



Full wwPDB X-ray Structure Validation Report

May 6, 2014 – 04:48 AM EDT

PDB ID : 4PS8
Title : Structure of PI3K gamma in complex with N-[6-(5,6-dimethoxypyridin-3-yl)-1,3-benzothiazol-2-yl]acetamide
Authors : Griffith, J.P.
Deposited on : 2014-03-06
Resolution : 2.99 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

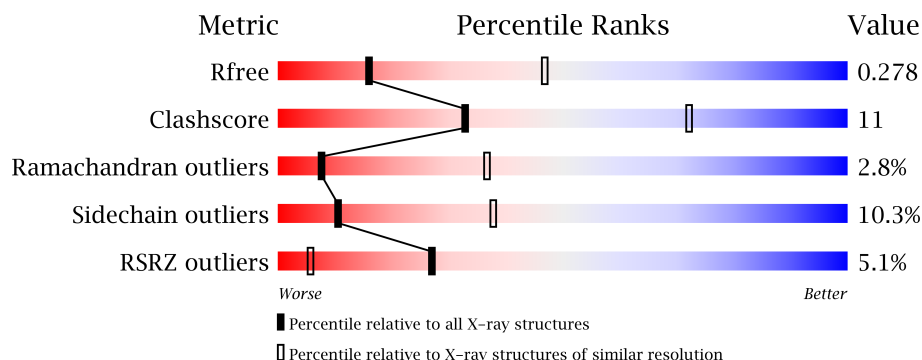
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable22978
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22978

1 Overall quality at a glance

The reported resolution of this entry is 2.99 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}	66092	1216 (3.00-3.00)
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (3.00-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	966	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6869 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

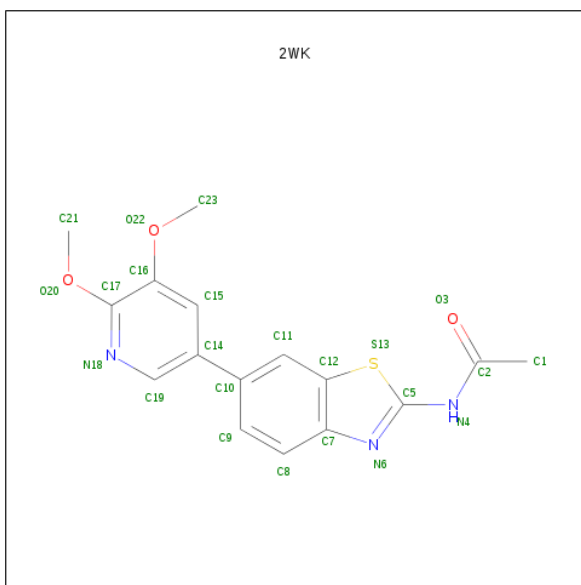
- Molecule 1 is a protein called Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform.

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-[6-(5,6-DIMETHOXYPYRIDIN-3-YL)-1,3-BENZOTHAZOL-2-YL]ACETAMIDE (three-letter code: 2WK) (formula: C₁₆H₁₅N₃O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			23	16	3	3	1		

- Molecule 3 is water.

