



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:30 AM GMT

PDB ID : 3M9G  
Title : Crystal structure of the three-PASTA-domain of a Ser/Thr kinase from Staphylococcus aureus  
Authors : Paracuellos, P.; Ballandras, A.; Robert, X.; Creze, C.; Cozzzone, A.J.; Duclos, B.; Gouet, P.  
Deposited on : 2010-03-22  
Resolution : 2.90 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.

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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

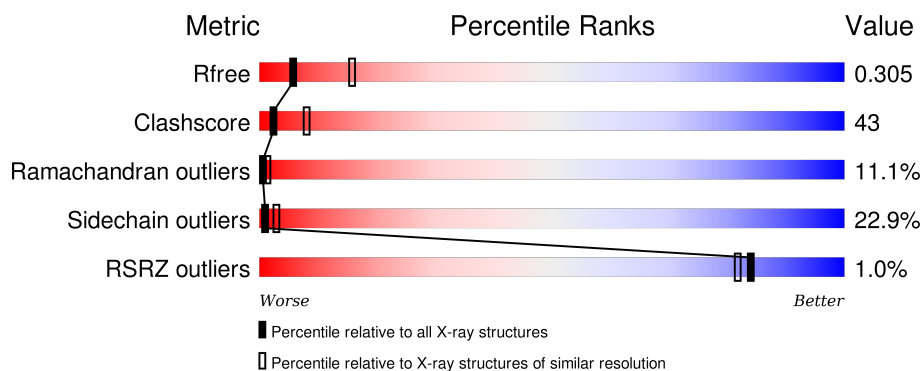
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	201	<div> <div></div> <div> <div></div> <div>37%</div> <div>40%</div> <div>19%</div> <div>.</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1644 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 Protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	201	Total	C	N	O	S	0	0	0
			1572	987	259	325	1			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total	Zn	0	0
			7	7		

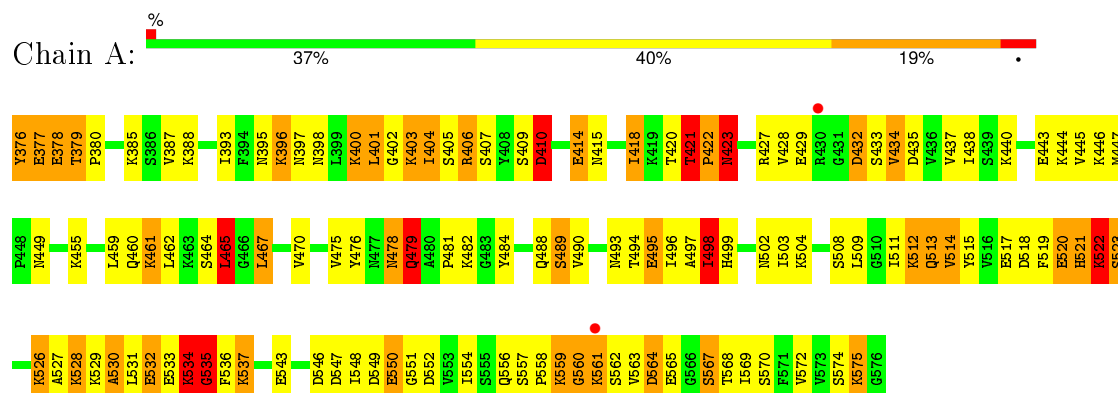
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	65	Total	O	0	0
			65	65		

### 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: Protein kinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.86Å 101.21Å 74.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.77 – 2.90 19.77 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.77-2.90) 99.5 (19.77-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.78 (at 2.88Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.224 , 0.305 0.228 , 0.305	Depositor DCC
$R_{free}$ test set	795 reflections (11.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	53.5	Xtriage
Anisotropy	0.734	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 64.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 7947 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	1644	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.02% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN

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	1.08	2/1594 (0.1%)	1.19	3/2140 (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	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	410	ASP	CB-CG	5.46	1.63	1.51
1	A	378	GLU	CB-CG	5.35	1.62	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	467	LEU	CA-CB-CG	-5.17	103.42	115.30
1	A	432	ASP	CB-CG-OD1	5.12	122.91	118.30
1	A	418	ILE	CB-CA-C	-5.06	101.47	111.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	409	SER	Peptide
1	A	421	THR	Peptide

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Mol	Chain	Res	Type	Group
1	A	535	GLY	Peptide
1	A	561	LYS	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	1572	0	1584	135	0
2	A	7	0	0	0	0
3	A	65	0	0	4	0
All	All	1644	0	1584	135	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 43.

