



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 2, 2026 – 01:03 pm BST

PDB ID : 9RU3 / pdb\_00009ru3  
Title : Streptococcus pneumoniae StkP catalytic domain T167A/T169A double mutant  
Authors : Gueguen-Chaignon, V.; Ravaud, S.; Grangeasse, C.  
Deposited on : 2025-07-03  
Resolution : 2.80 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

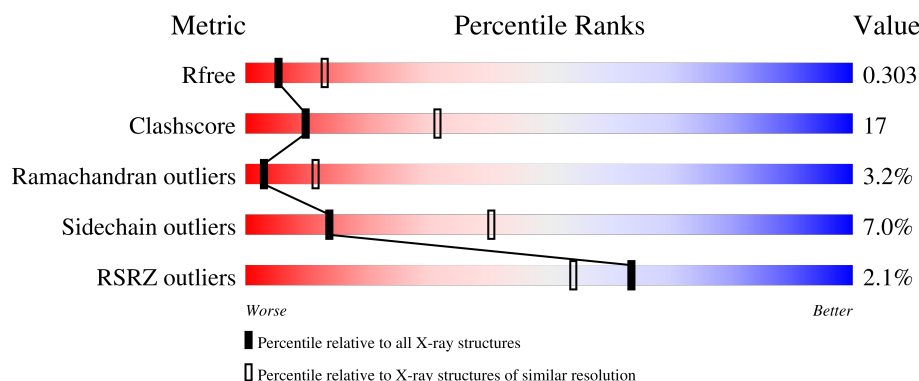
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	344	 2% 46% 26% 6% 23%
1	B	344	 % 49% 21% • 28%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4089 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 Serine/threonine-protein kinase StkP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	0
			2085	1315	368	394	8			
1	B	249	Total	C	N	O	S	0	0	0
			1941	1229	342	362	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	167	ALA	THR	engineered mutation	UNP Q8DNS0
A	169	ALA	THR	engineered mutation	UNP Q8DNS0
B	167	ALA	THR	engineered mutation	UNP Q8DNS0
B	169	ALA	THR	engineered mutation	UNP Q8DNS0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	40	Total	O	0	0
			40	40		
2	B	23	Total	O	0	0
			23	23		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.26Å 51.95Å 81.82Å 90.00° 103.41° 90.00°	Depositor
Resolution (Å)	46.39 – 2.80 46.39 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.39-2.80) 99.8 (46.39-2.80)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.30 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, $R_{free}$	0.223 , 0.304 0.222 , 0.303	Depositor DCC
$R_{free}$ test set	985 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.0	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 44.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4089	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.19% 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 [i](#)

### 5.1 Standard geometry [i](#)

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	0.46	0/2120	0.76	4/2868 (0.1%)
1	B	0.37	0/1973	0.63	0/2667
All	All	0.42	0/4093	0.70	4/5535 (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	B	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	93	VAL	CA-C-N	7.53	135.26	121.70
1	A	93	VAL	C-N-CA	7.53	135.26	121.70
1	A	84	GLY	CA-C-N	6.86	134.04	121.70
1	A	84	GLY	C-N-CA	6.86	134.04	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	106	TYR	Peptide

### 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	2085	0	2087	86	0
1	B	1941	0	1964	56	0
2	A	40	0	0	6	0
2	B	23	0	0	1	0
All	All	4089	0	4051	141	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.

