



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:40 PM GMT

PDB ID : 4A55
Title : Crystal structure of p110alpha in complex with iSH2 of p85alpha and the inhibitor PIK-108
Authors : Hon, W.-C.; Berndt, A.; Williams, R.L.
Deposited on : 2011-10-24
Resolution : 3.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

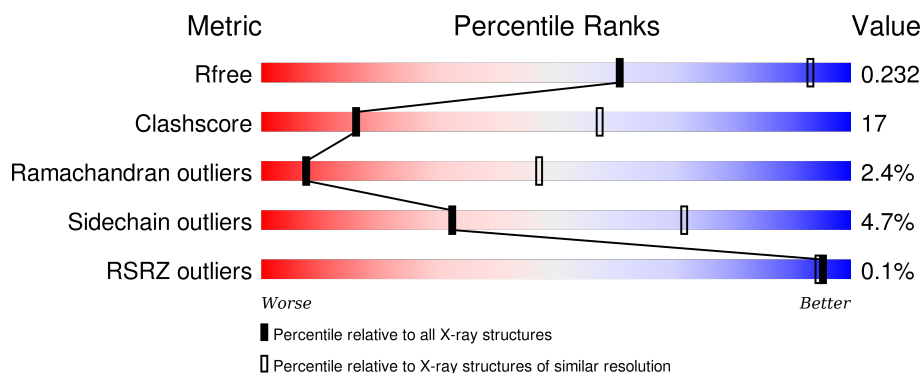
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 3.50 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}	91344	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)

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. 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	1096	 62% 26% • 9%
2	B	279	 38% 11% • 49%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9508 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 ALPHA ISOFORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1001	Total	C	N	O	S	0	0	0
			8214	5266	1397	1485	66			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	EXPRESSION TAG	UNP P42337
A	-26	SER	-	EXPRESSION TAG	UNP P42337
A	-25	TYR	-	EXPRESSION TAG	UNP P42337
A	-24	TYR	-	EXPRESSION TAG	UNP P42337
A	-23	HIS	-	EXPRESSION TAG	UNP P42337
A	-22	HIS	-	EXPRESSION TAG	UNP P42337
A	-21	HIS	-	EXPRESSION TAG	UNP P42337
A	-20	HIS	-	EXPRESSION TAG	UNP P42337
A	-19	HIS	-	EXPRESSION TAG	UNP P42337
A	-18	HIS	-	EXPRESSION TAG	UNP P42337
A	-17	ASP	-	EXPRESSION TAG	UNP P42337
A	-16	TYR	-	EXPRESSION TAG	UNP P42337
A	-15	ASP	-	EXPRESSION TAG	UNP P42337
A	-14	ILE	-	EXPRESSION TAG	UNP P42337
A	-13	PRO	-	EXPRESSION TAG	UNP P42337
A	-12	THR	-	EXPRESSION TAG	UNP P42337
A	-11	THR	-	EXPRESSION TAG	UNP P42337
A	-10	GLU	-	EXPRESSION TAG	UNP P42337
A	-9	ASN	-	EXPRESSION TAG	UNP P42337
A	-8	LEU	-	EXPRESSION TAG	UNP P42337
A	-7	TYR	-	EXPRESSION TAG	UNP P42337
A	-6	PHE	-	EXPRESSION TAG	UNP P42337
A	-5	GLN	-	EXPRESSION TAG	UNP P42337
A	-4	GLY	-	EXPRESSION TAG	UNP P42337
A	-3	ALA	-	EXPRESSION TAG	UNP P42337
A	-2	MET	-	EXPRESSION TAG	UNP P42337