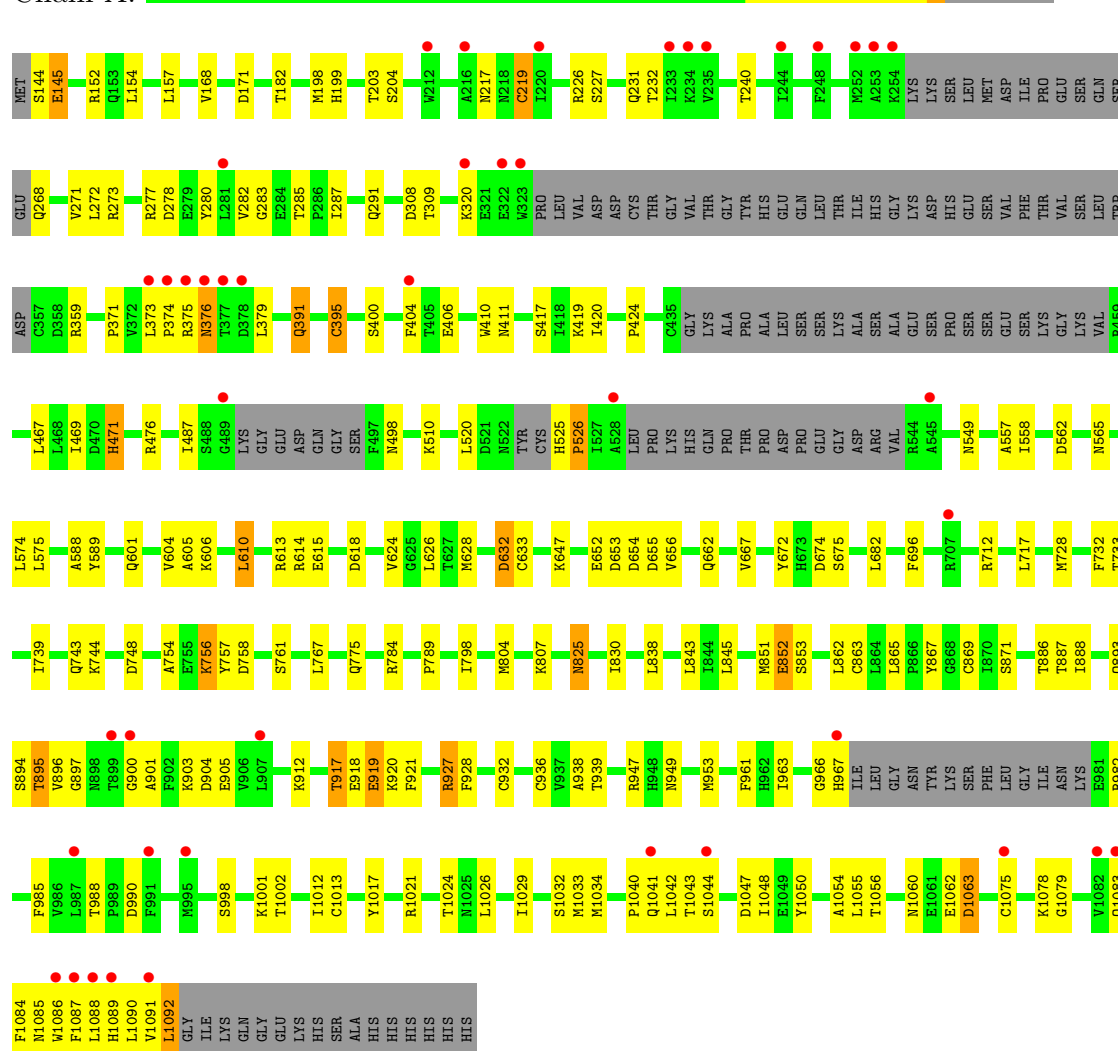
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	O	0	0
			2	2		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 gamma isoform

Chain A:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.57Å 67.68Å 106.54Å 90.00° 96.21° 90.00°	Depositor
Resolution (Å)	105.92 – 2.99 44.92 – 2.99	Depositor EDS
% Data completeness (in resolution range)	89.9 (105.92-2.99) 90.0 (44.92-2.99)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.193 , 0.279 0.200 , 0.278	Depositor DCC
R_{free} test set	960 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	83.9	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 57.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 18828 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6869	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 2WK

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	0.69	2/6992 (0.0%)	0.86	3/9457 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	918	GLU	CG-CD	6.89	1.62	1.51
1	A	904	ASP	CG-OD2	6.52	1.40	1.25

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	632	ASP	CB-CG-OD1	-6.59	112.37	118.30
1	A	830	ILE	CB-CA-C	-6.31	98.97	111.60
1	A	152	ARG	NE-CZ-NH2	-5.07	117.76	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6844	0	0	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	23	0	0	0	0
3	A	2	0	0	0	0
All	All	6869	0	0	77	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 11.

