



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 06:51 PM GMT

PDB ID : 3LI2  
Title : Closed Conformation of HtsA Complexed with Staphyloferrin A  
Authors : Grigg, J.C.; Murphy, M.E.P.  
Deposited on : 2010-01-23  
Resolution : 2.20 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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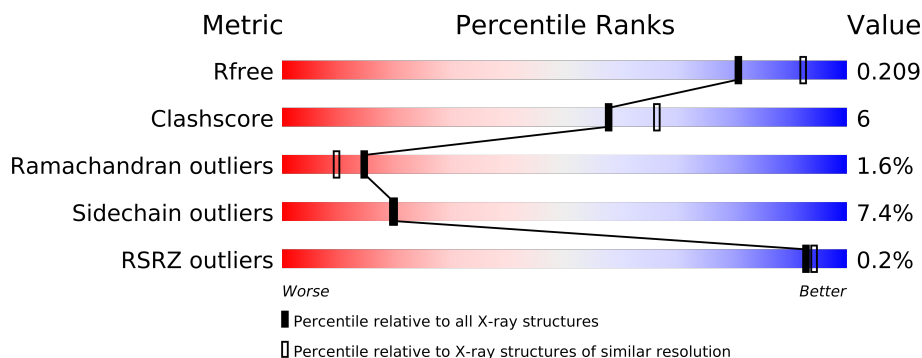
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.20 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))
$R_{free}$	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	296	
1	B	296	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4945 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Ferrichrome ABC transporter lipoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	4	0
			2316	1466	408	439	3			
1	B	289	Total	C	N	O	S	0	5	0
			2333	1478	410	442	3			

There are 14 discrepancies between the modelled and reference sequences:

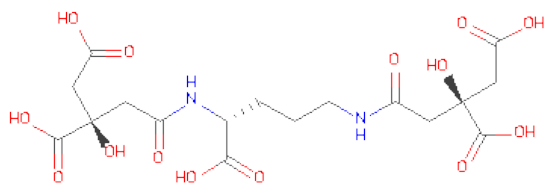
Chain	Residue	Modelled	Actual	Comment	Reference
A	32	GLY	-	EXPRESSION TAG	UNP A6QJ18
A	33	SER	-	EXPRESSION TAG	UNP A6QJ18
A	34	HIS	-	EXPRESSION TAG	UNP A6QJ18
A	35	MET	-	EXPRESSION TAG	UNP A6QJ18
A	36	ALA	-	EXPRESSION TAG	UNP A6QJ18
A	37	SER	-	EXPRESSION TAG	UNP A6QJ18
A	38	THR	-	EXPRESSION TAG	UNP A6QJ18
B	32	GLY	-	EXPRESSION TAG	UNP A6QJ18
B	33	SER	-	EXPRESSION TAG	UNP A6QJ18
B	34	HIS	-	EXPRESSION TAG	UNP A6QJ18
B	35	MET	-	EXPRESSION TAG	UNP A6QJ18
B	36	ALA	-	EXPRESSION TAG	UNP A6QJ18
B	37	SER	-	EXPRESSION TAG	UNP A6QJ18
B	38	THR	-	EXPRESSION TAG	UNP A6QJ18

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Fe	0	0
			1	1		
2	A	1	Total	Fe	0	0
			1	1		

- Molecule 3 is (2R)-2-(2-{[(1R)-1-CARBOXY-4-{[(3S)-3,4-DICARBOXY-3-HYDROXY

BUTANOYL]AMINO}BUTYL]AMINO}-2-OXOETHYL)-2-HYDROXYBUTANEDIOI  
CACID (three-letter code: SF8) (formula: C<sub>17</sub>H<sub>24</sub>N<sub>2</sub>O<sub>14</sub>).

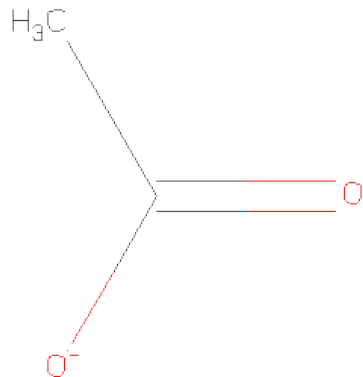


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			33	17	2	14		
3	B	1	Total	C	N	O	0	0
			33	17	2	14		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Zn	0	0
			4	4		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is water.

