



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:50 AM GMT

PDB ID : 2UZY  
Title : STRUCTURE OF THE HUMAN RECEPTOR TYROSINE KINASE MET  
IN COMPLEX WITH THE LISTERIA MONOCYTOGENES INVASION  
PROTEIN INLB: LOW RESOLUTION, CRYSTAL FORM II  
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Ferraris, D.; Gherardi, E.; Heinz, D.W.  
Deposited on : 2007-05-02  
Resolution : 4.00 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](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

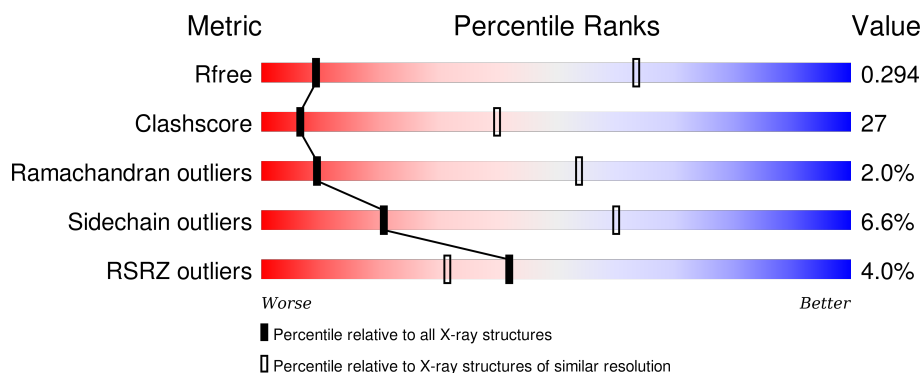
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 4.00 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	1010 (4.42-3.56)
Clashscore	102246	1052 (4.40-3.60)
Ramachandran outliers	100387	1005 (4.40-3.60)
Sidechain outliers	100360	1013 (4.42-3.58)
RSRZ outliers	91569	1013 (4.42-3.56)

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	289	<div> <div>4%</div> <div>55%</div> <div>41%</div> <div>..</div> </div>
1	C	289	<div> <div>%</div> <div>57%</div> <div>39%</div> <div>..</div> </div>
2	B	727	<div> <div>4%</div> <div>43%</div> <div>38%</div> <div>5%</div> <div>13%</div> </div>
2	D	727	<div> <div>4%</div> <div>43%</div> <div>37%</div> <div>5%</div> <div>15%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14329 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 INTERNALIN B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	0	0
			2252	1435	378	437	2			
1	C	286	Total	C	N	O	S	0	0	0
			2252	1435	378	437	2			

- Molecule 2 is a protein called HEPATOCYTE GROWTH FACTOR RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	630	Total	C	N	O	S	0	0	0
			4959	3151	835	938	35			
2	D	618	Total	C	N	O	S	0	0	0
			4866	3097	818	918	33			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	41	CYS	TYR	CONFLICT SEE REMARK 9	UNP P08581
B	344	ALA	GLY	CONFLICT SEE REMARK 9	UNP P08581
D	41	CYS	TYR	CONFLICT SEE REMARK 9	UNP P08581
D	344	ALA	GLY	CONFLICT SEE REMARK 9	UNP P08581