All (135) 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:521:HIS:O	1:A:522:LYS:HB2	1.38	1.10
1:A:557:SER:HB3	1:A:558:PRO:HD3	1.34	1.04
1:A:557:SER:HB3	1:A:558:PRO:CD	1.99	0.93
1:A:393:ILE:O	1:A:397:ASN:ND2	2.03	0.92
1:A:526:LYS:HD3	1:A:527:ALA:N	1.84	0.92
1:A:533:GLU:O	1:A:534:LYS:HB3	1.68	0.92
1:A:534:LYS:HG3	1:A:535:GLY:H	1.36	0.91
1:A:421:THR:CG2	1:A:435:ASP:HB2	2.02	0.89
1:A:519:PHE:CE2	1:A:526:LYS:HE3	2.10	0.85
1:A:557:SER:CB	1:A:558:PRO:HD3	2.06	0.85
1:A:547:ASP:O	1:A:548:ILE:HG13	1.77	0.85
1:A:421:THR:HG21	1:A:435:ASP:HB2	1.59	0.82
1:A:534:LYS:HG3	1:A:535:GLY:N	1.93	0.82
1:A:533:GLU:O	1:A:534:LYS:CB	2.25	0.82
1:A:407:SER:O	1:A:440:LYS:N	2.10	0.82
1:A:558:PRO:HD2	1:A:569:ILE:HG23	1.60	0.81
1:A:462:LEU:HB3	1:A:467:LEU:HB2	1.60	0.81
1:A:515:TYR:HA	1:A:563:VAL:HG12	1.60	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:ASN:H	1:A:478:ASN:ND2	1.81	0.78
1:A:429:GLU:O	1:A:432:ASP:HB2	1.84	0.78
1:A:400:LYS:NZ	1:A:433:SER:HB2	2.00	0.76
1:A:396:LYS:HG3	1:A:396:LYS:O	1.86	0.75
1:A:422:PRO:O	1:A:423:ASN:HB2	1.87	0.74
1:A:376:TYR:O	1:A:377:GLU:HB2	1.85	0.74
1:A:543:GLU:O	1:A:575:LYS:HB3	1.88	0.74
1:A:404:ILE:HD13	1:A:404:ILE:H	1.52	0.73
1:A:387:VAL:CG1	1:A:438:ILE:HD11	2.19	0.72
1:A:514:VAL:O	1:A:563:VAL:HA	1.90	0.71
1:A:421:THR:HG22	1:A:435:ASP:HB2	1.73	0.71
1:A:490:VAL:HG11	1:A:496:ILE:HG13	1.73	0.70
1:A:515:TYR:CE2	1:A:561:LYS:HA	2.27	0.70
1:A:497:ALA:O	1:A:499:HIS:N	2.27	0.67
1:A:519:PHE:HE2	1:A:526:LYS:HE3	1.58	0.66
1:A:532:GLU:O	1:A:534:LYS:O	2.12	0.66
1:A:446:LYS:HG3	1:A:446:LYS:O	1.96	0.65
1:A:543:GLU:O	1:A:575:LYS:N	2.30	0.64
1:A:445:VAL:HG12	1:A:446:LYS:N	2.12	0.64
1:A:478:ASN:C	1:A:479:GLN:HG2	2.19	0.63
1:A:400:LYS:HZ2	1:A:433:SER:HB2	1.63	0.63
1:A:559:LYS:O	1:A:560:GLY:O	2.17	0.63
1:A:446:LYS:HE2	1:A:493:ASN:OD1	1.99	0.62
1:A:475:VAL:C	1:A:509:LEU:HD12	2.20	0.62
1:A:526:LYS:HD3	1:A:527:ALA:H	1.62	0.62
1:A:515:TYR:CA	1:A:563:VAL:HG12	2.29	0.61
1:A:395:ASN:O	1:A:397:ASN:N	2.34	0.60
1:A:404:ILE:CD1	1:A:404:ILE:H	2.14	0.60
1:A:517:GLU:O	1:A:519:PHE:CE1	2.54	0.60
1:A:376:TYR:HB2	1:A:427:ARG:NH2	2.17	0.60
1:A:537:LYS:HG2	1:A:568:THR:HG23	1.84	0.59
1:A:490:VAL:O	1:A:490:VAL:HG12	2.01	0.59
1:A:549:ASP:O	1:A:551:GLY:N	2.36	0.59
1:A:517:GLU:O	1:A:519:PHE:CD1	2.56	0.58
1:A:518:ASP:OD2	1:A:519:PHE:N	2.36	0.58
1:A:400:LYS:O	1:A:433:SER:HA	2.03	0.57
1:A:395:ASN:C	1:A:397:ASN:H	2.08	0.57
1:A:378:GLU:O	1:A:378:GLU:HG3	2.04	0.57
1:A:521:HIS:O	1:A:522:LYS:CB	2.25	0.57
1:A:420:THR:O	1:A:423:ASN:ND2	2.38	0.57
1:A:543:GLU:C	1:A:575:LYS:HB3	2.24	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:VAL:HG13	1:A:438:ILE:HD11	1.85	0.57
1:A:497:ALA:N	3:A:1035:HOH:O	2.36	0.57
1:A:520:GLU:O	1:A:521:HIS:HB2	2.05	0.56
1:A:421:THR:CG2	1:A:435:ASP:CB	2.81	0.56
1:A:497:ALA:C	1:A:499:HIS:H	2.08	0.56
1:A:481:PRO:O	1:A:508:SER:HB3	2.06	0.56
1:A:557:SER:HB2	1:A:570:SER:HB2	1.89	0.54
1:A:445:VAL:O	1:A:496:ILE:N	2.27	0.54
1:A:497:ALA:C	1:A:499:HIS:N	2.61	0.54