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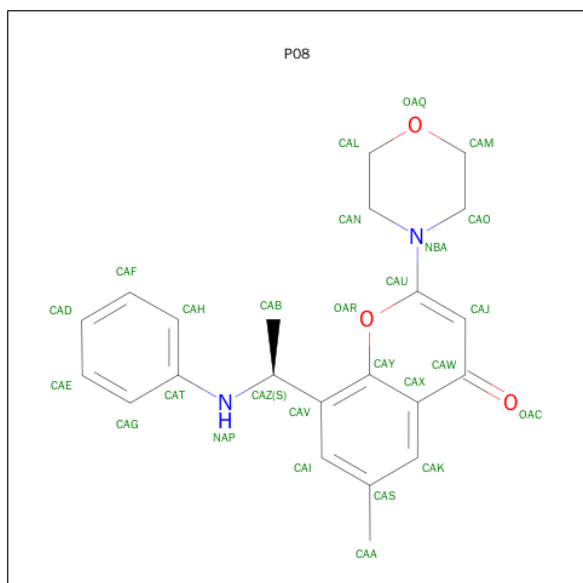
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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ASP	-	EXPRESSION TAG	UNP P42337
A	0	PRO	-	EXPRESSION TAG	UNP P42337

- Molecule 2 is a protein called PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	141	Total	C	N	O	S	0	0	0
			1240	772	224	239	5			

- Molecule 3 is PIK-108 (three-letter code: P08) (formula: C₂₂H₂₄N₂O₃).

