



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:34 PM GMT

PDB ID : 1PNZ  
Title : Crystal structure of ferric citrate transporter FecA in the unliganded form  
Authors : Yue, W.W.; Grizot, S.; Buchanan, S.K.  
Deposited on : 2003-06-13  
Resolution : 2.50 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

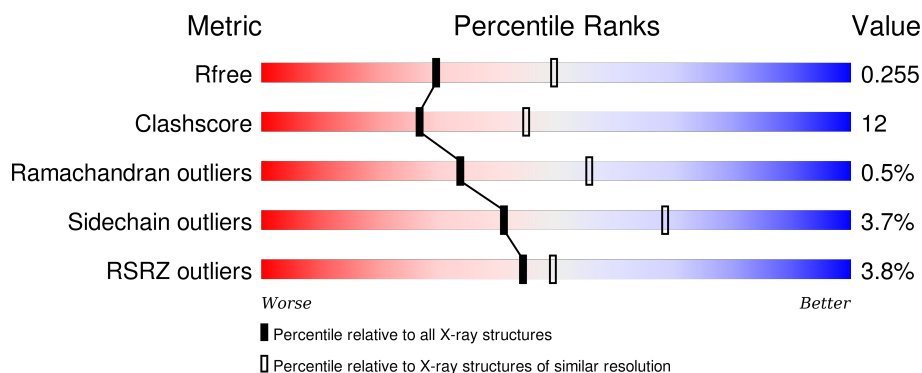
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	751	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5355 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 Iron(III) dicitrate transport protein fecA precursor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	661	Total	C	N	O	S	0	0	0
			5168	3236	907	1012	13			

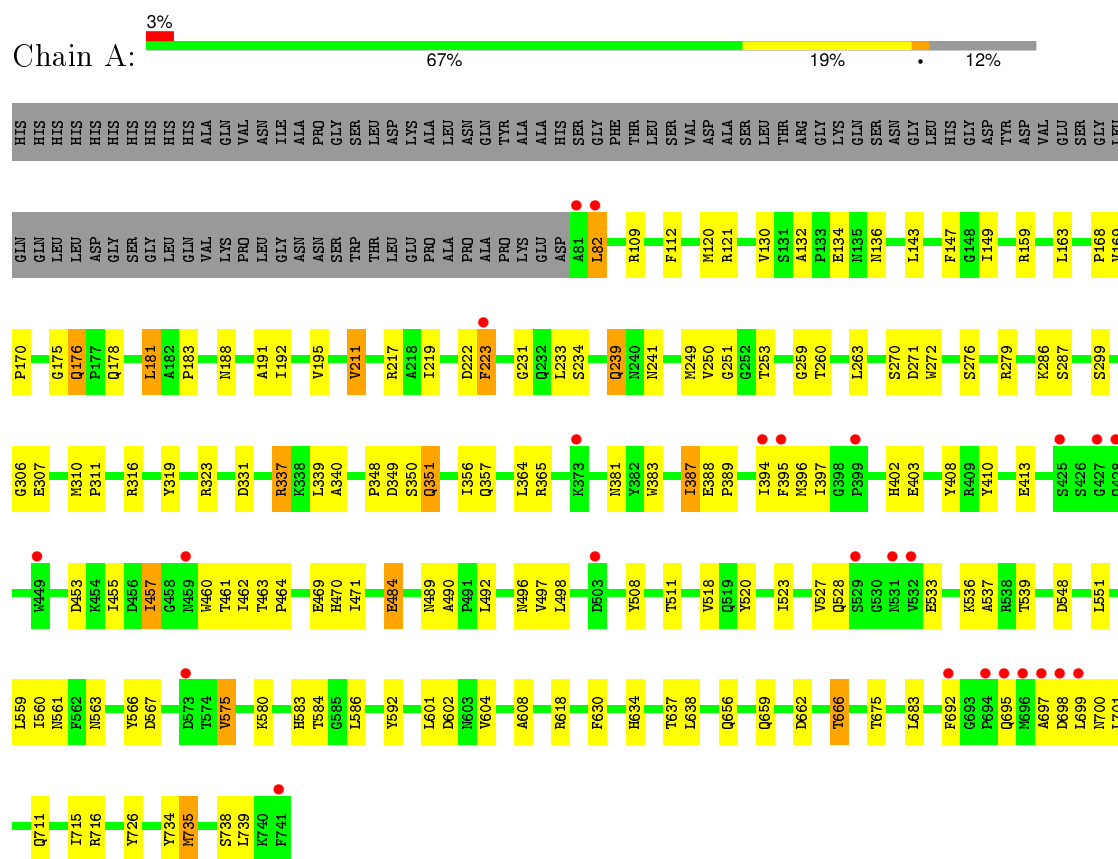
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	187	Total	O	0	0
			187	187		