1:A:494:THR:HG22	1:A:495:GLU:N	2.23	0.54
1:A:414:GLU:O	1:A:415:ASN:HB2	2.07	0.54
1:A:527:ALA:O	1:A:528:LYS:C	2.47	0.53
1:A:421:THR:HG21	1:A:435:ASP:CB	2.34	0.53
1:A:561:LYS:O	1:A:561:LYS:HG3	2.09	0.53
1:A:397:ASN:O	1:A:398:ASN:HB2	2.09	0.53
1:A:537:LYS:NZ	1:A:537:LYS:HB3	2.24	0.52
1:A:385:LYS:HG2	3:A:1014:HOH:O	2.09	0.52
1:A:418:ILE:HG22	1:A:418:ILE:O	2.08	0.52
1:A:400:LYS:HZ3	1:A:433:SER:HB2	1.75	0.52
1:A:447:MET:HG2	1:A:490:VAL:HG12	1.92	0.51
1:A:523:SER:OG	1:A:526:LYS:HG3	2.11	0.51
1:A:522:LYS:O	1:A:523:SER:C	2.50	0.50
1:A:532:GLU:O	1:A:533:GLU:C	2.50	0.50
1:A:546:ASP:HA	3:A:1044:HOH:O	2.11	0.50
1:A:526:LYS:HZ2	1:A:527:ALA:HA	1.75	0.50
1:A:482:LYS:HD2	1:A:509:LEU:O	2.12	0.50
1:A:421:THR:HG22	1:A:435:ASP:O	2.12	0.49
1:A:557:SER:HB2	1:A:570:SER:O	2.12	0.49
1:A:557:SER:CB	1:A:558:PRO:CD	2.70	0.48
1:A:513:GLN:HA	1:A:564:ASP:O	2.14	0.48
1:A:376:TYR:HB2	1:A:427:ARG:HH21	1.79	0.48
1:A:395:ASN:C	1:A:397:ASN:N	2.66	0.47
1:A:494:THR:CG2	1:A:495:GLU:N	2.77	0.47
1:A:422:PRO:HD2	1:A:434:VAL:HB	1.96	0.47
1:A:405:SER:C	1:A:406:ARG:HG2	2.35	0.47
1:A:543:GLU:O	1:A:575:LYS:CB	2.61	0.47
1:A:421:THR:HG23	1:A:422:PRO:HD3	1.96	0.47
1:A:514:VAL:O	1:A:563:VAL:CA	2.61	0.47
1:A:549:ASP:O	1:A:550:GLU:C	2.53	0.47
1:A:526:LYS:O	1:A:529:LYS:N	2.48	0.47
1:A:490:VAL:CG1	1:A:496:ILE:HG13	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:444:LYS:HG2	1:A:495:GLU:HG2	1.97	0.46
1:A:421:THR:O	1:A:421:THR:OG1	2.30	0.46
1:A:481:PRO:HB2	1:A:484:TYR:CD1	2.50	0.46
1:A:397:ASN:O	1:A:398:ASN:CB	2.64	0.45
1:A:460:GLN:O	1:A:461:LYS:C	2.54	0.45
1:A:519:PHE:CD2	1:A:526:LYS:HE3	2.49	0.45
1:A:554:ILE:HD11	1:A:574:SER:HA	1.97	0.45
1:A:522:LYS:H	1:A:552:ASP:HB3	1.80	0.45
1:A:476:TYR:CE1	1:A:512:LYS:HG3	2.52	0.45
1:A:528:LYS:HG2	1:A:532:GLU:OE1	2.15	0.45
1:A:530:ALA:O	1:A:533:GLU:O	2.35	0.45
1:A:494:THR:HG22	1:A:495:GLU:O	2.17	0.45
1:A:564:ASP:HB2	1:A:565:GLU:H	1.57	0.45
1:A:449:ASN:HA	1:A:488:GLN:HE22	1.82	0.44
1:A:428:VAL:HG22	1:A:432:ASP:HB2	1.99	0.44
1:A:379:THR:HG21	1:A:422:PRO:HB2	2.00	0.43
1:A:498:ILE:HG22	1:A:498:ILE:O	2.18	0.43
1:A:470:VAL:HG22	1:A:503:ILE:HB	1.99	0.43
1:A:557:SER:HB3	1:A:570:SER:H	1.82	0.43
1:A:379:THR:C	1:A:380:PRO:O	2.56	0.43
1:A:563:VAL:HG22	3:A:1001:HOH:O	2.18	0.43
1:A:418:ILE:O	1:A:418:ILE:CG2	2.67	0.43
1:A:445:VAL:CG1	1:A:446:LYS:N	2.79	0.42
1:A:467:LEU:HD23	1:A:467:LEU:HA	1.74	0.42
1:A:459:LEU:CD2	1:A:470:VAL:HG11	2.50	0.42
1:A:554:ILE:HD12	1:A:572:VAL:HG12	2.01	0.42
1:A:421:THR:HG21	1:A:435:ASP:OD1	2.21	0.41
1:A:534:LYS:O	1:A:535:GLY:C	2.59	0.41
1:A:401:LEU:HG	1:A:402:GLY:N	2.36	0.41
1:A:414:GLU:O	1:A:415:ASN:CB	2.68	0.40
1:A:513:GLN:CA	1:A:513:GLN:OE1	2.69	0.40
1:A:444:LYS:CG	1:A:495:GLU:HG2	2.51	0.40
1:A:465:LEU:HA	1:A:465:LEU:HD23	1.59	0.40
1:A:558:PRO:HG2	1:A:569:ILE:CD1	2.51	0.40
1:A:531:LEU:HD23	1:A:531:LEU:HA	1.85	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	199/201 (99%)	150 (75%)	27 (14%)	22 (11%)	<b>0</b> <b>1</b>