All (141) 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:84:GLY:HA3	1:A:85:GLN:HB2	1.45	0.98
1:A:190:THR:HG22	1:A:192:GLN:H	1.39	0.88
1:A:53:ILE:HD12	1:A:54:ALA:N	1.97	0.79
1:A:93:VAL:HA	1:A:94:ALA:HB3	1.68	0.75
1:A:67:ASP:HB3	1:A:130:ARG:HH12	1.54	0.73
1:A:53:ILE:HD12	1:A:54:ALA:H	1.54	0.72
1:A:11:ARG:HG3	1:A:33:ILE:HG12	1.74	0.70
1:A:229:LEU:HB2	1:A:251:THR:HG21	1.74	0.70
1:A:34:LEU:HB2	1:A:37:GLU:OE2	1.94	0.67
1:B:36:GLY:HA3	1:B:37:GLU:HG3	1.76	0.67
1:B:229:LEU:HD13	1:B:251:THR:HG21	1.77	0.66
1:A:233:ILE:HG12	1:A:239:VAL:HG13	1.77	0.66
1:A:46:THR:HG23	1:A:50:THR:HG21	1.78	0.65
1:A:38:GLU:H	1:A:38:GLU:CD	2.05	0.65
1:A:145:THR:HG22	1:A:147:ASP:H	1.62	0.64
1:B:233:ILE:HG23	1:B:237:SER:HA	1.79	0.62
1:A:84:GLY:CA	1:A:85:GLN:HB2	2.23	0.62
1:B:108:LEU:H	1:B:108:LEU:HD23	1.65	0.61
1:A:31:ASP:H	1:A:37:GLU:H	1.47	0.61
1:B:245:ASN:HA	1:B:248:ILE:HD12	1.83	0.60
1:A:200:ILE:HD12	1:A:211:PRO:HG3	1.83	0.60
1:A:200:ILE:HD13	1:A:229:LEU:HD21	1.84	0.58
1:B:231:SER:HB3	1:B:234:ALA:HB2	1.86	0.57
1:A:249:LYS:HD3	1:A:259:TYR:CE1	2.40	0.57
1:A:181:PRO:HD3	1:A:196:TYR:CE2	2.39	0.57
1:A:6:LYS:O	1:A:7:ILE:HG13	2.05	0.57
1:B:98:LEU:O	1:B:102:ILE:HG23	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:PRO:HD3	1:B:201:ILE:HG12	1.87	0.56
1:B:14:ILE:HD13	1:B:29:ALA:HB2	1.88	0.55
1:B:79:ILE:CD1	1:B:88:LEU:HD23	2.36	0.55
1:A:8:PHE:HB2	1:A:14:ILE:HD11	1.88	0.55
1:A:36:GLY:HA3	1:A:37:GLU:HG3	1.89	0.54
1:A:263:SER:O	1:A:267:VAL:HG13	2.08	0.54
1:B:117:MET:HE1	1:B:206:LEU:HD21	1.89	0.53
1:A:35:ASP:HB3	2:A:427:HOH:O	2.07	0.53
1:A:93:VAL:HA	1:A:94:ALA:CB	2.36	0.53
1:B:223:GLN:HG2	1:B:227:ASN:ND2	2.23	0.53
1:A:232:VAL:HB	1:A:244:GLU:HG3	1.91	0.53
1:A:216:SER:HB3	1:A:219:THR:HB	1.91	0.52
1:B:98:LEU:HB2	1:B:142:ILE:HB	1.92	0.52
1:B:109:SER:HB3	1:B:112:GLU:HB2	1.93	0.51
1:A:145:THR:HG22	1:A:147:ASP:N	2.26	0.51
1:B:78:ASP:HB3	1:B:89:ALA:HB3	1.91	0.51
1:B:106:TYR:CE1	1:B:108:LEU:HA	2.46	0.51
1:A:121:LEU:HD12	1:A:269:LEU:HD22	1.92	0.51
1:A:115:ARG:HH22	1:A:148:GLY:HA3	1.76	0.51
1:A:212:TYR:C	1:A:214:GLY:H	2.19	0.50
1:A:36:GLY:CA	1:A:37:GLU:HG3	2.42	0.50
1:A:58:PHE:HZ	1:A:88:LEU:HD11	1.77	0.50
1:B:252:ALA:HB3	1:B:258:ARG:HG2	1.92	0.50
1:A:20:ARG:H	1:A:20:ARG:HE	1.60	0.49
1:A:134:HIS:O	1:A:135:ARG:HB2	2.11	0.49
1:A:46:THR:HG22	2:A:421:HOH:O	2.12	0.49
1:A:72:HIS:HB2	1:A:123:ALA:HB2	1.95	0.49
1:A:143:LEU:CD1	1:A:153:THR:HG21	2.42	0.49
1:A:279:ASN:HB3	2:A:412:HOH:O	2.11	0.49
1:A:182:GLU:H	1:A:182:GLU:CD	2.20	0.49
1:A:203:TYR:CE1	1:A:211:PRO:HA	2.49	0.48
1:B:219:THR:O	1:B:223:GLN:HG3	2.12	0.48
1:B:93:VAL:HG11	1:B:143:LEU:HD13	1.96	0.48
1:A:46:THR:HG23	1:A:50:THR:CG2	2.43	0.48
1:B:28:LEU:HD11	1:B:38:GLU:HG3	1.95	0.48
1:B:117:MET:CB	1:B:269:LEU:HD21	2.44	0.48
1:B:99:LYS:HB2	1:B:139:PRO:HB2	1.94	0.48
1:A:33:ILE:HG22	1:A:34:LEU:HD23	1.96	0.47
1:A:58:PHE:CZ	1:A:88:LEU:HD11	2.49	0.47
1:B:232:VAL:HB	1:B:244:GLU:HG3	1.96	0.47
1:A:78:ASP:HB3	1:A:89:ALA:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:PHE:CE2	1:B:86:GLN:HB3	2.50	0.47
1:A:58:PHE:HZ	1:A:88:LEU:CD1	2.28	0.47
1:A:67:ASP:HB3	1:A:130:ARG:NH1	2.27	0.47
1:B:17:GLN:HG2	1:B:27:TYR:CE2	2.50	0.47