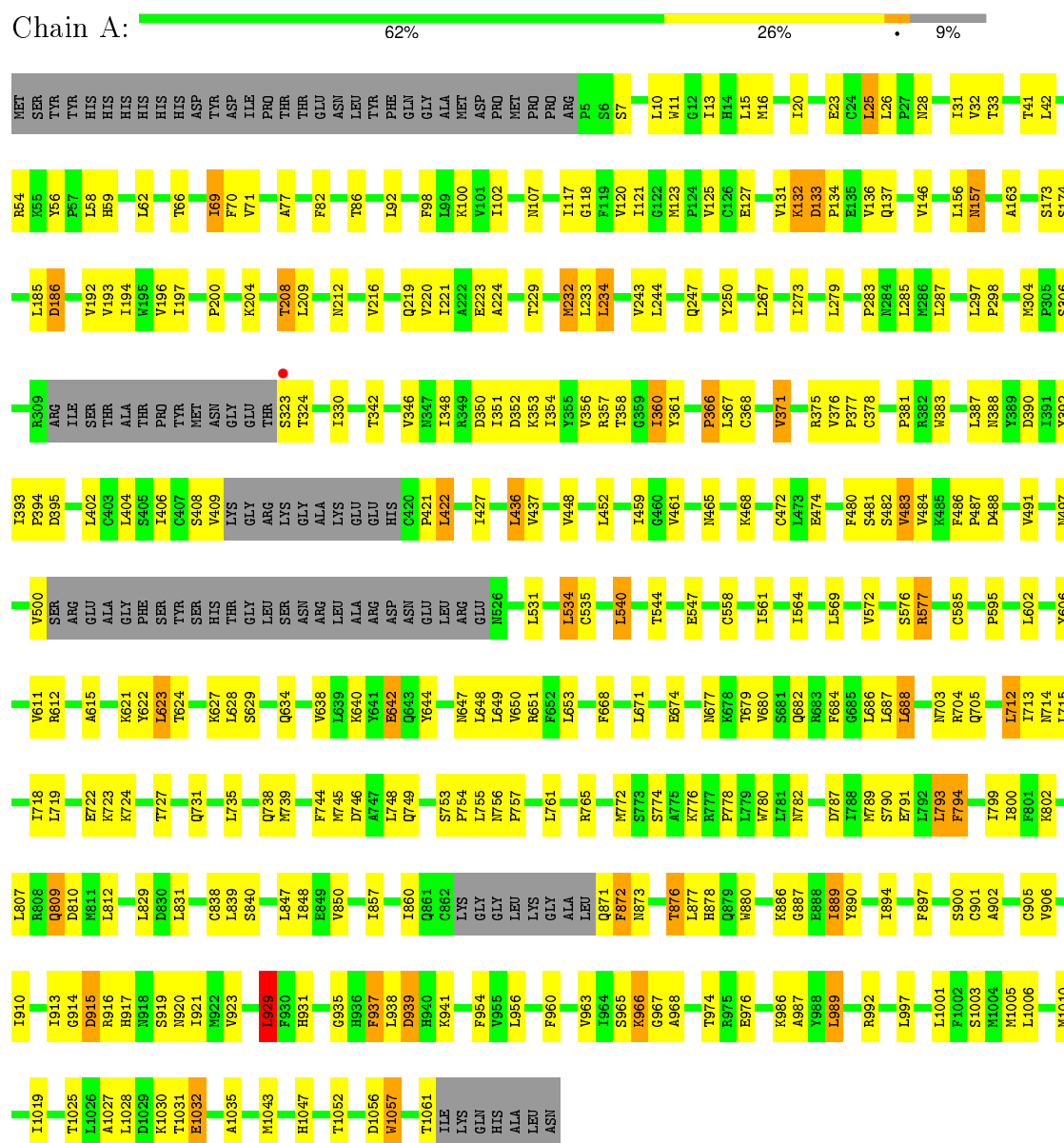


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			27	22	2	3		
3	A	1	Total	C	N	O	0	0
			27	22	2	3		

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 ALPHA ISOFORM



- Molecule 2: PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT ALPHA

Response	Percentage
Yes	38%
No	11%
Don't know	49%

Y580	ILE	LYS	MET
L581	GLU	ILE	ASN
M582	ALA	PHE	ASN
TRP	VAL	HIS	ASN
LEU	GLY	ARG	MET
THR	LYS	ASP	SER
GLN	R448	GLY	LEU
LYS	L449	LYS	GLN
VAL	H450	TYR	ASP
ARG		GLY	ALA
GLN	R453	PHE	GLU
LYS	T454	SER	TYR
		ASP	TRP
K593	L466	PRO	TRP
L594		LEU	GLY
M595	T473	THR	ASP
E596		PHE	ILE
M597	I477	SER	SER
L598		SER	ARG
GLY	A483	VAL	GLU
ASN		VAL	GLU
	A486	GLU	VAL
		LEU	ASN
	T490	ILE	GLU
	I491	ASN	LYS
	R492	HIS	LEU
	I493	TYR	ARG
		ARG	ASP
	N517	ASN	THR
	E518	GLU	ALA
	R519	SER	ASP
		LEU	GLY
	L531	ALA	THR
		GLN	PHE
	E536	TYR	LEU
		ASN	VAL
	E538	PRO	ARG
	I539	LYS	ASP
		LEU	ALA
	L549	ASP	SER
	K550	VAL	THR
	R551	LYS	LYS
	Q552	LEU	MET
	A553	LEU	HIS
	A554	TYR	GLY
	E555	PRO	ASP
		VAL	TYR
	I559	SER	THR
		LYS	LEU
	M563	TYR	THR
	N564	GLN	LEU
	S565	GLN	ARG
		ASP	LYS
	I571	GLY	GLY
		VAL	ASN
	R575	VAL	ASN
	R577	LYS	ASN
	D578	GLU	LYS
		ASP	LEU

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	136.09Å 147.18Å 226.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	123.41 – 3.50 68.05 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (123.41-3.50) 100.0 (68.05-3.50)	Depositor EDS
R_{merge}	0.28	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 3.49Å)	Xtriage
Refinement program	REFMAC 5.7.0002	Depositor
R, R_{free}	0.183 , 0.228 0.188 , 0.232	Depositor DCC
R_{free} test set	1484 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	124.3	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 94.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 29055 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9508	wwPDB-VP
Average B, all atoms (Å ²)	142.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: P08

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	1/8403 (0.0%)	0.79	3/11365 (0.0%)
2	B	0.53	0/1256	0.67	0/1670
All	All	0.62	1/9659 (0.0%)	0.78	3/13035 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	915	ASP	CB-CG	5.63	1.63	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1028	LEU	CA-CB-CG	6.51	130.26	115.30
1	A	938	LEU	CA-CB-CG	5.22	127.30	115.30
1	A	929	LEU	CA-CB-CG	5.02	126.84	115.30

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	8214	0	8219	292	0
2	B	1240	0	1234	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	54	0	48	7	0
All	All	9508	0	9501	322	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 17.

