



# Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 10:00 pm BST

PDB ID : 2H34  
Title : Apoenzyme crystal structure of the tuberculosis serine/threonine kinase, PknE  
Authors : Gay, L.M.; Ng, H.L.; Alber, T.  
Deposited on : 2006-05-22  
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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

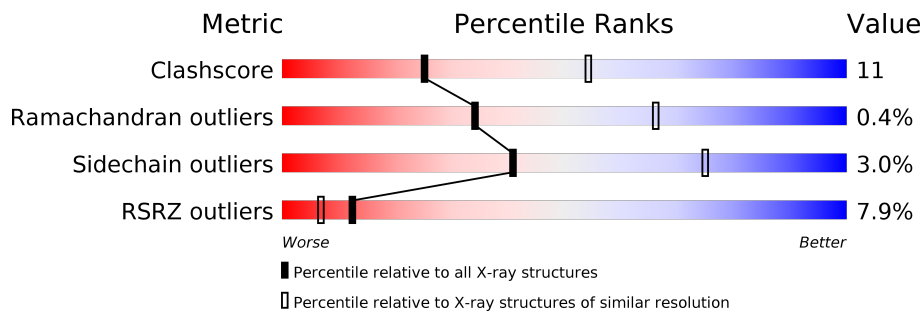
# 1 Overall quality at a glance

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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 on 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	309	 7% 62% 15% .. 21%
1	B	309	 5% 60% 19% 21%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 3645 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 pknE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	243	1812	1144	314	343	3	8	0	0	0
1	B	243	1830	1153	323	343	3	8	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP P72001
A	-18	GLY	-	EXPRESSION TAG	UNP P72001
A	-17	SER	-	EXPRESSION TAG	UNP P72001
A	-16	SER	-	EXPRESSION TAG	UNP P72001
A	-15	HIS	-	EXPRESSION TAG	UNP P72001
A	-14	HIS	-	EXPRESSION TAG	UNP P72001
A	-13	HIS	-	EXPRESSION TAG	UNP P72001
A	-12	HIS	-	EXPRESSION TAG	UNP P72001
A	-11	HIS	-	EXPRESSION TAG	UNP P72001
A	-10	HIS	-	EXPRESSION TAG	UNP P72001
A	-9	SER	-	EXPRESSION TAG	UNP P72001
A	-8	SER	-	EXPRESSION TAG	UNP P72001
A	-7	GLY	-	EXPRESSION TAG	UNP P72001
A	-6	LEU	-	EXPRESSION TAG	UNP P72001
A	-5	VAL	-	EXPRESSION TAG	UNP P72001
A	-4	PRO	-	EXPRESSION TAG	UNP P72001
A	17	ARG	-	EXPRESSION TAG	UNP P72001
A	-2	GLY	-	EXPRESSION TAG	UNP P72001
A	-1	SER	-	EXPRESSION TAG	UNP P72001
A	0	HIS	-	EXPRESSION TAG	UNP P72001
A	27	MSE	MET	MODIFIED RESIDUE	UNP P72001
A	47	MSE	MET	MODIFIED RESIDUE	UNP P72001
A	61	MSE	MET	MODIFIED RESIDUE	UNP P72001
A	93	MSE	MET	MODIFIED RESIDUE	UNP P72001
A	104	MSE	MET	MODIFIED RESIDUE	UNP P72001

