



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 17, 2017 – 09:33 AM EDT

PDB ID : 5MO6  
Title : Crystal Structure of CK2alpha with N-(3-(((2-chloro-[1,1'-biphenyl]-4-yl)methyl)amino)propyl)methanesulfonamide bound  
Authors : Brear, P.; De Fusco, C.; Georgiou, K.; Iegre, J.; Sore, H.; Hyvonen, M.; Spring, D.  
Deposited on : unknown  
Resolution : 1.82 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](mailto: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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029824  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : rb-20029824

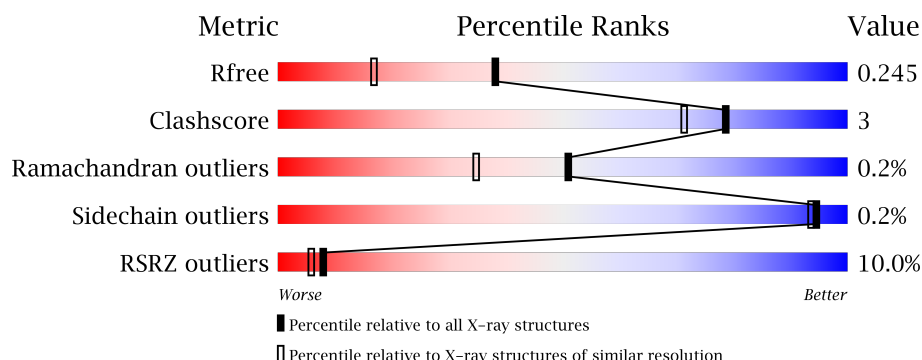
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.82 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))
$R_{free}$	100719	5868 (1.84-1.80)
Clashscore	112137	6856 (1.84-1.80)
Ramachandran outliers	110173	6780 (1.84-1.80)
Sidechain outliers	110143	6780 (1.84-1.80)
RSRZ outliers	101464	5947 (1.84-1.80)

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  $\geq 3$ , 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	352	
1	B	352	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5809 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 Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	324	Total	C	N	O	S	0	4	0
			2770	1775	487	497	11			
1	A	325	Total	C	N	O	S	0	2	0
			2756	1766	482	497	11			

There are 50 discrepancies between the modelled and reference sequences:

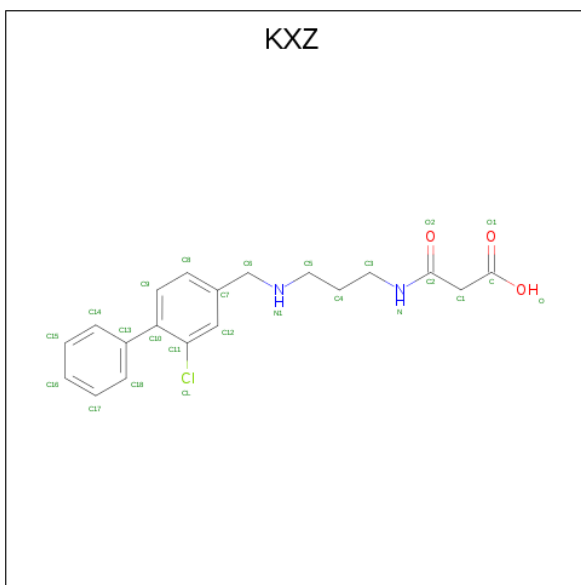
Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	GLY	-	expression tag	UNP P68400
B	-21	SER	-	expression tag	UNP P68400
B	-20	MET	-	expression tag	UNP P68400
B	-19	ASP	-	expression tag	UNP P68400
B	-18	ILE	-	expression tag	UNP P68400
B	-17	GLU	-	expression tag	UNP P68400
B	-16	PHE	-	expression tag	UNP P68400
B	-15	ASP	-	expression tag	UNP P68400
B	-14	ASP	-	expression tag	UNP P68400
B	-13	ASP	-	expression tag	UNP P68400
B	-12	ALA	-	expression tag	UNP P68400
B	-11	ASP	-	expression tag	UNP P68400
B	-10	ASP	-	expression tag	UNP P68400
B	-9	ASP	-	expression tag	UNP P68400
B	-8	GLY	-	expression tag	UNP P68400
B	-7	SER	-	expression tag	UNP P68400
B	-6	GLY	-	expression tag	UNP P68400
B	-5	SER	-	expression tag	UNP P68400
B	-4	GLY	-	expression tag	UNP P68400
B	-3	SER	-	expression tag	UNP P68400
B	-2	GLY	-	expression tag	UNP P68400
B	-1	SER	-	expression tag	UNP P68400
B	0	GLY	-	expression tag	UNP P68400
B	1	SER	-	expression tag	UNP P68400
B	21	SER	ARG	engineered mutation	UNP P68400