The worst 5 of 322 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:910:ILE:HA	1:A:1025:THR:HG21	1.22	1.18
1:A:535:CYS:HB3	1:A:564:ILE:HG22	1.38	1.06
1:A:279:LEU:O	1:A:279:LEU:HD13	1.62	0.99
1:A:23:GLU:OE1	1:A:33:THR:HG22	1.63	0.99
1:A:992:ARG:NH1	1:A:1027:ALA:HB3	1.81	0.96

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	991/1096 (90%)	855 (86%)	109 (11%)	27 (3%)	6	44
2	B	137/279 (49%)	130 (95%)	7 (5%)	0	100	100
All	All	1128/1375 (82%)	985 (87%)	116 (10%)	27 (2%)	7	47

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	132	LYS
1	A	200	PRO
1	A	366	PRO

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Mol	Chain	Res	Type
1	A	577	ARG
1	A	723	LYS

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	924/1003 (92%)	880 (95%)	44 (5%)	31	71
2	B	136/259 (52%)	130 (96%)	6 (4%)	35	73
All	All	1060/1262 (84%)	1010 (95%)	50 (5%)	32	72

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	585	CYS
1	A	705	GLN
2	B	535	ILE
1	A	623	LEU
1	A	642	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	605	ASN
1	A	705	GLN
2	B	478	GLN
1	A	630	GLN
1	A	731	GLN

5.3.3 RNA ⓘ

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 carbohydrates 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	$\# Z > 2$
3	P08	A	2062	-	27,30,30	1.73	7 (25%)	34,42,42	1.26	4 (11%)
3	P08	A	2063	-	27,30,30	1.96	6 (22%)	34,42,42	1.70	6 (17%)

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	P08	A	2062	-	-	0/10/20/20	0/4/4/4
3	P08	A	2063	-	-	0/10/20/20	0/4/4/4

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2063	P08	CAV-CAZ	-5.69	1.42	1.52
3	A	2062	P08	CAV-CAZ	-5.18	1.42	1.52
3	A	2063	P08	CAT-NAP	-5.11	1.29	1.39
3	A	2063	P08	CAA-CAS	-3.36	1.38	1.51
3	A	2063	P08	CAZ-NAP	-2.44	1.43	1.46

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2063	P08	CAI-CAV-CAZ	-4.26	114.57	120.63
3	A	2063	P08	CAO-NBA-CAU	-2.88	113.36	120.22
3	A	2062	P08	CAO-NBA-CAU	-2.32	114.71	120.22
3	A	2063	P08	OAR-CAY-CAX	-2.15	118.94	121.21
3	A	2063	P08	CAK-CAX-CAY	2.15	118.99	116.42

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2062	P08	3	0
3	A	2063	P08	4	0

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	1001/1096 (91%)	-0.18	1 (0%) 95 94	87, 134, 179, 231	0
2	B	141/279 (50%)	-0.28	0 100 100	116, 173, 226, 244	0
All	All	1142/1375 (83%)	-0.19	1 (0%) 95 94	87, 138, 191, 244	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	323	SER	2.3

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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	P08	A	2062	27/27	0.93	0.33	1.36	108,123,150,152	0
3	P08	A	2063	27/27	0.93	0.39	1.26	107,116,137,148	0

6.5 Other polymers [i](#)

There are no such residues in this entry.