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Chain	Residue	Modelled	Actual	Comment	Reference
A	182	MSE	MET	MODIFIED RESIDUE	UNP P72001
A	223	MSE	MET	MODIFIED RESIDUE	UNP P72001
A	253	MSE	MET	MODIFIED RESIDUE	UNP P72001
B	1	MET	-	EXPRESSION TAG	UNP P72001
B	-18	GLY	-	EXPRESSION TAG	UNP P72001
B	-17	SER	-	EXPRESSION TAG	UNP P72001
B	-16	SER	-	EXPRESSION TAG	UNP P72001
B	-15	HIS	-	EXPRESSION TAG	UNP P72001
B	-14	HIS	-	EXPRESSION TAG	UNP P72001
B	-13	HIS	-	EXPRESSION TAG	UNP P72001
B	-12	HIS	-	EXPRESSION TAG	UNP P72001
B	-11	HIS	-	EXPRESSION TAG	UNP P72001
B	-10	HIS	-	EXPRESSION TAG	UNP P72001
B	-9	SER	-	EXPRESSION TAG	UNP P72001
B	-8	SER	-	EXPRESSION TAG	UNP P72001
B	-7	GLY	-	EXPRESSION TAG	UNP P72001
B	-6	LEU	-	EXPRESSION TAG	UNP P72001
B	-5	VAL	-	EXPRESSION TAG	UNP P72001
B	-4	PRO	-	EXPRESSION TAG	UNP P72001
B	17	ARG	-	EXPRESSION TAG	UNP P72001
B	-2	GLY	-	EXPRESSION TAG	UNP P72001
B	-1	SER	-	EXPRESSION TAG	UNP P72001
B	0	HIS	-	EXPRESSION TAG	UNP P72001
B	27	MSE	MET	MODIFIED RESIDUE	UNP P72001
B	47	MSE	MET	MODIFIED RESIDUE	UNP P72001
B	61	MSE	MET	MODIFIED RESIDUE	UNP P72001
B	93	MSE	MET	MODIFIED RESIDUE	UNP P72001
B	104	MSE	MET	MODIFIED RESIDUE	UNP P72001
B	182	MSE	MET	MODIFIED RESIDUE	UNP P72001
B	223	MSE	MET	MODIFIED RESIDUE	UNP P72001
B	253	MSE	MET	MODIFIED RESIDUE	UNP P72001

- Molecule 2 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Br 1 1	0	0

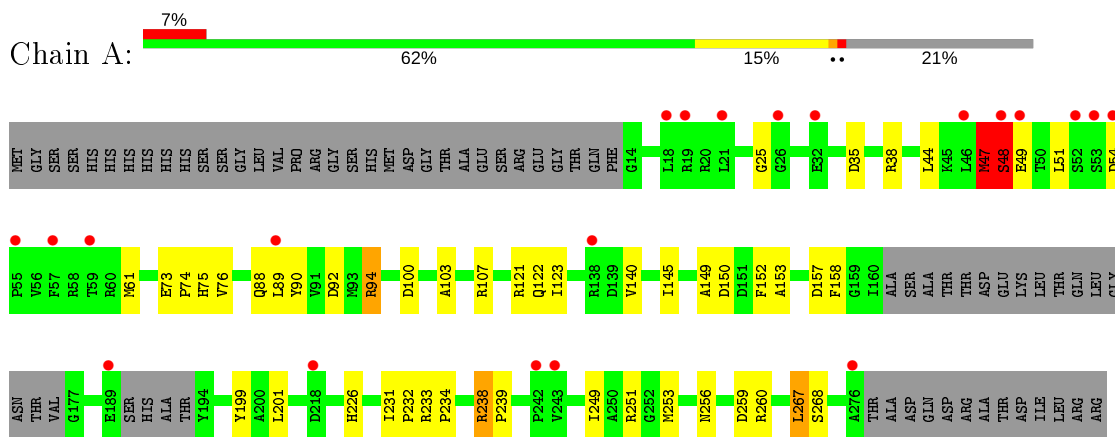
- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	B	1	Total 1	Na 1	0	0
3	A	1	Total 1	Na 1	0	0

