



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 8, 2017 – 03:32 PM EST

PDB ID : 4LC9  
Title : Structural Basis for Regulation of Human Glucokinase by Glucokinase Regulatory Protein  
Authors : Beck, T.; Miller, B.G.  
Deposited on : unknown  
Resolution : 3.40 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-20030345  
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-20030345

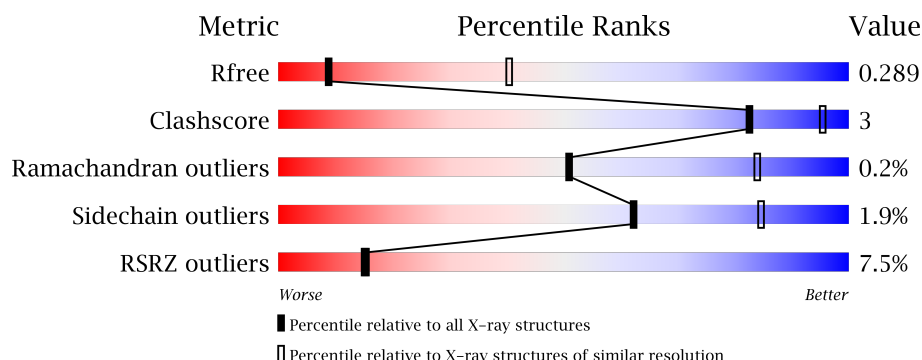
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


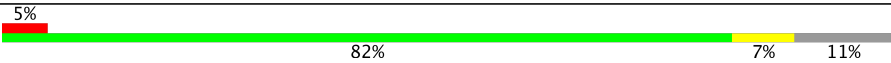
The reported resolution of this entry is 3.40 Å.

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	1679 (3.50-3.30)
Clashscore	112137	1832 (3.50-3.30)
Ramachandran outliers	110173	1789 (3.50-3.30)
Sidechain outliers	110143	1789 (3.50-3.30)
RSRZ outliers	101464	1709 (3.50-3.30)

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	636	
2	B	472	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7699 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 Glucokinase regulatory protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	567	4375	2783	754	815	23	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	628	SER	-	EXPRESSION TAG	UNP Q07071
A	629	LEU	-	EXPRESSION TAG	UNP Q07071
A	630	GLU	-	EXPRESSION TAG	UNP Q07071
A	631	HIS	-	EXPRESSION TAG	UNP Q07071
A	632	HIS	-	EXPRESSION TAG	UNP Q07071
A	633	HIS	-	EXPRESSION TAG	UNP Q07071
A	634	HIS	-	EXPRESSION TAG	UNP Q07071
A	635	HIS	-	EXPRESSION TAG	UNP Q07071
A	636	HIS	-	EXPRESSION TAG	UNP Q07071

- Molecule 2 is a protein called Glucokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	422	3307	2051	575	649	32	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

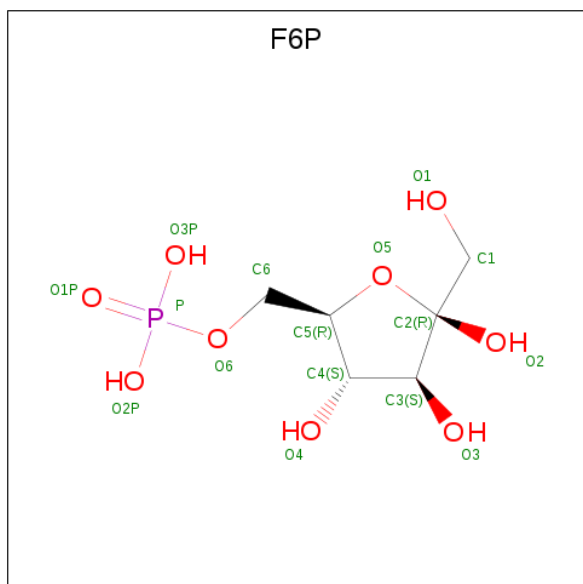
Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	MET	-	EXPRESSION TAG	UNP P35557
B	-5	HIS	-	EXPRESSION TAG	UNP P35557
B	-4	HIS	-	EXPRESSION TAG	UNP P35557
B	-3	HIS	-	EXPRESSION TAG	UNP P35557
B	-2	HIS	-	EXPRESSION TAG	UNP P35557
B	-1	HIS	-	EXPRESSION TAG	UNP P35557
B	0	HIS	-	EXPRESSION TAG	UNP P35557

