:ILE:HG23	1.97	0.46
1:A:760:SER:O	1:A:763:VAL:HG12	2.14	0.46
1:A:359:ARG:HH11	1:A:359:ARG:HG2	1.81	0.46
1:A:239:ASP:O	1:A:287:ILE:HG13	2.16	0.45
1:A:271:VAL:CG2	1:A:282:VAL:HG11	2.46	0.45
1:A:896:VAL:HG23	1:A:897:GLY:H	1.81	0.45
1:A:228:THR:O	1:A:228:THR:CG2	2.64	0.45
1:A:742:LEU:HD22	1:A:813:LEU:HD11	1.98	0.45
1:A:896:VAL:CG2	1:A:903:LYS:HD2	2.46	0.45
1:A:498:ASN:OD1	1:A:498:ASN:C	2.55	0.45
1:A:939:THR:CG2	1:A:945:GLY:HA2	2.46	0.45
1:A:1088:LEU:O	1:A:1091:VAL:HG22	2.16	0.45
1:A:665:GLN:NE2	1:A:702:GLU:OE2	2.36	0.45
1:A:743:GLN:C	1:A:745:VAL:H	2.21	0.44



		Interatomic	Clash
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)
1:A:887:THR:HG22	1:A:889:ALA:N	2.33	0.44
1:A:910:TRP:O	1:A:914:LYS:HG2	2.18	0.44
1:A:369:ASP:N	1:A:369:ASP:OD1	2.51	0.43
1:A:923:ALA:O	1:A:926:GLU:HB3	2.17	0.43
1:A:1040:PRO:HB2	1:A:1041:GLN:H	1.65	0.43
1:A:317:GLU:O	1:A:726:THR:HG23	2.18	0.43
1:A:466:LEU:HD11	1:A:476:ARG:HD3	2.00	0.43
1:A:745:VAL:C	1:A:747:LEU:H	2.21	0.43
1:A:287:ILE:HG13	1:A:287:ILE:H	1.68	0.43
1:A:1017:TYR:OH	1:A:1056:THR:HG22	2.19	0.43
1:A:697:TRP:CZ3	1:A:872:THR:HG22	2.54	0.43
1:A:168:VAL:HG13	1:A:170:ASP:O	2.18	0.43
1:A:378:ASP:O	1:A:379:LEU:O	2.36	0.43
1:A:552:ARG:CZ	1:A:552:ARG:HB2	2.49	0.43
1:A:743:GLN:C	1:A:745:VAL:N	2.72	0.43
1:A:363:VAL:HG23	1:A:520:LEU:HD13	2.00	0.42
1:A:804:MET:HB2	1:A:810:PRO:HG2	2.01	0.42
1:A:834:HIS:CD2	1:A:835:GLY:CA	3.02	0.42
1:A:497:PHE:HD1	1:A:1041:GLN:NE2	2.10	0.42
1:A:910:TRP:HA	1:A:913:GLU:HG2	2.01	0.42
1:A:562:ASP:HB2	1:A:563:PRO:CD	2.50	0.42
1:A:470:ASP:HB3	1:A:476:ARG:NH2	2.34	0.41
1:A:199:HIS:O	1:A:200:PRO:C	2.59	0.41
1:A:410:TRP:HB3	1:A:412:VAL:HG22	2.00	0.41
1:A:467:LEU:HB2	1:A:476:ARG:HH12	1.85	0.41
1:A:561:THR:HG23	1:A:565:ASN:CB	2.50	0.41
1:A:1055:LEU:C	1:A:1056:THR:HG22	2.41	0.41
1:A:460:LEU:HG	1:A:487:ILE:HD13	2.03	0.41
1:A:500:ASP:HB3	1:A:708:HIS:CD2	2.55	0.41
1:A:724:CYS:HB2	1:A:728:MET:HE2	1.99	0.41
1:A:960:LEU:HD23	1:A:961:PHE:N	2.36	0.41
1:A:463:TYR:CE1	1:A:501:LYS:HA	2.55	0.41
1:A:497:PHE:HB3	1:A:1041:GLN:HE22	1.84	0.41
1:A:158:ILE:HG12	1:A:717:LEU:HD13	2.02	0.41
1:A:245:LEU:O	1:A:249:PHE:HD1	2.03	0.41
1:A:416:PHE:HB3	1:A:418:ILE:HD12	2.02	0.41
1:A:1045:LYS:O	1:A:1046:GLU:CG	2.69	0.41
1:A:1091:VAL:O	1:A:1091:VAL:HG23	2.21	0.41
2:A:2093:090:OAU	2:A:2093:090:NAL	2.51	0.41
1:A:168:VAL:HG13	1:A:169:HIS:N	2.35	0.41
1:A:178:ARG:NH1	1:A:178:ARG:CG	2.83	0.41