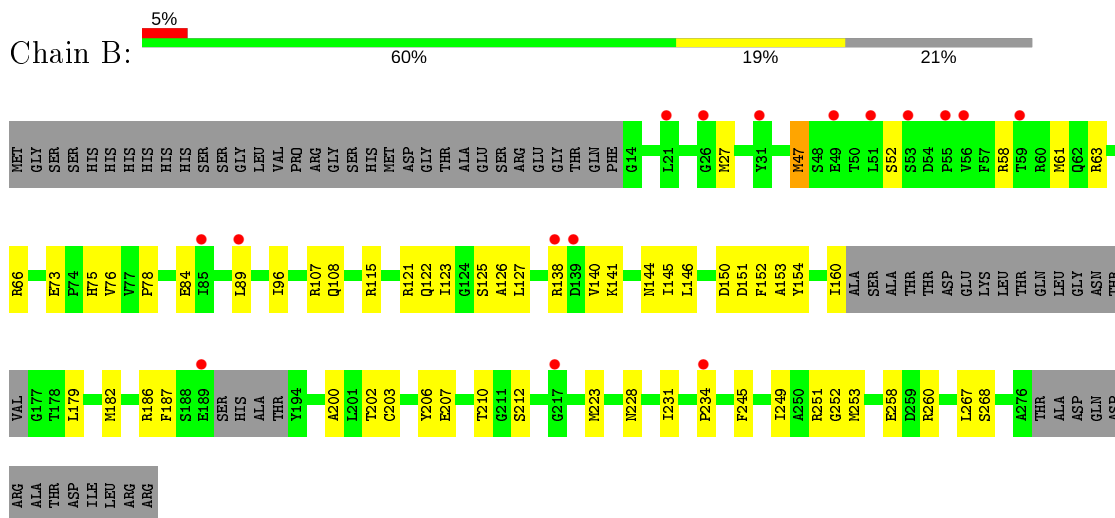
### 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Serine/threonine-protein kinase pknE



- Molecule 1: Serine/threonine-protein kinase pknE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.08Å 77.08Å 221.02Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.10 – 2.80 34.15 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.10-2.80) 99.8 (34.15-2.80)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.65 (at 2.81Å)	Xtrriage
Refinement program	REFMAC refmac_5.2.0005	Depositor
R, $R_{free}$	0.216 , 0.265 0.231 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	68.9	Xtrriage
Anisotropy	0.072	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 75.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.047 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	3645	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.70% 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

Bond lengths and bond angles in the following residue types are not validated in this section: NA, BR

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	0.55	1/1840 (0.1%)	0.64	1/2492 (0.0%)
1	B	0.48	0/1858	0.62	0/2513
All	All	0.52	1/3698 (0.0%)	0.63	1/5005 (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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	48	SER	C-N	-12.23	1.05	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	MSE	O-C-N	-7.21	111.17	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	47	MSE	Mainchain



## 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	1812	0	1760	36	0
1	B	1830	0	1794	42	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	3645	0	3554	77	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 11.