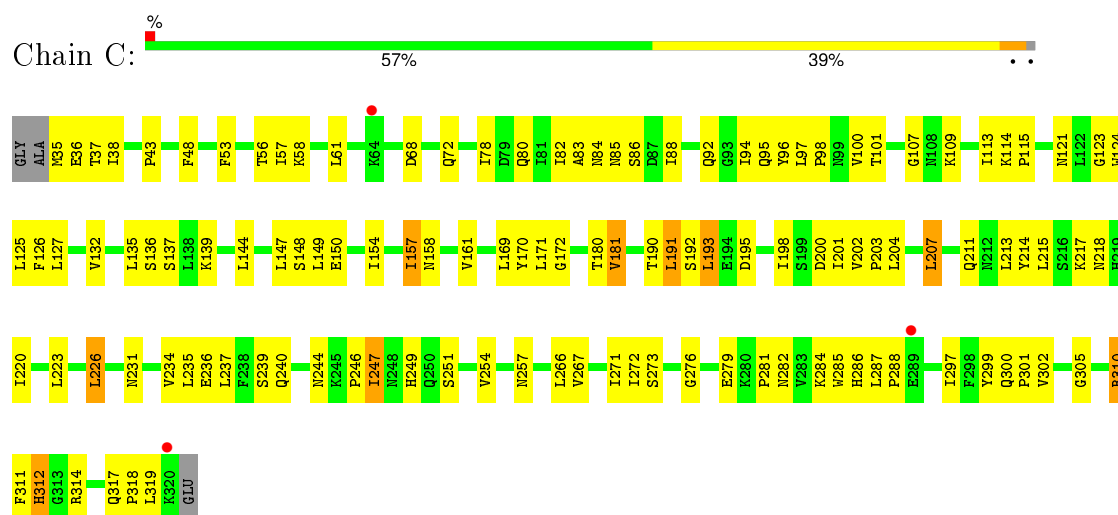
### 3 Residue-property plots

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.