All (77) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:217:ASN:ND2	1:A:219:CYS:SG	2.66	0.69
1:A:894:SER:OG	1:A:895:THR:N	2.27	0.68
1:A:863:CYS:SG	1:A:927:ARG:NH1	2.68	0.66
1:A:988:THR:OG1	1:A:990:ASP:OD1	2.17	0.62
1:A:144:SER:OG	1:A:145:GLU:N	2.34	0.61
1:A:618:ASP:O	1:A:647:LYS:NZ	2.36	0.59
1:A:919:GLU:OE2	1:A:920:LYS:N	2.35	0.58
1:A:308:ASP:OD1	1:A:308:ASP:N	2.36	0.58
1:A:917:THR:OG1	1:A:919:GLU:OE2	2.25	0.55
1:A:467:LEU:O	1:A:476:ARG:NH1	2.40	0.54
1:A:756:LYS:O	1:A:758:ASP:O	2.26	0.53
1:A:655:ASP:O	1:A:656:VAL:C	2.46	0.53
1:A:154:LEU:O	1:A:157:LEU:N	2.42	0.53
1:A:391:GLN:OE1	1:A:633:CYS:SG	2.67	0.53
1:A:283:GLY:O	1:A:285:THR:N	2.45	0.50
1:A:966:GLY:O	1:A:967:HIS:O	2.30	0.50
1:A:562:ASP:OD1	1:A:565:ASN:N	2.45	0.50
1:A:1050:TYR:C	1:A:1050:TYR:CD1	2.84	0.49
1:A:391:GLN:OE1	1:A:633:CYS:CB	2.60	0.49
1:A:1086:TRP:CE3	1:A:1087:PHE:CA	2.95	0.49
1:A:411:ASN:O	1:A:411:ASN:CG	2.51	0.48
1:A:273:ARG:NH1	1:A:277:ARG:O	2.47	0.48
1:A:851:MET:O	1:A:852:GLU:C	2.52	0.48
1:A:395:CYS:SG	1:A:417:SER:OG	2.71	0.47
1:A:1021:ARG:O	1:A:1024:THR:OG1	2.33	0.47
1:A:674:ASP:C	1:A:674:ASP:OD1	2.52	0.46
1:A:758:ASP:N	1:A:758:ASP:OD1	2.48	0.46
1:A:604:VAL:O	1:A:605:ALA:C	2.50	0.46
1:A:1033:MET:O	1:A:1034:MET:C	2.54	0.46
1:A:653:ASP:O	1:A:654:ASP:C	2.53	0.46
1:A:932:CYS:O	1:A:936:CYS:SG	2.74	0.46
1:A:887:THR:O	1:A:888:ILE:C	2.53	0.46
1:A:419:LYS:O	1:A:420:ILE:C	2.54	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:204:SER:OG	1:A:652:GLU:OE2	2.33	0.45
1:A:893:GLN:CA	1:A:897:GLY:CA	2.94	0.45
1:A:825:ASN:ND2	1:A:825:ASN:N	2.63	0.45
1:A:917:THR:O	1:A:920:LYS:N	2.50	0.45
1:A:947:ARG:NH2	1:A:963:ILE:O	2.49	0.45
1:A:171:ASP:OD1	1:A:471:HIS:NE2	2.50	0.44