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	EXPRESSION TAG	UNP P35557
B	2	VAL	-	EXPRESSION TAG	UNP P35557

- Molecule 3 is FRUCTOSE-6-PHOSPHATE (three-letter code: F6P) (formula:  $C_6H_{13}O_9P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			16	6	9	1		

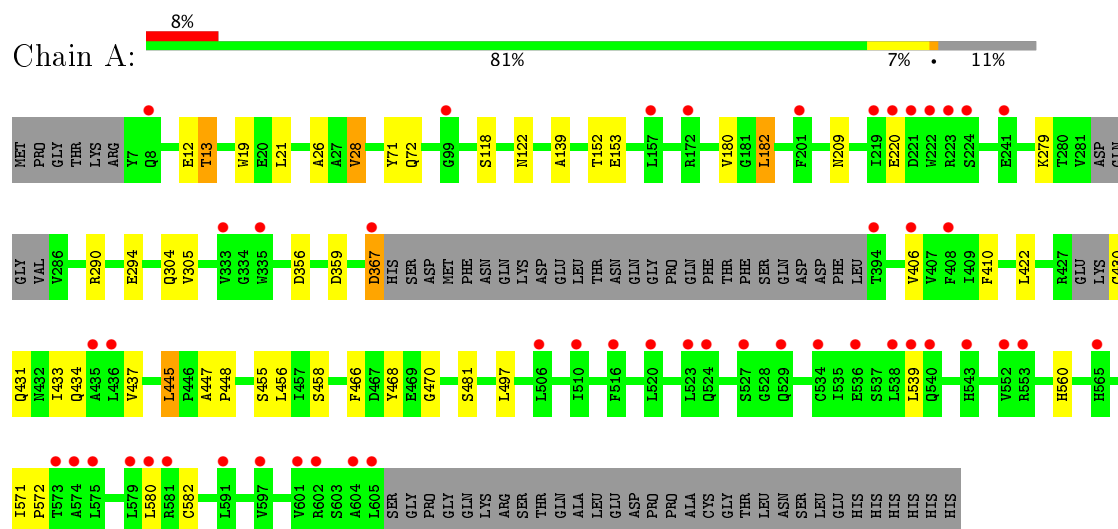
- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Na	0	0
			1	1		

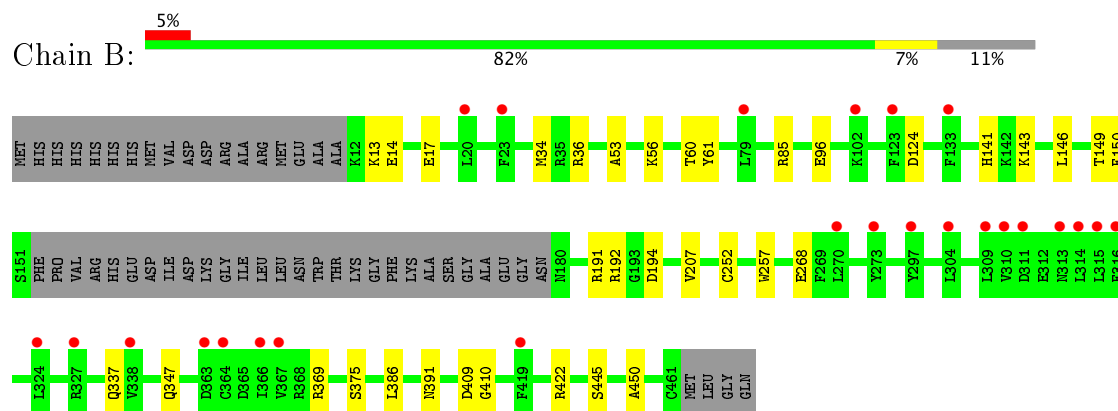
### 3 Residue-property plots [i](#)

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: Glucokinase regulatory protein



- Molecule 2: Glucokinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.66Å 105.31Å 132.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.93 – 3.40 48.93 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.93-3.40) 94.1 (48.93-3.40)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.38 (at 3.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.244 , 0.292 0.243 , 0.289	Depositor DCC
$R_{free}$ test set	920 reflections (5.16%)	DCC
Wilson B-factor (Å <sup>2</sup> )	131.4	Xtriage
Anisotropy	0.344	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 59.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7699	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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: NA, F6P

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	0.31	0/4448	0.53	0/6016
2	B	0.32	0/3353	0.46	0/4501
All	All	0.32	0/7801	0.50	0/10517

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	4375	0	4486	27	0
2	B	3307	0	3256	18	0
3	A	16	0	11	1	0
4	B	1	0	0	0	0
All	All	7699	0	7753	44	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 3.