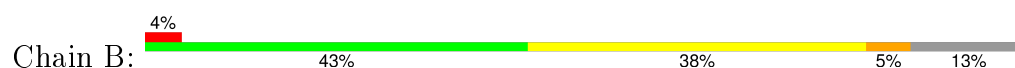
#### • Molecule 1: INTERNALIN B

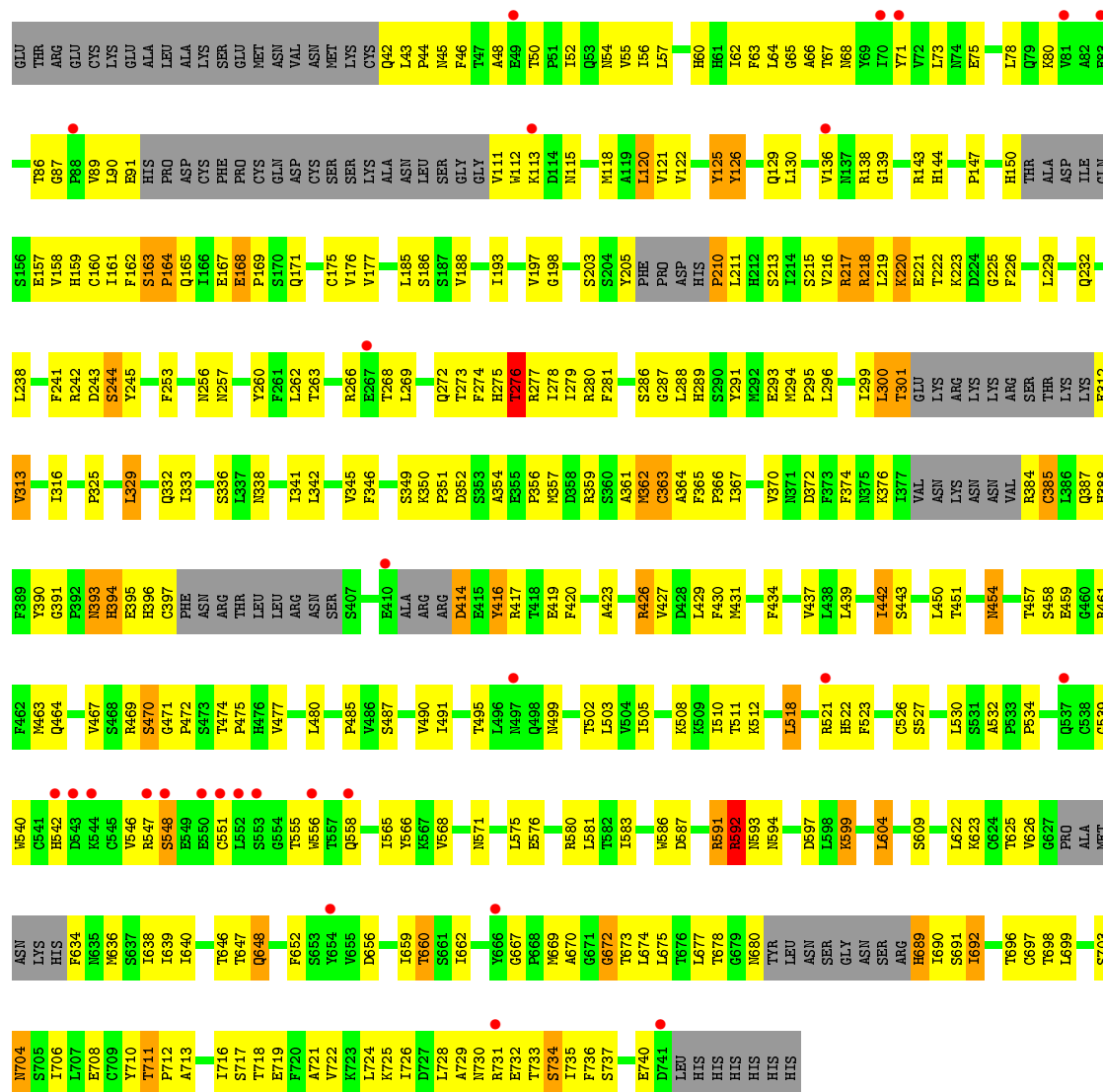


#### • Molecule 1: INTERNALIN B

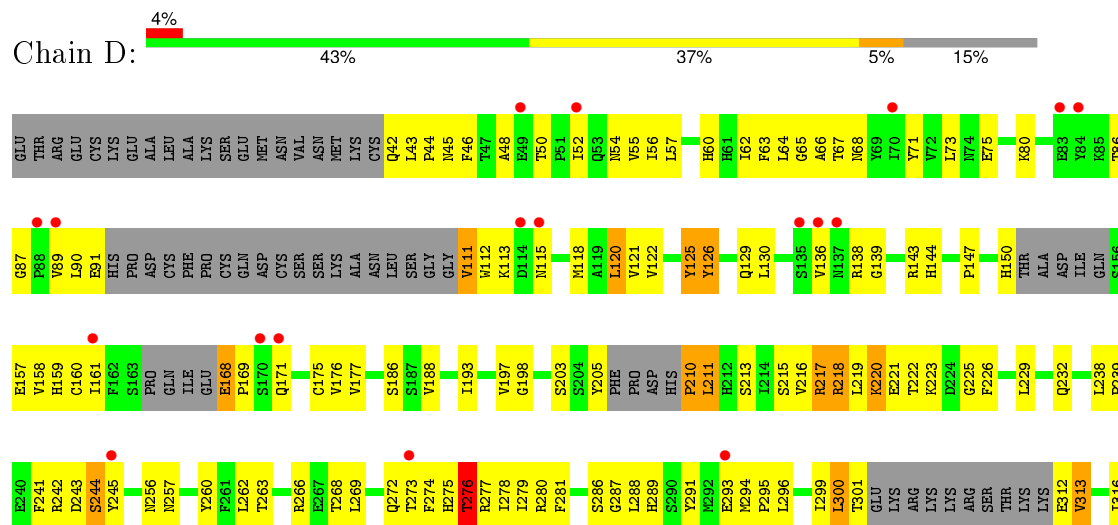


#### • Molecule 2: HEPATOCYTE GROWTH FACTOR RECEPTOR





• Molecule 2: HEPATOCYTE GROWTH FACTOR RECEPTOR



E719	F720	A721	V722	K723	L724	K725	I726	D727	L728	A729	N730	R731	E732	I733	S734	I735	F736	S737	E740	D741	LEU	HIS	HIS	HIS	HIS	HIS	HIS																						
Q648	F652	D656	I659	T660	S661	I662	G667	R668	M669	G671	G672	T673	L674	L675	T676	L677	T678	G679	M680	TYR	LEU	ASN	SER	GLY	ASN	SER	ARG																						
L562	I565	Y566	K567	V568	N571	P574	L575	E576	R580	T581	L582	I583	N586	R591	N592	N593	N594	D597	L598	K599	L604	S609	L614	L622	K623	C624	T625	V626	G627	PRO	ALA	MET	ASN	LYS	HIS	F634	N635	R636	T638	I639	I640	R644	G645	T646	T647				
R469	S470	T474	H475	V477	L480	P485	V486	S487	V490	I491	T502	L503	I505	K508	K509	I510	T511	K512	I513	P514	L518	R521	H522	F523	C526	L530	S531	A532	G539	N540	C541	R542	D543	V546	R547	S548	C551	L552	S553	G554	T555	M556	T557	Q558					
GLU	HIS	CYS	PHE	ASN	ARG	THR	LEU	LEU	ARG	ASN	SER	GLY	CYS	GLU	ALA	ARG	D414	E415	Y416	R417	T418	E419	F420	A423	R426	V427	D428	L429	F430	F434	V437	L438	L439	I442	S443	T451	I452	A453	N454	T457	S458	E459	Q460	R461	F462	M463	Q464	V467	S468
P325	L329	Q332	I333	S336	L337	N338	I341	L342	V345	F346	S349	K350	P351	D352	S353	A354	P355	P356	R359	S360	A361	N362	C363	A364	F365	P366	I367	V370	R371	D372	F373	F374	N375	K376	I377	VAL	ASN	LYS	ASN	ASN	VAL	R384	C385	L386	Q387	H388	P392	N393	HIS