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:569:ALA:O	1:A:573:GLU:HG3	2.20	0.41
1:A:1092:LEU:HD23	1:A:1093:GLY:N	2.36	0.41
1:A:851:MET:HE2	1:A:851:MET:HB2	1.94	0.40
1:A:724:CYS:O	1:A:728:MET:HE2	2.21	0.40
1:A:743:GLN:O	1:A:745:VAL:N	2.54	0.40
1:A:568:THR:HG22	1:A:570:GLU:H	1.85	0.40
1:A:1002:THR:HG23	1:A:1003:SER:H	1.85	0.40
1:A:1041:GLN:OE1	1:A:1041:GLN:HA	2.21	0.40
1:A:1018:LEU:HD13	1:A:1061:GLU:OE1	2.21	0.40

There are no symmetry-related clashes.

## 3.3 Torsion angles (i)

#### 3.3.1 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	А	827/966~(86%)	760~(92%)	49 (6%)	18 (2%)	6 10

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	376	ASN
1	А	754	ALA
1	А	966	GLY
1	А	1040	PRO
1	А	1090	LEU
1	А	527	ILE
1	А	744	LYS
1	А	746	THR
1	А	806	SER
1	А	949	ASN
1	А	1046	GLU
1	А	374	PRO



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Mol	Chain	Res	Type
1	А	747	LEU
1	А	1092	LEU
1	А	216	ALA
1	А	251	LYS
1	А	509	ASP
1	А	897	GLY

#### 3.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	757/864~(88%)	667~(88%)	90 (12%)	5 10

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	145	GLU
1	А	153	GLN
1	А	178	ARG
1	А	190	SER
1	А	202	VAL
1	А	213	LYS
1	А	214	LYS
1	А	219	CYS
1	А	227	SER
1	А	228	THR
1	А	254	LYS
1	А	271	VAL
1	А	281	LEU
1	А	282	VAL
1	А	305	VAL
1	А	309	THR
1	А	358	ASP
1	А	366	ARG
1	А	369	ASP
1	А	373	LEU



Mol	Chain	Res	Type
1	А	375	ARG
1	А	377	THR
1	А	379	LEU
1	А	381	VAL
1	А	391	GLN
1	А	393	VAL
1	А	406	GLU
1	А	412	VAL
1	А	418	ILE
1	А	459	ARG
1	А	487	ILE
1	А	520	LEU
1	А	570	GLU
1	A	574	LEU
1	А	575	LEU
1	А	601	GLN
1	А	610	LEU
1	А	613	ARG
1	А	626	LEU
1	А	646	GLN
1	А	647	LYS
1	А	652	GLU
1	А	682	LEU
1	А	717	LEU
1	А	739	ILE
1	А	744	LYS
1	А	747	LEU
1	А	748	ASP
1	А	751	SER
1	А	756	LYS
1	A	757	TYR
1	A	763	VAL
1	A	766	GLN
1	A	767	LEU
1	A	773	ASN
1	A	777	SER
1	A	791	LEU
1	A	799	GLU
1	A	802	LYS
1	A	806	SER
1	A	807	LYS
1	A	811	LEU



Mol	Chain	Res	Type
1	А	823	LEU
1	А	834	HIS
1	А	836	ASP
1	А	843	LEU
1	А	845	LEU
1	А	848	LEU
1	А	858	GLU
1	А	865	LEU
1	А	871	SER
1	А	886	THR
1	А	890	LYS
1	А	895	THR
1	А	898	ASN
1	А	907	LEU
1	А	939	THR
1	А	967	HIS
1	А	982	ARG
1	А	983	VAL
1	А	997	THR
1	А	1002	THR
1	А	1026	LEU
1	А	1029	ILE
1	A	1041	GLN
1	A	1042	LEU
1	A	1043	THR
1	A	1045	LYS
1	А	1052	ARG
1	А	1078	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	А	148	GLN
1	А	225	HIS
1	А	231	GLN
1	А	304	HIS
1	А	639	ASN
1	А	766	GLN
1	А	773	ASN
1	А	775	GLN
1	А	825	ASN
1	А	834	HIS



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Mol	Chain	Res	Type
1	А	898	ASN
1	А	948	HIS
1	А	959	ASN
1	А	1007	GLN
1	А	1023	HIS
1	А	1041	GLN
1	А	1083	GLN

#### 3.3.3 RNA (i)

There are no RNA molecules in this entry.