### 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: Iron(III) dicitrate transport protein fecA precursor



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	117.05Å 88.46Å 95.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.82 – 2.50 49.87 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.82-2.50) 99.8 (49.87-2.50)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.03 (at 2.51Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.223 , 0.259 0.221 , 0.255	Depositor DCC
$R_{free}$ test set	1742 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.1	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 45.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 34927 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	5355	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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	0.36	0/5299	0.63	0/7201

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 [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	5168	0	4870	121	0
2	A	187	0	0	5	0
All	All	5355	0	4870	121	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 12.

All (121) 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:82:LEU:HD11	1:A:396:MET:HG2	1.41	0.98
1:A:253:THR:HG22	1:A:259:GLY:HA3	1.53	0.87
1:A:395:PHE:HE1	1:A:397:ILE:HD11	1.51	0.76
1:A:175:GLY:HA3	1:A:520:TYR:CE2	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:VAL:HB	1:A:211:VAL:HG13	1.73	0.71
1:A:692:PHE:CD1	1:A:699:LEU:HD12	2.27	0.69
1:A:351:GLN:HE21	1:A:351:GLN:N	1.93	0.65
1:A:700:ASN:HB2	1:A:738:SER:OG	1.97	0.64
1:A:287:SER:HB2	1:A:299:SER:OG	1.96	0.64
1:A:181:LEU:HD13	1:A:183:PRO:HD3	1.80	0.63
1:A:662:ASP:OD2	1:A:666:THR:HG23	1.98	0.63
1:A:395:PHE:CE1	1:A:397:ILE:HD11	2.33	0.63
1:A:715:ILE:HG12	1:A:716:ARG:H	1.65	0.62
1:A:217:ARG:HG3	1:A:263:LEU:HD22	1.83	0.60
1:A:457:ILE:HG23	1:A:457:ILE:O	2.01	0.59
1:A:175:GLY:HA3	1:A:520:TYR:CZ	2.38	0.58
1:A:563:ASN:HD21	1:A:580:LYS:NZ	2.02	0.58
1:A:356:ILE:HD11	1:A:387:ILE:HD11	1.86	0.58
1:A:470:HIS:ND1	1:A:489:ASN:ND2	2.52	0.57
1:A:176:GLN:NE2	1:A:178:GLN:OE1	2.38	0.57
1:A:453:ASP:O	1:A:464:PRO:HD2	2.04	0.57
1:A:191:ALA:C	1:A:192:ILE:HD12	2.25	0.57
1:A:699:LEU:HD23	1:A:739:LEU:HD21	1.86	0.56
1:A:715:ILE:HG12	1:A:716:ARG:N	2.21	0.56
1:A:143:LEU:HD21	1:A:306:GLY:C	2.27	0.55
1:A:461:THR:HB	1:A:498:LEU:HB3	1.89	0.55
1:A:388:GLU:HG3	1:A:408:TYR:O	2.06	0.54
1:A:260:THR:HG22	1:A:287:SER:OG	2.07	0.54
1:A:130:VAL:HG22	1:A:149:ILE:CD1	2.36	0.54
1:A:239:GLN:NE2	1:A:270:SER:HB2	2.22	0.54
1:A:634:HIS:O	1:A:656:GLN:HA	2.08	0.53
1:A:233:LEU:HG	1:A:234:SER:N	2.24	0.53
1:A:136:ASN:HA	1:A:726:TYR:CE2	2.44	0.53
1:A:395:PHE:HE1	1:A:397:ILE:CD1	2.21	0.52
1:A:387:ILE:HD13	1:A:388:GLU:N	2.25	0.51
1:A:470:HIS:HA	1:A:489:ASN:HD22	1.76	0.51
1:A:121:ARG:NH2	1:A:134:GLU:HG3	2.26	0.51
1:A:457:ILE:C	1:A:457:ILE:HD13	2.30	0.50
1:A:169:VAL:N	1:A:170:PRO:CD	2.74	0.50
1:A:402:HIS:CD2	1:A:455:ILE:HG23	2.47	0.50
1:A:364:LEU:HD23	1:A:381:ASN:OD1	2.11	0.50
1:A:462:ILE:HD12	1:A:462:ILE:N	2.27	0.50
1:A:711:GLN:HG2	2:A:815:HOH:O	2.11	0.49
1:A:394:ILE:HA	1:A:402:HIS:O	2.13	0.49
1:A:697:ALA:O	1:A:698:ASP:C	2.50	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:GLN:HG3	1:A:394:ILE:HD11	1.96	0.48
1:A:537:ALA:HA	1:A:561:ASN:O	2.13	0.48
1:A:188:ASN:O	1:A:217:ARG:HG2	2.13	0.48