1:A:38:GLU:CD	1:A:38:GLU:N	2.71	0.47
1:A:182:GLU:CD	1:A:258:ARG:HH22	2.23	0.47
1:B:134:HIS:CE1	1:B:155:PHE:HA	2.49	0.47
1:B:56:ALA:O	1:B:60:ARG:HG3	2.14	0.46
1:B:252:ALA:HB1	1:B:257:ASN:HB2	1.96	0.46
1:A:121:LEU:HA	1:A:121:LEU:HD23	1.61	0.46
1:A:211:PRO:HG2	2:A:435:HOH:O	2.15	0.46
1:A:284:ILE:HA	2:A:431:HOH:O	2.16	0.46
1:A:155:PHE:N	1:A:155:PHE:CD1	2.84	0.46
1:A:264:GLU:HB2	2:A:405:HOH:O	2.16	0.45
1:A:68:LEU:HD22	1:A:126:LEU:HD13	1.99	0.45
1:B:106:TYR:HD1	1:B:107:PRO:C	2.24	0.45
1:A:232:VAL:HG12	1:A:239:VAL:HG11	1.98	0.45
1:B:117:MET:HE1	1:B:206:LEU:CD2	2.46	0.45
1:A:94:ALA:O	1:A:146:PRO:HD3	2.17	0.45
1:A:246:VAL:HG11	1:A:269:LEU:HB2	1.98	0.45
1:A:236:ASN:O	1:A:239:VAL:HG12	2.17	0.44
1:A:125:ARG:HD2	1:A:263:SER:OG	2.17	0.44
1:A:135:ARG:HG2	1:A:189:ALA:HB3	1.98	0.44
1:B:24:ALA:HB1	1:B:42:LYS:HG2	1.98	0.44
1:A:104:GLU:O	1:A:104:GLU:HG3	2.17	0.44
1:B:68:LEU:HD13	1:B:73:ILE:HD13	1.99	0.44
1:B:74:VAL:HG21	1:B:153:THR:HB	2.00	0.44
1:B:79:ILE:HD12	1:B:87:TYR:O	2.17	0.44
1:B:106:TYR:HD1	1:B:107:PRO:O	2.00	0.44
1:B:117:MET:HB3	1:B:269:LEU:HD21	1.98	0.43
1:A:128:HIS:CE1	1:A:191:VAL:HG13	2.53	0.43
1:A:239:VAL:HG23	1:A:243:LEU:HD23	2.01	0.43
1:A:15:VAL:HG12	1:A:16:LYS:H	1.83	0.43
1:A:53:ILE:H	1:A:53:ILE:HG13	1.54	0.43
1:A:115:ARG:HH21	1:A:116:ILE:HD11	1.83	0.43
1:B:115:ARG:HE	1:B:115:ARG:HB3	1.71	0.43
1:A:71:PRO:HD3	1:B:125:ARG:CZ	2.48	0.43
1:B:61:GLU:O	1:B:65:MET:HG3	2.19	0.43
1:B:180:SER:HA	1:B:196:TYR:CD1	2.54	0.43
1:A:4:ILE:O	1:A:5:GLY:C	2.60	0.43
1:A:74:VAL:HG13	1:A:91:GLU:HG2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:LEU:HD22	1:A:126:LEU:O	2.19	0.43
1:A:135:ARG:HG2	1:A:189:ALA:CB	2.48	0.43
1:A:121:LEU:HD12	1:A:269:LEU:CD2	2.49	0.43
1:B:93:VAL:HG13	1:B:94:ALA:N	2.34	0.42
1:B:210:ILE:HD12	1:B:210:ILE:O	2.18	0.42
1:B:17:GLN:HG2	1:B:27:TYR:CD2	2.54	0.42
1:B:79:ILE:HD12	1:B:79:ILE:HA	1.73	0.42
1:B:115:ARG:O	1:B:119:GLN:HG3	2.20	0.42
1:A:98:LEU:HD21	1:A:205:MET:HE2	2.01	0.42
1:B:104:GLU:O	1:B:104:GLU:HG3	2.18	0.42
1:B:183:GLN:HG3	2:B:406:HOH:O	2.20	0.42
1:B:233:ILE:HA	1:B:236:ASN:O	2.19	0.42
1:B:137:LEU:HD13	1:B:198:MET:HG3	2.02	0.42
1:B:229:LEU:HD21	1:B:247:ILE:HG22	2.01	0.42
1:A:212:TYR:O	1:A:214:GLY:N	2.48	0.42
1:A:277:ARG:HD2	1:A:280:GLU:OE2	2.20	0.42
1:A:59:GLN:HB3	1:A:63:ARG:NH1	2.35	0.41
1:A:121:LEU:HD22	1:A:262:VAL:HG13	2.02	0.41
1:B:53:ILE:H	1:B:53:ILE:HG13	1.60	0.41
1:B:106:TYR:CD1	1:B:108:LEU:HA	2.56	0.41
1:A:57:ARG:HA	1:A:60:ARG:CZ	2.50	0.41
1:A:84:GLY:HA3	1:A:85:GLN:CB	2.34	0.41
1:A:99:LYS:HD2	1:A:139:PRO:HG2	2.02	0.41
1:B:6:LYS:HD3	1:B:6:LYS:HA	1.75	0.41
1:A:74:VAL:CG2	1:A:153:THR:HG22	2.51	0.41
1:B:7:ILE:HG13	1:B:13:ARG:HG3	2.02	0.40
1:B:247:ILE:O	1:B:251:THR:HB	2.20	0.40
1:A:75:ARG:HG2	1:A:91:GLU:OE2	2.20	0.40
1:B:65:MET:HA	1:B:68:LEU:HG	2.04	0.40
1:A:115:ARG:HH22	1:A:148:GLY:CA	2.34	0.40
1:A:190:THR:CG2	1:A:191:VAL:N	2.84	0.40
1:A:284:ILE:HA	1:A:284:ILE:HD12	1.99	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	262/344 (76%)	224 (86%)	26 (10%)	12 (5%)	2	6
1	B	243/344 (71%)	214 (88%)	25 (10%)	4 (2%)	7	27
All	All	505/688 (73%)	438 (87%)	51 (10%)	16 (3%)	3	11