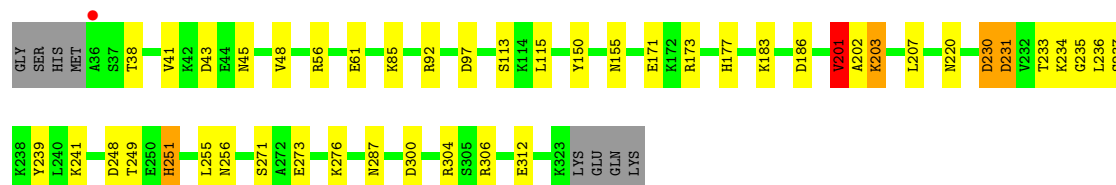
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	102	Total	O	0	0
			102	102		
6	B	118	Total	O	0	0
			118	118		

### 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.

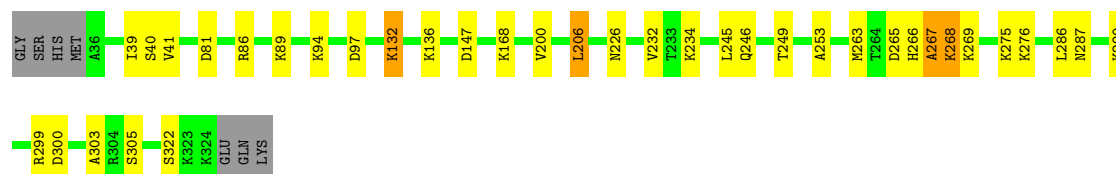
- Molecule 1: Ferrichrome ABC transporter lipoprotein

Chain A: 



- Molecule 1: Ferrichrome ABC transporter lipoprotein

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.28Å 148.60Å 52.27Å 90.00° 117.14° 90.00°	Depositor
Resolution (Å)	33.15 – 2.20 33.15 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.0 (33.15-2.20) 99.1 (33.15-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.75 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.165 , 0.216 0.163 , 0.209	Depositor DCC
$R_{free}$ test set	1785 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.4	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 23.2	EDS
Estimated twinning fraction	0.509 for H, K, L 0.491 for L, -K, H 0.017 for l,k,-h-l 0.017 for -h-l,k,h 0.023 for -h-l,-k,l 0.022 for h,-k,-h-l 0.477 for l,-k,h	Xtriage
Reported twinning fraction	0.509 for H, K, L 0.491 for L, -K, H	Depositor
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 35627 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4945	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.19% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, FE, SF8, ACT

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	0.61	0/2349	0.69	0/3154
1	B	0.59	0/2366	0.70	0/3173
All	All	0.60	0/4715	0.70	0/6327

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
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	201	VAL	Peptide
1	B	269	LYS	Peptide

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the



chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2316	0	0	18	0
1	B	2333	0	0	12	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	33	0	17	2	0
3	B	33	0	17	2	0
4	A	4	0	0	0	0
5	A	4	0	3	0	0
6	A	102	0	0	3	0
6	B	118	0	0	2	0
All	All	4945	0	37	30	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (30) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:248:ASP:OD2	1:A:251:HIS:N	2.13	0.80
1:B:200:VAL:O	1:B:206:LEU:O	2.02	0.78
1:B:132[A]:LYS:CB	1:B:132[A]:LYS:NZ	2.50	0.73
1:A:201:VAL:CG2	1:A:201:VAL:O	2.48	0.61
1:A:203:LYS:NZ	6:A:414:HOH:O	2.35	0.58
1:B:299:ARG:NH2	3:B:501:SF8:H8A	2.20	0.57
1:B:263:MET:CE	1:B:303:ALA:CB	2.83	0.56
1:A:306:ARG:NH1	3:A:501:SF8:O33	2.40	0.54
1:A:173[A]:ARG:NH2	1:A:312:GLU:OE2	2.44	0.51
1:A:233:THR:O	1:A:235:GLY:O	2.30	0.50
1:B:300:ASP:O	1:B:305:SER:OG	2.31	0.49
1:A:61:GLU:OE2	1:A:306:ARG:NH2	2.46	0.49
1:A:183:LYS:NZ	6:A:407:HOH:O	2.45	0.48
1:A:202:ALA:O	1:A:203:LYS:CB	2.61	0.48
1:A:56:ARG:NH2	1:A:115:LEU:O	2.46	0.47
1:B:81:ASP:OD2	1:B:86:ARG:NH1	2.48	0.46
1:A:239:TYR:CE1	3:A:501:SF8:H8	2.51	0.46
1:B:168:LYS:NZ	6:B:391:HOH:O	2.48	0.46
1:B:299:ARG:NH2	3:B:501:SF8:O23	2.50	0.44
1:B:286:LEU:O	1:B:287:ASN:C	2.56	0.44
1:A:202:ALA:CB	1:A:207:LEU:CD2	2.95	0.44
1:A:256:ASN:OD1	1:A:287:ASN:N	2.50	0.43
1:B:267:ALA:N	6:B:10:HOH:O	2.52	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:300:ASP:OD1	1:A:304:ARG:NH1	2.51	0.43
1:A:43:ASP:OD1	1:A:45:ASN:N	2.53	0.42
1:B:266:HIS:O	1:B:268:LYS:N	2.53	0.41
1:A:41:VAL:O	1:A:48:VAL:N	2.53	0.41
1:A:150:TYR:OH	1:A:177:HIS:NE2	2.54	0.41
1:A:220:ASN:ND2	6:A:392:HOH:O	2.53	0.41
1:B:249:THR:O	1:B:253:ALA:N	2.55	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	290/296 (98%)	271 (93%)	13 (4%)	6 (2%)	11	5
1	B	292/296 (99%)	275 (94%)	14 (5%)	3 (1%)	22	18
All	All	582/592 (98%)	546 (94%)	27 (5%)	9 (2%)	14	10