1:A:339:LEU:C	1:A:339:LEU:HD23	2.34	0.48
1:A:222:ASP:O	1:A:223:PHE:C	2.53	0.47
1:A:82:LEU:HB3	1:A:394:ILE:HD12	1.96	0.47
1:A:176:GLN:HG3	2:A:863:HOH:O	2.13	0.47
1:A:159:ARG:NH2	2:A:745:HOH:O	2.06	0.47
1:A:249:MET:HG2	1:A:263:LEU:HD23	1.96	0.47
1:A:231:GLY:O	1:A:734:TYR:HA	2.14	0.47
1:A:638:LEU:N	1:A:638:LEU:HD23	2.31	0.46
1:A:319:TYR:CE1	1:A:323:ARG:HB2	2.51	0.46
1:A:551:LEU:HD13	1:A:551:LEU:C	2.36	0.46
1:A:463:THR:HB	1:A:496:ASN:ND2	2.30	0.46
1:A:699:LEU:HD23	1:A:739:LEU:CD2	2.45	0.46
1:A:351:GLN:HG3	1:A:394:ILE:HG13	1.98	0.46
1:A:460:TRP:HB3	1:A:462:ILE:HD11	1.98	0.46
1:A:697:ALA:HB3	1:A:739:LEU:HD22	1.98	0.46
1:A:364:LEU:HD13	1:A:364:LEU:C	2.36	0.45
1:A:533:GLU:HG3	1:A:536:LYS:HE3	1.97	0.45
1:A:176:GLN:HE21	1:A:176:GLN:CA	2.28	0.45
1:A:497:VAL:O	1:A:508:TYR:HA	2.17	0.45
1:A:394:ILE:HG22	1:A:403:GLU:HB2	1.98	0.45
1:A:490:ALA:O	1:A:492:LEU:HD22	2.18	0.44
1:A:350:SER:C	1:A:351:GLN:HE21	2.21	0.44
1:A:217:ARG:HG2	1:A:217:ARG:H	1.64	0.44
1:A:169:VAL:O	1:A:337:ARG:NH2	2.43	0.44
1:A:339:LEU:HD23	1:A:340:ALA:N	2.33	0.44
1:A:316:ARG:HD3	1:A:316:ARG:O	2.18	0.44
1:A:551:LEU:HB2	1:A:592:TYR:CD1	2.53	0.44
1:A:469:GLU:HB3	1:A:471:ILE:HD11	1.98	0.44
1:A:559:LEU:HD13	1:A:584:THR:HG22	1.99	0.44
1:A:699:LEU:HD13	1:A:699:LEU:C	2.37	0.44
1:A:250:VAL:HG23	1:A:250:VAL:O	2.18	0.44
1:A:271:ASP:HB2	1:A:272:TRP:CE3	2.53	0.43
1:A:520:TYR:HA	1:A:523:ILE:HG13	2.00	0.43
1:A:533:GLU:HG3	1:A:536:LYS:CE	2.48	0.43
1:A:518:VAL:HG22	1:A:566:TYR:CE1	2.53	0.43
1:A:508:TYR:CD1	1:A:508:TYR:C	2.92	0.43
1:A:560:ILE:HB	1:A:583:HIS:HB2	2.01	0.43
1:A:618:ARG:HD3	1:A:618:ARG:HA	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:ARG:NE	1:A:307:GLU:OE2	2.47	0.43
1:A:630:PHE:HA	1:A:659:GLN:OE1	2.18	0.43
1:A:586:LEU:HD23	1:A:586:LEU:C	2.38	0.43
1:A:348:PRO:HG2	1:A:349:ASP:H	1.84	0.43
1:A:253:THR:HA	1:A:259:GLY:HA2	2.01	0.42
1:A:192:ILE:HD12	1:A:192:ILE:N	2.34	0.42
1:A:457:ILE:CG2	1:A:457:ILE:O	2.67	0.42
1:A:121:ARG:CZ	1:A:134:GLU:HG3	2.50	0.42
1:A:389:PRO:HD2	1:A:408:TYR:O	2.19	0.42
1:A:735:MET:O	1:A:735:MET:HG3	2.19	0.42
1:A:239:GLN:NE2	1:A:241:ASN:O	2.50	0.42
1:A:608:ALA:HA	1:A:637:THR:O	2.20	0.42
1:A:601:LEU:O	1:A:604:VAL:HB	2.19	0.42
1:A:563:ASN:HD21	1:A:580:LYS:HZ2	1.67	0.42
1:A:511:THR:HA	1:A:539:THR:O	2.20	0.42
1:A:176:GLN:HE21	1:A:176:GLN:HA	1.84	0.41
1:A:460:TRP:HB3	1:A:462:ILE:CD1	2.50	0.41
1:A:548:ASP:C	1:A:548:ASP:OD1	2.58	0.41
1:A:692:PHE:CE1	1:A:699:LEU:HD12	2.55	0.41
1:A:349:ASP:HB3	2:A:924:HOH:O	2.19	0.41
1:A:528:GLN:NE2	1:A:575:VAL:HG21	2.36	0.41
1:A:260:THR:HA	1:A:286:LYS:O	2.19	0.41
1:A:387:ILE:HG22	1:A:410:TYR:HB3	2.03	0.41
1:A:484:GLU:HG2	1:A:527:VAL:HG21	2.01	0.41
1:A:310:MET:HB2	1:A:331:ASP:HB3	2.02	0.41
1:A:383:TRP:O	1:A:413:GLU:HA	2.19	0.41
1:A:223:PHE:HA	1:A:251:GLY:O	2.21	0.41
1:A:147:PHE:CD1	1:A:147:PHE:C	2.94	0.41
1:A:276:SER:HB3	1:A:311:PRO:HG3	2.02	0.41
1:A:394:ILE:HG22	1:A:403:GLU:CB	2.51	0.40
1:A:163:LEU:HD23	1:A:168:PRO:HA	2.03	0.40
1:A:219:ILE:HD12	1:A:219:ILE:N	2.37	0.40
1:A:121:ARG:HB2	1:A:132:ALA:HB1	2.03	0.40
1:A:159:ARG:NH1	2:A:772:HOH:O	2.37	0.40
1:A:109:ARG:HA	1:A:112:PHE:CE2	2.57	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	659/751 (88%)	631 (96%)	25 (4%)	3 (0%)	34	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	LEU
1	A	695	GLN
1	A	223	PHE