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	83	ASP
1	A	85	GLN
1	A	278	ARG
1	A	279	ASN
1	B	36	GLY
1	B	106	TYR
1	A	5	GLY
1	A	106	TYR
1	A	154	ASP
1	A	237	SER
1	B	236	ASN
1	A	15	VAL
1	A	94	ALA
1	A	213	ASP
1	A	216	SER
1	B	11	ARG

### 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	222/293 (76%)	203 (91%)	19 (9%)	10	31
1	B	206/293 (70%)	195 (95%)	11 (5%)	20	52
All	All	428/586 (73%)	398 (93%)	30 (7%)	14	40

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	20	ARG
1	A	41	VAL
1	A	63	ARG
1	A	75	ARG
1	A	79	ILE
1	A	97	ASP
1	A	107	PRO
1	A	126	LEU
1	A	155	PHE
1	A	182	GLU
1	A	229	LEU
1	A	239	VAL
1	A	261	SER
1	A	263	SER
1	A	267	VAL
1	A	269	LEU
1	A	278	ARG
1	A	281	SER
1	B	6	LYS
1	B	7	ILE
1	B	15	VAL
1	B	53	ILE
1	B	102	ILE
1	B	108	LEU
1	B	251	THR
1	B	256	THR
1	B	263	SER
1	B	270	SER
1	B	272	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	241	GLN
1	A	245	ASN
1	B	85	GLN
1	B	177	HIS
1	B	226	GLN

### 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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 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	266/344 (77%)	-0.01	6 (2%) 61 51	24, 40, 61, 68	0
1	B	249/344 (72%)	0.16	5 (2%) 65 56	34, 51, 73, 90	0
All	All	515/688 (74%)	0.07	11 (2%) 63 54	24, 46, 68, 90	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	279	ASN	4.2
1	A	107	PRO	3.4
1	A	278	ARG	2.9
1	A	185	ARG	2.7
1	B	219	THR	2.6
1	B	107	PRO	2.5
1	A	215	ASP	2.3
1	B	46	THR	2.3
1	A	15	VAL	2.3
1	B	50	THR	2.2
1	B	213	ASP	2.1

### 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 oligosaccharides in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.