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	139.00Å 144.98Å 150.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 4.00 48.16 – 4.00	Depositor EDS
% Data completeness (in resolution range)	97.5 (15.00-4.00) 99.6 (48.16-4.00)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 4.00Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.251 , 0.301 0.260 , 0.294	Depositor DCC
$R_{free}$ test set	1302 reflections (4.98%)	DCC
Wilson B-factor (Å <sup>2</sup> )	119.6	Xtriage
Anisotropy	0.833	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 92.1	EDS
Estimated twinning fraction	0.088 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 26224 reflections	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	14329	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	136.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.29% 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 [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	0.23	0/2288	0.42	0/3105
1	C	0.24	0/2288	0.42	0/3105
2	B	0.33	1/5068 (0.0%)	0.47	1/6868 (0.0%)
2	D	0.33	2/4972 (0.0%)	0.48	0/6738
All	All	0.30	3/14616 (0.0%)	0.46	1/19816 (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
2	B	0	1
2	D	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	113	LYS	C-N	12.95	1.63	1.34
2	D	113	LYS	C-N	9.64	1.56	1.34
2	D	111	VAL	CB-CG2	-5.24	1.41	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	414	ASP	N-CA-C	-6.07	94.61	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
2	B	300	LEU	Peptide
2	D	300	LEU	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	2252	0	2323	125	0
1	C	2252	0	2323	111	0
2	B	4959	0	4832	301	0
2	D	4866	0	4760	270	0
All	All	14329	0	14238	781	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 27.

The worst 5 of 781 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:310:ARG:HG3	1:A:310:ARG:HH11	1.32	0.94
1:C:310:ARG:HH11	1:C:310:ARG:HG3	1.33	0.92
1:A:193:LEU:HD22	1:A:198:ILE:HD11	1.53	0.90
1:C:193:LEU:HD22	1:C:198:ILE:HD11	1.52	0.90
2:B:521:ARG:HE	2:B:546:VAL:HG23	1.37	0.90

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	284/289 (98%)	226 (80%)	54 (19%)	4 (1%)	14	59
1	C	284/289 (98%)	227 (80%)	53 (19%)	4 (1%)	14	59
2	B	610/727 (84%)	494 (81%)	101 (17%)	15 (2%)	7	49
2	D	598/727 (82%)	489 (82%)	96 (16%)	13 (2%)	8	52
All	All	1776/2032 (87%)	1436 (81%)	304 (17%)	36 (2%)	9	54

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	LEU
2	B	163	SER
2	B	164	PRO
2	B	211	LEU
2	B	276	THR

### 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	264/265 (100%)	251 (95%)	13 (5%)	31	69
1	C	264/265 (100%)	251 (95%)	13 (5%)	31	69
2	B	566/654 (86%)	524 (93%)	42 (7%)	17	56
2	D	555/654 (85%)	514 (93%)	41 (7%)	17	56
All	All	1649/1838 (90%)	1540 (93%)	109 (7%)	21	60

5 of 109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	648	GLN
1	C	207	LEU
2	D	599	LYS
2	B	660	THR
1	C	37	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	571	ASN
1	C	80	GLN
2	D	559	GLN
2	B	594	ASN
2	B	704	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](#)

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	286/289 (98%)	0.16	11 (3%) 44 34	89, 125, 174, 201	0
1	C	286/289 (98%)	0.07	3 (1%) 84 77	76, 112, 158, 191	0
2	B	630/727 (86%)	0.33	28 (4%) 38 28	87, 139, 208, 245	0
2	D	618/727 (85%)	0.41	31 (5%) 32 24	87, 137, 191, 236	0
All	All	1820/2032 (89%)	0.29	73 (4%) 42 31	76, 132, 192, 245	0

The worst 5 of 73 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	136	VAL	6.2
2	B	552	LEU	5.5
2	D	555	THR	5.3
2	D	135	SER	4.5
2	D	741	ASP	4.1

### 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 carbohydrates 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.