### 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	540/617 (88%)	520 (96%)	20 (4%)	41	68

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	120	MET
1	A	176	GLN
1	A	181	LEU
1	A	211	VAL
1	A	239	GLN
1	A	337	ARG
1	A	351	GLN
1	A	357	GLN

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Mol	Chain	Res	Type
1	A	365	ARG
1	A	387	ILE
1	A	457	ILE
1	A	484	GLU
1	A	567	ASP
1	A	575	VAL
1	A	602	ASP
1	A	666	THR
1	A	675	THR
1	A	683	LEU
1	A	701	LEU
1	A	735	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	176	GLN
1	A	240	ASN
1	A	325	GLN
1	A	351	GLN
1	A	489	ASN
1	A	496	ASN
1	A	563	ASN
1	A	729	GLN

### 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

There are no ligands in this entry.

## 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	661/751 (88%)	-0.00	25 (3%)	44 49	6, 19, 39, 81	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	696	MET	6.6
1	A	695	GLN	6.5
1	A	81	ALA	5.8
1	A	697	ALA	4.7
1	A	694	PRO	4.2
1	A	532	VAL	3.8
1	A	741	PHE	3.8
1	A	428	GLN	3.6
1	A	503	ASP	3.3
1	A	698	ASP	3.2
1	A	82	LEU	3.1
1	A	529	SER	2.8
1	A	427	GLY	2.7
1	A	699	LEU	2.7
1	A	395	PHE	2.6
1	A	531	ASN	2.6
1	A	399	PRO	2.5
1	A	223	PHE	2.5
1	A	692	PHE	2.4
1	A	573	ASP	2.4
1	A	425	SER	2.4
1	A	373	LYS	2.4
1	A	394	ILE	2.3
1	A	449	TRP	2.3
1	A	459	ASN	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 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.