1:A:1089:HIS:C	1:A:1091:VAL:N	2.69	0.44
1:A:1060:ASN:ND2	1:A:1063:ASP:OD2	2.50	0.44
1:A:1055:LEU:O	1:A:1056:THR:CG2	2.65	0.44
1:A:400:SER:O	1:A:410:TRP:NE1	2.51	0.43
1:A:606:LYS:O	1:A:610:LEU:N	2.51	0.43
1:A:743:GLN:O	1:A:744:LYS:C	2.56	0.43
1:A:614:ARG:O	1:A:615:GLU:C	2.55	0.43
1:A:588:ALA:O	1:A:589:TYR:C	2.57	0.43
1:A:985:PHE:O	1:A:1075:CYS:SG	2.77	0.43
1:A:557:ALA:O	1:A:558:ILE:C	2.58	0.42
1:A:784:ARG:NH1	1:A:789:PRO:O	2.53	0.42
1:A:953:MET:O	1:A:961:PHE:N	2.53	0.42
1:A:1089:HIS:O	1:A:1091:VAL:N	2.53	0.42
1:A:928:PHE:C	1:A:928:PHE:CD1	2.93	0.42
1:A:1062:GLU:O	1:A:1063:ASP:C	2.58	0.42
1:A:469:ILE:O	1:A:672:TYR:OH	2.37	0.42
1:A:632:ASP:C	1:A:632:ASP:OD1	2.56	0.42
1:A:1083:GLN:O	1:A:1084:PHE:C	2.58	0.42
1:A:411:ASN:O	1:A:411:ASN:ND2	2.52	0.42
1:A:1043:THR:N	1:A:1047:ASP:OD2	2.52	0.42
1:A:198:MET:O	1:A:199:HIS:C	2.58	0.42
1:A:1089:HIS:O	1:A:1092:LEU:N	2.53	0.41
1:A:280:TYR:CD1	1:A:280:TYR:N	2.88	0.41
1:A:732:PHE:O	1:A:733:THR:C	2.58	0.41
1:A:624:VAL:O	1:A:628:MET:N	2.53	0.41
1:A:171:ASP:OD1	1:A:171:ASP:C	2.58	0.41
1:A:667:VAL:O	1:A:712:ARG:NH1	2.54	0.41
1:A:988:THR:CB	1:A:990:ASP:OD1	2.69	0.41
1:A:1012:ILE:O	1:A:1013:CYS:C	2.59	0.41
1:A:696:PHE:CD1	1:A:696:PHE:C	2.94	0.41
1:A:920:LYS:O	1:A:921:PHE:C	2.58	0.41
1:A:1017:TYR:OH	1:A:1054:ALA:O	2.39	0.41
1:A:271:VAL:N	1:A:308:ASP:O	2.54	0.40
1:A:990:ASP:OD1	1:A:990:ASP:N	2.54	0.40
1:A:851:MET:CE	1:A:938:ALA:CB	2.99	0.40
1:A:744:LYS:O	1:A:748:ASP:OD1	2.39	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:271:VAL:CG2	1:A:272:LEU:N	2.84	0.40
1:A:525:HIS:CB	1:A:526:PRO:CD	3.00	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	827/966 (86%)	713 (86%)	91 (11%)	23 (3%)	8 37