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	GLY	-	expression tag	UNP P68400
A	-21	SER	-	expression tag	UNP P68400
A	-20	MET	-	expression tag	UNP P68400
A	-19	ASP	-	expression tag	UNP P68400
A	-18	ILE	-	expression tag	UNP P68400
A	-17	GLU	-	expression tag	UNP P68400
A	-16	PHE	-	expression tag	UNP P68400
A	-15	ASP	-	expression tag	UNP P68400
A	-14	ASP	-	expression tag	UNP P68400
A	-13	ASP	-	expression tag	UNP P68400
A	-12	ALA	-	expression tag	UNP P68400
A	-11	ASP	-	expression tag	UNP P68400
A	-10	ASP	-	expression tag	UNP P68400
A	-9	ASP	-	expression tag	UNP P68400
A	-8	GLY	-	expression tag	UNP P68400
A	-7	SER	-	expression tag	UNP P68400
A	-6	GLY	-	expression tag	UNP P68400
A	-5	SER	-	expression tag	UNP P68400
A	-4	GLY	-	expression tag	UNP P68400
A	-3	SER	-	expression tag	UNP P68400
A	-2	GLY	-	expression tag	UNP P68400
A	-1	SER	-	expression tag	UNP P68400
A	0	GLY	-	expression tag	UNP P68400
A	1	SER	-	expression tag	UNP P68400
A	21	SER	ARG	engineered mutation	UNP P68400

- Molecule 2 is 3-[3-[(3-chloranyl-4-phenyl-phenyl)methylamino]propylamino]-3-oxidanylidene-propanoic acid (three-letter code: KXZ) (formula: C<sub>19</sub>H<sub>21</sub>ClN<sub>2</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			25	19	1	2	3		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).



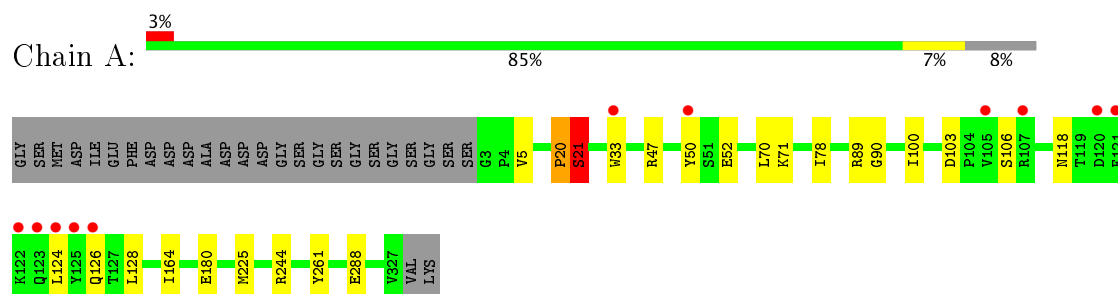
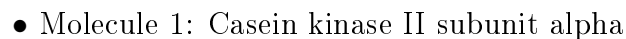
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	49	Total	O	0	0
			49	49		
5	A	191	Total	O	0	0
			191	191		



- Molecule 1: Casein kinase II subunit alpha



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.51Å 68.69Å 334.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	167.08 – 1.82 167.08 – 1.82	Depositor EDS
% Data completeness (in resolution range)	98.2 (167.08-1.82) 99.7 (167.08-1.82)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.29 (at 1.82Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, $R_{free}$	0.213 , 0.231 0.226 , 0.245	Depositor DCC
$R_{free}$ test set	3345 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.7	Xtriage
Anisotropy	0.409	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 36.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5809	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.90% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, KXZ, ACT

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	0.82	3/2831 (0.1%)	0.71	3/3830 (0.1%)
1	B	0.47	0/2849	0.63	0/3854
All	All	0.67	3/5680 (0.1%)	0.67	3/7684 (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	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	20	PRO	C-N	-28.78	0.67	1.34
1	A	21	SER	C-N	-11.75	1.07	1.34
1	A	180	GLU	CD-OE2	-5.00	1.20	1.25

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	126	GLN	CB-CA-C	12.55	135.50	110.40
1	A	20	PRO	C-N-CA	9.44	145.31	121.70
1	A	126	GLN	N-CA-C	-6.19	94.29	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	19[A]	ARG	Sidechain

## 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	2756	0	2689	21	0
1	B	2770	0	2709	18	1
2	A	25	0	0	1	0
3	A	8	0	6	0	0
4	A	10	0	0	0	0
5	A	191	0	0	2	1
5	B	49	0	0	0	1
All	All	5809	0	5404	36	2

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 3.