All (44) 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)
2:B:13:LYS:O	2:B:14:GLU:HG2	1.64	0.96
2:B:13:LYS:O	2:B:14:GLU:CG	2.35	0.73
1:A:12:GLU:OE1	1:A:13:THR:N	2.30	0.65
2:B:17:GLU:OE2	2:B:369:ARG:NH1	2.34	0.61
2:B:337:GLN:NE2	2:B:347:GLN:OE1	2.36	0.58
1:A:434:GLN:NE2	1:A:455:SER:O	2.38	0.57
1:A:118:SER:O	1:A:122:ASN:ND2	2.38	0.56
1:A:26:ALA:HB1	1:A:28:VAL:HG12	1.89	0.55
2:B:13:LYS:C	2:B:14:GLU:HG2	2.28	0.53
1:A:182:LEU:CD1	1:A:209:ASN:HB2	2.40	0.52
2:B:409:ASP:OD2	2:B:410:GLY:N	2.44	0.50
1:A:26:ALA:HB1	1:A:28:VAL:CG1	2.42	0.50
2:B:96:GLU:N	2:B:96:GLU:OE2	2.44	0.49
2:B:124:ASP:OD1	2:B:191:ARG:NH2	2.45	0.49
1:A:220:GLU:N	1:A:220:GLU:OE1	2.47	0.47
1:A:466:PHE:HB2	1:A:470:GLY:HA2	1.97	0.46
1:A:180:VAL:N	3:A:701:F6P:O3P	2.46	0.45
1:A:356:ASP:OD1	1:A:359:ASP:N	2.50	0.45
1:A:21:LEU:HG	1:A:71:TYR:CE2	2.52	0.44
2:B:36:ARG:NH2	2:B:268:GLU:OE2	2.50	0.44
1:A:406:VAL:CG1	1:A:433:ILE:HD11	2.47	0.44
2:B:192:ARG:NE	2:B:194:ASP:OD2	2.47	0.44
1:A:410:PHE:CZ	1:A:437:VAL:CG1	3.01	0.44
2:B:60:THR:OG1	2:B:252:CYS:O	2.35	0.44
2:B:375:SER:OG	2:B:422:ARG:NH1	2.50	0.44
2:B:445:SER:HB3	2:B:450:ALA:HA	1.98	0.43
2:B:61:TYR:CZ	2:B:143:LYS:HD3	2.54	0.43
1:A:431:GLN:N	1:A:431:GLN:OE1	2.51	0.43
1:A:290:ARG:NH1	1:A:294:GLU:OE2	2.52	0.43
1:A:456:LEU:CD1	1:A:458:SER:HB2	2.48	0.43
2:B:34:MET:SD	2:B:391:ASN:ND2	2.92	0.43
1:A:304:GLN:HG3	1:A:305:VAL:N	2.33	0.42
1:A:139:ALA:CB	1:A:153:GLU:HG3	2.50	0.42
1:A:539:LEU:HD22	1:A:560:HIS:CD2	2.54	0.42
1:A:367:ASP:N	1:A:367:ASP:OD1	2.54	0.41
1:A:19:TRP:CZ2	1:A:21:LEU:HD22	2.56	0.41
1:A:571:ILE:N	1:A:572:PRO:HD2	2.35	0.41
1:A:445:LEU:CD1	1:A:445:LEU:H	2.34	0.41
2:B:85:ARG:HH11	2:B:85:ARG:HG2	1.86	0.41
1:A:139:ALA:HB1	1:A:152:THR:HG23	2.02	0.41
1:A:447:ALA:N	1:A:448:PRO:CD	2.84	0.41
1:A:279:LYS:HE3	1:A:466:PHE:CD2	2.56	0.41

Continued on next page...