All (77) 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:47:MSE:HG3	1:A:61:MSE:HE3	1.51	0.92
1:A:234:PRO:HG3	1:A:249:ILE:HD13	1.56	0.87
1:A:238:ARG:HG3	1:A:239:PRO:HD2	1.59	0.84
1:A:61:MSE:HE2	1:A:89:LEU:HD12	1.61	0.82
1:A:73:GLU:O	1:A:76:VAL:HG22	1.80	0.81
1:A:199:TYR:OH	1:A:226:HIS:HD2	1.69	0.76
1:B:73:GLU:O	1:B:76:VAL:HG22	1.86	0.76
1:B:73:GLU:OE2	1:B:125:SER:HB3	1.87	0.74
1:A:73:GLU:OE2	1:A:74:PRO:HD2	1.89	0.72
1:B:231:ILE:HG23	1:B:253:MSE:HE2	1.73	0.71
1:B:123:ILE:HG12	1:B:145:ILE:HG12	1.73	0.70
1:A:35:ASP:OD2	1:A:38:ARG:HD3	1.93	0.69
1:B:122:GLN:NE2	1:B:153:ALA:H	1.88	0.69
1:A:100:ASP:HB2	1:A:103:ALA:H	1.57	0.67
1:B:63:ARG:HA	1:B:66:ARG:HG3	1.79	0.65
1:B:127:LEU:HD11	1:B:140:VAL:HG21	1.79	0.64
1:A:121:ARG:HA	1:A:268:SER:OG	1.98	0.64
1:B:179:LEU:HD23	1:B:182:MSE:SE	2.50	0.61
1:A:122:GLN:NE2	1:A:153:ALA:H	1.99	0.60
1:A:238:ARG:HG3	1:A:239:PRO:CD	2.30	0.60
1:B:84:GLU:HB3	1:B:89:LEU:HD23	1.84	0.60
1:B:122:GLN:HE22	1:B:152:PHE:HA	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:ASN:HB3	1:A:259:ASP:OD2	2.04	0.57
1:B:47:MSE:HG2	1:B:61:MSE:SE	2.55	0.57
1:B:75:HIS:NE2	1:B:122:GLN:HG2	2.19	0.57
1:B:123:ILE:HD11	1:B:145:ILE:HG23	1.86	0.56
1:B:27:MSE:SE	1:B:61:MSE:HB3	2.57	0.55
1:B:146:LEU:HD13	1:B:160:ILE:HD13	1.88	0.54
1:A:44:LEU:HD11	1:A:90:TYR:HB2	1.90	0.54
1:A:122:GLN:HE22	1:A:152:PHE:HA	1.72	0.54
1:A:73:GLU:CD	1:A:74:PRO:HD2	2.28	0.54
1:A:103:ALA:O	1:A:107:ARG:HG3	2.09	0.52
1:B:47:MSE:HE2	1:B:61:MSE:HB2	1.91	0.52
1:B:202:THR:HG21	1:B:252:GLY:HA3	1.92	0.51
1:A:92:ASP:C	1:A:92:ASP:OD1	2.49	0.50
1:A:201:LEU:HD23	1:A:267:LEU:HD13	1.94	0.49
1:A:122:GLN:HE22	1:A:153:ALA:H	1.60	0.49
1:B:96:ILE:HG12	1:B:154:TYR:CE1	2.48	0.48
1:A:251:ARG:O	1:A:260:ARG:HA	2.14	0.48
1:B:121:ARG:HA	1:B:268:SER:OG	2.14	0.48
1:A:48:SER:HG	1:A:49:GLU:N	2.11	0.47
1:A:94:ARG:NH1	1:B:78:PRO:HA	2.30	0.46
1:A:157:ASP:OD1	1:A:158:PHE:HD2	1.97	0.46
1:B:115:ARG:HD2	1:B:151:ASP:OD2	2.16	0.46
1:A:73:GLU:O	1:A:76:VAL:CG2	2.58	0.46
1:B:52:SER:O	1:B:58:ARG:HD3	2.15	0.46
1:A:47:MSE:HE3	1:A:61:MSE:HG3	1.99	0.45
1:B:122:GLN:HE22	1:B:153:ALA:H	1.61	0.45
1:A:123:ILE:HD11	1:A:145:ILE:HG23	1.98	0.44
1:A:199:TYR:OH	1:A:226:HIS:CD2	2.58	0.44
1:B:107:ARG:HH21	1:B:108:GLN:HE21	1.65	0.44
1:B:234:PRO:HG3	1:B:249:ILE:HG13	2.00	0.44
1:B:150:ASP:O	1:B:151:ASP:HB2	2.17	0.44
1:B:207:GLU:HA	1:B:212:SER:O	2.17	0.44
1:B:258:GLU:OE2	1:B:258:GLU:HA	2.18	0.43
1:B:186:ARG:HG3	1:B:186:ARG:O	2.18	0.43
1:B:58:ARG:NH1	1:B:84:GLU:OE2	2.50	0.43
1:B:123:ILE:HD11	1:B:153:ALA:HB1	2.00	0.43
1:B:141:LYS:HG2	1:B:144:ASN:ND2	2.33	0.43
1:B:251:ARG:O	1:B:260:ARG:HA	2.18	0.43
1:A:25:GLY:HA2	1:A:158:PHE:HB3	1.99	0.43
1:A:231:ILE:HA	1:A:232:PRO:HD3	1.91	0.42
1:A:75:HIS:CD2	1:A:122:GLN:HE21	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:PHE:CZ	1:B:223:MSE:HG3	2.54	0.42
1:B:52:SER:HA	1:B:61:MSE:HE2	2.00	0.42
1:A:75:HIS:CD2	1:A:122:GLN:HB3	2.54	0.42
1:B:206:TYR:CZ	1:B:210:THR:HG21	2.55	0.41
1:B:245:PHE:O	1:B:249:ILE:HG12	2.20	0.41
1:A:49:GLU:O	1:A:49:GLU:HG3	2.20	0.41
1:B:138:ARG:HB3	1:B:186:ARG:NH1	2.35	0.41
1:B:138:ARG:HD3	1:B:186:ARG:NH2	2.35	0.41
1:B:200:ALA:O	1:B:203:CYS:HB2	2.21	0.41
1:A:233:ARG:HA	1:A:234:PRO:HD2	1.85	0.41
1:A:47:MSE:HG2	1:A:89:LEU:O	2.21	0.41
1:B:76:VAL:CG1	1:B:126:ALA:HB1	2.51	0.41
1:A:249:ILE:O	1:A:253:MSE:HG2	2.21	0.41
1:B:187:PHE:CE1	1:B:223:MSE:HG3	2.56	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	237/309 (77%)	218 (92%)	17 (7%)	2 (1%)	19	49
1	B	237/309 (77%)	221 (93%)	16 (7%)	0	100	100
All	All	474/618 (77%)	439 (93%)	33 (7%)	2 (0%)	34	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	ALA
1	A	48	SER