All (36) 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:20:PRO:CA	1:A:21:SER:N	1.96	1.27
1:A:20:PRO:C	1:A:21:SER:CA	2.05	1.23
1:A:20:PRO:O	1:A:21:SER:N	1.67	1.22
1:A:20:PRO:C	1:A:21:SER:N	0.67	0.72
1:A:225:MET:HG3	2:A:401:KXZ:C15	2.21	0.69
1:B:224:SER:HB3	1:B:230:GLU:HG2	1.74	0.69
1:A:124:LEU:HD23	1:A:128:LEU:HD21	1.80	0.63
1:A:33:TRP:CE3	1:A:100:ILE:HG22	2.34	0.62
1:B:105:VAL:HG11	1:A:20:PRO:HD2	1.84	0.59
1:B:107:ARG:HH22	1:A:89:ARG:HH11	1.51	0.57
1:B:124:LEU:O	1:B:128:LEU:HG	2.07	0.54
1:A:33:TRP:CZ3	1:A:100:ILE:HG22	2.42	0.54
1:B:118:ASN:HD22	1:B:164:ILE:H	1.54	0.54
1:B:50:TYR:CD1	1:B:73:VAL:HG21	2.44	0.52
1:A:118:ASN:HD22	1:A:164:ILE:H	1.57	0.51
1:B:124:LEU:HD22	1:B:128:LEU:HD21	1.92	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:GLU:HG3	5:A:557:HOH:O	2.13	0.48
1:B:5:VAL:HB	1:B:261:TYR:HA	1.94	0.48
1:A:124:LEU:CD2	1:A:128:LEU:HD21	2.42	0.47
1:A:5:VAL:HB	1:A:261:TYR:HA	1.96	0.46
1:A:47:ARG:HG3	1:A:52:GLU:HG3	1.96	0.46
1:B:103:ASP:HB3	1:B:106:SER:OG	2.16	0.46
1:B:36:GLN:HG3	1:B:101:VAL:HG21	1.98	0.44
1:B:47:ARG:HG3	1:B:52:GLU:HG3	1.99	0.44
1:B:255:TYR:HA	1:B:258:ILE:HG12	1.98	0.44
1:B:255:TYR:CD1	1:B:258:ILE:HD11	2.52	0.43
1:A:103:ASP:HB3	1:A:106:SER:OG	2.19	0.43
1:B:125:TYR:HA	1:B:128:LEU:HD12	2.01	0.42
1:B:14:ASP:HB3	1:B:17:THR:OG1	2.19	0.42
1:A:244:ARG:HD3	5:A:610:HOH:O	2.19	0.42
1:B:31:VAL:HG13	1:B:100:ILE:HD12	2.01	0.42
1:A:70:LEU:HD13	1:A:78:ILE:HG12	2.02	0.41
1:A:20:PRO:HA	1:A:21:SER:N	2.19	0.41
1:A:50:TYR:HB3	1:A:71:LYS:HB2	2.03	0.41
1:B:33:TRP:CD1	1:A:90:GLY:HA3	2.56	0.40
1:B:50:TYR:HB3	1:B:71:LYS:HB2	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:662:HOH:O	5:A:662:HOH:O[4_597]	1.08	1.12
1:B:74:LYS:CE	5:B:427:HOH:O[5_545]	2.04	0.16

## 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	325/352 (92%)	311 (96%)	13 (4%)	1 (0%)	44	28
1	B	326/352 (93%)	314 (96%)	12 (4%)	0	100	100
All	All	651/704 (92%)	625 (96%)	25 (4%)	1 (0%)	51	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	21	SER

### 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	301/319 (94%)	301 (100%)	0	100	100
1	B	303/319 (95%)	302 (100%)	1 (0%)	94	93
All	All	604/638 (95%)	603 (100%)	1 (0%)	94	93