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:53:ALA:O	2:B:56:LYS:NZ	2.37	0.41
1:A:468:TYR:H	2:B:141:HIS:HB3	1.87	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	559/636 (88%)	535 (96%)	22 (4%)	2 (0%)	38	75
2	B	418/472 (89%)	396 (95%)	22 (5%)	0	100	100
All	All	977/1108 (88%)	931 (95%)	44 (4%)	2 (0%)	51	84

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	28	VAL

### 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	482/543 (89%)	472 (98%)	10 (2%)	59	83
2	B	364/404 (90%)	358 (98%)	6 (2%)	68	86

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	846/947 (89%)	830 (98%)	16 (2%)	62 84

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	THR
1	A	182	LEU
1	A	367	ASP
1	A	422	LEU
1	A	430	CYS
1	A	445	LEU
1	A	481	SER
1	A	497	LEU
1	A	580	LEU
1	A	582	CYS
2	B	146	LEU
2	B	149	THR
2	B	150	PHE
2	B	207	VAL
2	B	257	TRP
2	B	386	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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
3	F6P	A	701	-	15,16,16	0.95	1 (6%)	17,25,25	0.77	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
3	F6P	A	701	-	-	0/9/28/28	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	701	F6P	O2-C2	2.87	1.45	1.40

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
3	A	701	F6P	1	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 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	567/636 (89%)	0.59	49 (8%)	11 12	46, 107, 153, 170	0
2	B	422/472 (89%)	0.39	25 (5%)	23 22	39, 78, 118, 146	0
All	All	989/1108 (89%)	0.51	74 (7%)	15 15	39, 92, 146, 170	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	527	SER	6.5
1	A	540	GLN	5.6
2	B	315	LEU	5.3
1	A	219	ILE	4.9
1	A	580	LEU	4.8
2	B	314	LEU	4.5
1	A	223	ARG	4.4
2	B	364	CYS	4.2
1	A	573	THR	4.1
1	A	605	LEU	3.8
1	A	224	SER	3.8
2	B	313	ASN	3.8
1	A	581	ARG	3.8
1	A	529	GLN	3.7
1	A	534	CYS	3.7
2	B	297	TYR	3.4
1	A	536	GLU	3.4
1	A	222	TRP	3.3
1	A	394	THR	3.1
1	A	538	LEU	3.1
2	B	324	LEU	3.0
1	A	520	LEU	2.9
1	A	524	GLN	2.9
1	A	523	LEU	2.9

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
2	B	419	PHE	2.9
1	A	597	VAL	2.8
2	B	23	PHE	2.8
1	A	241	GLU	2.7
1	A	367	ASP	2.7
2	B	316	PHE	2.7
2	B	270	LEU	2.7
1	A	591	LEU	2.7
1	A	506	LEU	2.7
1	A	552	VAL	2.6
1	A	602	ARG	2.6
2	B	311	ASP	2.6
2	B	273	TYR	2.6
2	B	133	PHE	2.6
2	B	363	ASP	2.6
1	A	172	ARG	2.5
1	A	553	ARG	2.5
1	A	8	GLN	2.5
2	B	366	ILE	2.5
1	A	333	VAL	2.5
1	A	579	LEU	2.5
2	B	20	LEU	2.5
2	B	310	VAL	2.4
1	A	575	LEU	2.4
1	A	157	LEU	2.3
1	A	408	PHE	2.3
1	A	335	TRP	2.3
1	A	543	HIS	2.3
1	A	201	PHE	2.3
1	A	516	PHE	2.3
1	A	539	LEU	2.3
1	A	436	LEU	2.3
1	A	435	ALA	2.2
2	B	338	VAL	2.2
2	B	102	LYS	2.2
2	B	367	VAL	2.2
2	B	327	ARG	2.2
1	A	604	ALA	2.1
1	A	221	ASP	2.1
1	A	510	ILE	2.1
1	A	601	VAL	2.1
2	B	309	LEU	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
2	B	304	LEU	2.1
1	A	99	GLY	2.1
1	A	406	VAL	2.1
2	B	79	LEU	2.1
1	A	220	GLU	2.1
1	A	574	ALA	2.1
2	B	123	PHE	2.0
1	A	565	HIS	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	NA	B	501	1/1	0.88	0.25	0.85	34,34,34,34	0
3	F6P	A	701	16/16	0.83	0.26	-0.07	87,105,123,125	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.