#### 3.4 Non-standard residues in protein, DNA, RNA chains (i)

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

#### 3.5 Carbohydrates (i)

There are no monosaccharides in this entry.

#### 3.6 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).

Mal	l Type Chain Res Lin	Chain	Ros Link		Bo	ond leng	ths	B	ond ang	les
WIOI			Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2		
2	090	А	2093	-	25,29,29	1.24	2 (8%)	31,41,41	1.98	7 (22%)

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	090	А	2093	-	-	0/12/12/12	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms		Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
2	А	2093	090	CAH-CAB	4.41	1.53	1.36
2	А	2093	090	CAJ-CAK	-2.10	1.39	1.42

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms		$Observed(^{o})$	$Ideal(^{o})$
2	А	2093	090	CAB-CAH-NAG	-8.26	100.04	106.83
2	А	2093	090	CAK-CAE-CAF	-2.83	117.85	119.98
2	А	2093	090	CAX-NAR-CAQ	2.74	121.58	116.85
2	А	2093	090	CAP-CAQ-NAR	-2.70	119.50	123.49
2	А	2093	090	OAS-CAI-CAJ	2.51	120.00	116.49
2	А	2093	090	CAE-CAK-NAL	-2.26	120.21	123.33
2	А	2093	090	OAS-CAI-CAC	-2.16	120.67	124.37

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	$\mathbf{Res}$	Type	Clashes	Symm-Clashes
2	А	2093	090	2	0

## 3.7 Other polymers (i)

There are no such residues in this entry.

## 3.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



## 4 Fit of model and data (i)

## 4.1 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,  $95^{th}$  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	А	843/966~(87%)	0.54	51 (6%) 21 22	20, 46, 74, 108	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	1044	SER	7.1
1	А	376	ASN	5.7
1	А	1045	LYS	5.7
1	А	374	PRO	5.6
1	А	226	ARG	5.5
1	А	757	TYR	5.2
1	А	307	LEU	4.7
1	А	216	ALA	4.5
1	А	377	THR	4.4
1	А	375	ARG	4.0
1	А	1092	LEU	3.9
1	А	254	LYS	3.8
1	А	897	GLY	3.8
1	А	825	ASN	3.7
1	А	228	THR	3.6
1	А	1086	TRP	3.6
1	А	378	ASP	3.6
1	А	777	SER	3.5
1	А	229	THR	3.3
1	А	874	ASP	3.2
1	А	234	LYS	3.1
1	А	528	ALA	3.1
1	А	489	GLY	3.0
1	А	1066	LYS	3.0
1	А	754	ALA	3.0
1	А	403	PRO	3.0
1	А	253	ALA	2.9



Mol	Chain	Res	Type	RSRZ
1	А	215	ILE	2.8
1	А	1043	THR	2.8
1	А	545	ALA	2.8
1	А	461	LEU	2.6
1	А	823	LEU	2.6
1	А	213	LYS	2.6
1	А	251	LYS	2.6
1	А	774	LEU	2.5
1	А	219	CYS	2.5
1	А	231	GLN	2.5
1	А	527	ILE	2.4
1	А	252	MET	2.4
1	А	220	ILE	2.3
1	А	613	ARG	2.2
1	А	303	ILE	2.2
1	А	1041	GLN	2.2
1	А	755	GLU	2.2
1	А	1046	GLU	2.2
1	А	248	PHE	2.1
1	А	753	SER	2.1
1	А	237	PRO	2.1
1	А	898	ASN	2.1
1	A	834	HIS	2.1
1	А	460	LEU	2.0

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## 4.2 Non-standard residues in protein, DNA, RNA chains (i)

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

#### 4.3 Carbohydrates (i)

There are no monosaccharides in this entry.

#### 4.4 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,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	090	А	2093	26/26	0.94	0.17	44,47,48,50	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.



## 4.5 Other polymers (i)

There are no such residues in this entry.