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	227	SER
1	A	374	PRO
1	A	406	GLU
1	A	471	HIS
1	A	949	ASN
1	A	371	PRO
1	A	376	ASN
1	A	756	LYS
1	A	867	TYR
1	A	1085	ASN
1	A	1090	LEU
1	A	391	GLN
1	A	754	ALA
1	A	1063	ASP
1	A	526	PRO
1	A	900	GLY
1	A	901	ALA
1	A	1040	PRO
1	A	1044	SER
1	A	601	GLN
1	A	757	TYR

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Mol	Chain	Res	Type
1	A	1079	GLY
1	A	424	PRO

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%)	679 (90%)	78 (10%)	10	38

All (78) 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	203	THR
1	A	219	CYS
1	A	226	ARG
1	A	231	GLN
1	A	232	THR
1	A	240	THR
1	A	268	GLN
1	A	278	ASP
1	A	282	VAL
1	A	287	ILE
1	A	291	GLN
1	A	309	THR
1	A	320	LYS
1	A	359	ARG
1	A	373	LEU
1	A	375	ARG
1	A	376	ASN
1	A	379	LEU
1	A	395	CYS
1	A	404	PHE
1	A	487	ILE
1	A	498	ASN
1	A	510	LYS

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Mol	Chain	Res	Type
1	A	520	LEU
1	A	549	ASN
1	A	574	LEU
1	A	575	LEU
1	A	610	LEU
1	A	613	ARG
1	A	626	LEU
1	A	662	GLN
1	A	675	SER
1	A	682	LEU
1	A	717	LEU
1	A	728	MET
1	A	739	ILE
1	A	761	SER
1	A	767	LEU
1	A	775	GLN
1	A	798	ILE
1	A	804	MET
1	A	807	LYS
1	A	825	ASN
1	A	838	LEU
1	A	843	LEU
1	A	845	LEU
1	A	852	GLU
1	A	853	SER
1	A	862	LEU
1	A	865	LEU
1	A	869	CYS
1	A	871	SER
1	A	886	THR
1	A	895	THR
1	A	896	VAL
1	A	903	LYS
1	A	905	GLU
1	A	912	LYS
1	A	917	THR
1	A	919	GLU
1	A	927	ARG
1	A	939	THR
1	A	982	ARG
1	A	998	SER
1	A	1001	LYS

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Mol	Chain	Res	Type
1	A	1002	THR
1	A	1026	LEU
1	A	1029	ILE
1	A	1032	SER
1	A	1041	GLN
1	A	1042	LEU
1	A	1048	ILE
1	A	1078	LYS
1	A	1088	LEU
1	A	1092	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	2WK	A	1201	-	25,25,25	1.04	1 (4%)	35,35,35	2.17	12 (34%)

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	2WK	A	1201	-	-	0/10/12/12	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	2WK	C5-N6	-2.99	1.30	1.34

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	2WK	S13-C5-N6	-5.14	110.86	120.99
2	A	1201	2WK	C5-S13-C12	4.46	90.69	88.89
2	A	1201	2WK	C5-N6-C7	4.01	116.56	108.64
2	A	1201	2WK	C16-C17-N18	-3.94	119.67	123.51
2	A	1201	2WK	O22-C16-C15	-3.42	118.35	124.23
2	A	1201	2WK	C7-C12-S13	-3.12	108.11	112.03
2	A	1201	2WK	C11-C12-S13	2.65	129.72	124.84
2	A	1201	2WK	C8-C7-C12	-2.65	116.76	121.01
2	A	1201	2WK	O3-C2-C1	-2.57	117.11	122.04
2	A	1201	2WK	C19-N18-C17	2.52	122.36	116.67
2	A	1201	2WK	C12-C7-N6	2.47	113.78	108.08
2	A	1201	2WK	C14-C19-N18	-2.01	120.94	124.34

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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	843/966 (87%)	0.10	43 (5%) 27 6	45, 90, 153, 192	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1088	LEU	9.5
1	A	374	PRO	8.3
1	A	322	GLU	7.3
1	A	899	THR	6.1
1	A	323	TRP	6.1
1	A	377	THR	5.6
1	A	1044	SER	5.6
1	A	376	ASN	5.4
1	A	254	LYS	5.1
1	A	995	MET	5.0
1	A	375	ARG	4.9
1	A	1086	TRP	4.9
1	A	253	ALA	4.8
1	A	545	ALA	4.0
1	A	1082	VAL	3.9
1	A	216	ALA	3.8
1	A	1091	VAL	3.8
1	A	907	LEU	3.5
1	A	248	PHE	3.5
1	A	212	TRP	3.4
1	A	1075	CYS	3.4
1	A	252	MET	3.3
1	A	373	LEU	3.3
1	A	900	GLY	3.3
1	A	404	PHE	3.3
1	A	1087	PHE	3.2
1	A	991	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	1089	HIS	3.1
1	A	489	GLY	3.0
1	A	967	HIS	2.9
1	A	987	LEU	2.9
1	A	220	ILE	2.8
1	A	1041	GLN	2.7
1	A	281	LEU	2.6
1	A	378	ASP	2.5
1	A	244	ILE	2.4
1	A	235	VAL	2.4
1	A	1083	GLN	2.3
1	A	233	ILE	2.3
1	A	320	LYS	2.2
1	A	707	ARG	2.1
1	A	528	ALA	2.1
1	A	234	LYS	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q < 0.9
2	2WK	A	1201	23/23	0.16	-0.34	59,72,80,83	0

6.5 Other polymers ⓘ

There are no such residues in this entry.