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

Mol	Chain	Res	Type
1	B	288	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	118	ASN
1	B	262	ASN
1	B	270	ASN
1	A	118	ASN
1	A	168	HIS
1	A	262	ASN
1	A	270	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

5 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	$\# Z  > 2$
2	KXZ	A	401	-	23,26,26	0.20	0	29,33,33	0.32	0
3	ACT	A	402	-	1,3,3	5.56	1 (100%)	0,3,3	0.00	-
3	ACT	A	403	-	1,3,3	5.50	1 (100%)	0,3,3	0.00	-
4	PO4	A	404	-	4,4,4	2.71	1 (25%)	6,6,6	0.64	0
4	PO4	A	405	-	4,4,4	2.64	1 (25%)	6,6,6	0.60	0

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	KXZ	A	401	-	-	0/15/17/17	0/2/2/2
3	ACT	A	402	-	-	0/0/0/0	0/0/0/0
3	ACT	A	403	-	-	0/0/0/0	0/0/0/0
4	PO4	A	404	-	-	0/0/0/0	0/0/0/0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PO4	A	405	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	405	PO4	P-O1	4.67	1.60	1.50
4	A	404	PO4	P-O1	4.83	1.60	1.50
3	A	403	ACT	CH3-C	5.50	1.55	1.48
3	A	402	ACT	CH3-C	5.56	1.55	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	KXZ	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	21:SER	C	22:GLU	N	1.07
1	A	20:PRO	C	21:SER	N	0.67

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	325/352 (92%)	-0.01	11 (3%) 46 40	13, 27, 58, 103	0
1	B	324/352 (92%)	0.84	54 (16%) 2 1	26, 62, 107, 124	0
All	All	649/704 (92%)	0.41	65 (10%) 8 6	13, 43, 99, 124	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	124	LEU	10.1
1	B	125	TYR	9.2
1	A	125	TYR	8.6
1	B	50	TYR	8.5
1	A	121	PHE	8.5
1	B	121	PHE	6.7
1	A	123	GLN	6.2
1	B	123	GLN	5.0
1	B	122	LYS	4.9
1	A	50	TYR	4.5
1	B	282	GLU	4.4
1	A	122	LYS	4.4
1	B	48	GLY	4.4
1	B	288	GLU	4.3
1	B	128	LEU	4.2
1	B	126	GLN	4.1
1	A	120	ASP	4.1
1	B	49	LYS	4.0
1	B	267	PRO	3.8
1	B	292	LEU	3.7
1	B	270	ASN	3.7
1	B	47	ARG	3.7
1	B	283	ARG	3.6
1	B	284	PHE	3.6

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	33	TRP	3.5
1	B	257	TYR	3.5
1	B	271	ASP	3.4
1	B	272	ILE	3.2
1	A	105	VAL	3.1
1	B	117	ASN	3.1
1	B	252	GLU	3.0
1	B	72	PRO	3.0
1	B	258	ILE	2.9
1	B	248	VAL	2.8
1	B	35	ASN	2.8
1	B	5	VAL	2.6
1	B	302	ASP	2.6
1	B	124	LEU	2.6
1	B	52	GLU	2.5
1	B	327	VAL	2.5
1	B	326	THR	2.5
1	A	33	TRP	2.5
1	B	286	HIS	2.4
1	B	105	VAL	2.4
1	B	76	LYS	2.4
1	B	307	TYR	2.4
1	B	100	ILE	2.4
1	B	280	ARG	2.3
1	B	43	ARG	2.3
1	B	239	TYR	2.2
1	B	298	LEU	2.2
1	A	126	GLN	2.2
1	B	265	LEU	2.2
1	B	18	HIS	2.2
1	B	30	VAL	2.2
1	B	182	TYR	2.2
1	B	119	THR	2.1
1	B	103	ASP	2.1
1	B	225	MET	2.1
1	B	254	LEU	2.1
1	A	107	ARG	2.1
1	B	167	GLU	2.1
1	B	251	THR	2.0
1	B	300	PHE	2.0
1	B	206	TYR	2.0



## 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	PO4	A	404	5/5	0.88	0.11	1.21	50,51,54,56	0
3	ACT	A	402	4/4	0.89	0.11	0.89	31,32,34,37	0
2	KXZ	A	401	25/25	0.58	0.24	0.59	41,53,74,75	0
3	ACT	A	403	4/4	0.98	0.08	-0.37	28,32,35,40	0
4	PO4	A	405	5/5	0.87	0.12	-	55,57,60,64	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.