### 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	182/237 (77%)	174 (96%)	8 (4%)	28	61
1	B	185/237 (78%)	182 (98%)	3 (2%)	62	88
All	All	367/474 (77%)	356 (97%)	11 (3%)	41	75

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LEU
1	A	54	ASP
1	A	88	GLN
1	A	94	ARG
1	A	140	VAL
1	A	150	ASP
1	A	238	ARG
1	A	267	LEU
1	B	47	MSE
1	B	228	ASN
1	B	267	LEU

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

Mol	Chain	Res	Type
1	A	122	GLN
1	A	226	HIS
1	B	108	GLN
1	B	122	GLN
1	B	144	ASN
1	B	226	HIS
1	B	228	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 3 ligands modelled in this entry, 3 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	48:SER	C	49:GLU	N	1.05

## 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	235/309 (76%)	0.47	21 (8%) <b>9</b> <b>5</b>	60, 75, 95, 101	0
1	B	235/309 (76%)	0.43	16 (6%) <b>17</b> <b>10</b>	61, 72, 87, 95	0
All	All	470/618 (76%)	0.45	37 (7%) <b>12</b> <b>7</b>	60, 74, 92, 101	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	138	ARG	6.5
1	B	26	GLY	5.6
1	A	276	ALA	5.5
1	B	85	ILE	4.7
1	A	89	LEU	4.4
1	B	217	GLY	4.1
1	B	53	SER	3.9
1	A	55	PRO	3.8
1	A	59	THR	3.5
1	A	57	PHE	3.3
1	B	139	ASP	3.1
1	B	189	GLU	3.1
1	B	56	VAL	3.0
1	B	234	PRO	3.0
1	A	49	GLU	2.9
1	A	243	VAL	2.9
1	A	53	SER	2.8
1	B	49	GLU	2.5
1	A	32	GLU	2.5
1	A	138	ARG	2.5
1	B	59	THR	2.4
1	A	18	LEU	2.4
1	B	21	LEU	2.4
1	B	55	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	48	SER	2.3
1	A	21	LEU	2.3
1	A	19	ARG	2.2
1	B	31	TYR	2.2
1	A	189	GLU	2.2
1	B	51	LEU	2.1
1	A	26	GLY	2.1
1	A	242	PRO	2.1
1	A	52	SER	2.1
1	B	89	LEU	2.1
1	A	46	LEU	2.0
1	A	218	ASP	2.0
1	A	54	ASP	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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NA	B	290	1/1	0.78	0.16	59,59,59,59	0
3	NA	A	301	1/1	0.94	0.10	53,53,53,53	0
2	BR	A	300	1/1	0.94	0.16	150,150,150,150	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.