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	377	GLU
1	A	465	LEU
1	A	498	ILE
1	A	522	LYS
1	A	534	LYS
1	A	550	GLU
1	A	560	GLY
1	A	396	LYS
1	A	423	ASN
1	A	530	ALA
1	A	535	GLY
1	A	559	LYS
1	A	403	LYS
1	A	479	GLN
1	A	489	SER
1	A	567	SER
1	A	521	HIS
1	A	464	SER
1	A	520	GLU
1	A	410	ASP
1	A	532	GLU
1	A	421	THR

### 5.3.2 Protein sidechains [i](#)

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	179/179 (100%)	138 (77%)	41 (23%)	<b>1</b> <b>3</b>

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	376	TYR
1	A	379	THR
1	A	388	LYS
1	A	400	LYS
1	A	401	LEU
1	A	403	LYS
1	A	404	ILE
1	A	406	ARG
1	A	410	ASP
1	A	414	GLU
1	A	422	PRO
1	A	423	ASN
1	A	434	VAL
1	A	437	VAL
1	A	443	GLU
1	A	455	LYS
1	A	461	LYS
1	A	465	LEU
1	A	478	ASN
1	A	479	GLN
1	A	489	SER
1	A	495	GLU
1	A	498	ILE
1	A	502	ASN
1	A	504	LYS
1	A	511	ILE
1	A	512	LYS
1	A	513	GLN
1	A	514	VAL
1	A	522	LYS
1	A	523	SER
1	A	526	LYS
1	A	528	LYS
1	A	534	LYS
1	A	536	PHE

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Mol	Chain	Res	Type
1	A	537	LYS
1	A	556	GLN
1	A	562	SER
1	A	564	ASP
1	A	567	SER
1	A	575	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	395	ASN
1	A	423	ASN
1	A	449	ASN
1	A	478	ASN
1	A	488	GLN
1	A	502	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 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	201/201 (100%)	-0.25	2 (0%) 84 82	24, 42, 57, 65	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	561	LYS	3.4
1	A	430	ARG	3.3

### 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, 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(Å <sup>2</sup> )	Q<0.9
2	ZN	A	2000	1/1	0.98	0.09	-2.14	53,53,53,53	0
2	ZN	A	2003	1/1	0.99	0.04	-4.25	60,60,60,60	0
2	ZN	A	2004	1/1	0.97	0.04	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	A	2005	1/1	0.84	0.15	-	65,65,65,65	0
2	ZN	A	2002	1/1	0.98	0.06	-	63,63,63,63	0
2	ZN	A	2001	1/1	0.97	0.06	-	45,45,45,45	0
2	ZN	A	2006	1/1	0.98	0.06	-	65,65,65,65	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.