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	203	LYS
1	A	236	LEU
1	A	271	SER
1	B	267	ALA
1	A	230	ASP
1	A	231	ASP
1	B	268	LYS
1	A	234	LYS
1	B	290	LYS

### 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	254/257 (99%)	236 (93%)	18 (7%)	21	21
1	B	256/257 (100%)	236 (92%)	20 (8%)	18	17
All	All	510/514 (99%)	472 (92%)	38 (8%)	20	19

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	THR
1	A	85	LYS
1	A	92	ARG
1	A	97	ASP
1	A	113	SER
1	A	155	ASN
1	A	171	GLU
1	A	186	ASP
1	A	201	VAL
1	A	230	ASP
1	A	231	ASP
1	A	237	SER
1	A	241	LYS
1	A	249	THR
1	A	251	HIS
1	A	255	LEU
1	A	273	GLU
1	A	276	LYS
1	B	39	ILE
1	B	40	SER
1	B	41	VAL
1	B	89	LYS
1	B	94	LYS
1	B	97	ASP
1	B	132[A]	LYS
1	B	132[B]	LYS
1	B	136	LYS
1	B	147	ASP
1	B	206	LEU

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Mol	Chain	Res	Type
1	B	226	ASN
1	B	232	VAL
1	B	234	LYS
1	B	245	LEU
1	B	246	GLN
1	B	265	ASP
1	B	275	LYS
1	B	276	LYS
1	B	322	SER

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 chains 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 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	$\# Z  > 2$
5	ACT	A	14	-	1,3,3	1.39	0	0,3,3	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SF8	A	501	2	32,32,32	0.87	1 (3%)	45,45,45	1.82	8 (17%)
3	SF8	B	501	2	32,32,32	1.18	2 (6%)	45,45,45	1.87	12 (26%)

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
5	ACT	A	14	-	-	0/0/0/0	0/0/0/0
3	SF8	A	501	2	-	0/47/47/47	0/0/0/0
3	SF8	B	501	2	-	0/47/47/47	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	SF8	C3-C20	-4.01	1.48	1.53
3	B	501	SF8	C13-C12	2.67	1.54	1.51
3	A	501	SF8	C3-C20	-2.08	1.51	1.53

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	SF8	O31-C28-C14	6.85	122.85	112.89
3	B	501	SF8	O31-C28-C14	4.59	119.56	112.89
3	A	501	SF8	O29-C14-C28	-4.44	102.56	108.95
3	B	501	SF8	O21-C20-C3	-4.34	116.22	122.20
3	B	501	SF8	O22-C20-C3	4.08	118.83	112.89
3	B	501	SF8	C8-C7-N6	3.35	117.22	110.83
3	B	501	SF8	O30-C28-C14	-3.26	117.71	122.20
3	A	501	SF8	O30-C28-C14	-3.15	117.85	122.20
3	A	501	SF8	O19-C3-C20	-3.15	104.41	108.95
3	B	501	SF8	O19-C3-C20	-3.08	104.51	108.95
3	B	501	SF8	C13-C12-N11	3.03	119.04	115.68
3	A	501	SF8	O23-C5-C4	-2.86	118.30	121.88
3	A	501	SF8	O22-C20-C3	2.77	116.92	112.89
3	A	501	SF8	C4-C5-N6	2.74	118.89	115.85
3	B	501	SF8	O27-C12-C13	-2.44	118.83	121.88
3	B	501	SF8	O17-C1-C2	-2.27	115.54	122.74
3	B	501	SF8	C3-C4-C5	-2.20	108.39	113.77
3	A	501	SF8	O18-C1-C2	2.19	122.34	114.63
3	B	501	SF8	O23-C5-C4	-2.11	119.24	121.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	SF8	O18-C1-C2	2.01	121.73	114.63

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	288/296 (97%)	-0.48	1 (0%) 91 93	17, 35, 57, 70	0
1	B	289/296 (97%)	-0.44	0 100 100	17, 36, 54, 61	0
All	All	577/592 (97%)	-0.46	1 (0%) 93 94	17, 36, 56, 70	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	36	ALA	3.2

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	SF8	A	501	33/33	0.11	-0.29	15,24,36,37	0
4	ZN	A	2	1/1	0.11	-0.30	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	ZN	A	3	1/1	0.11	-0.42	23,23,23,23	0
4	ZN	A	4	1/1	0.10	-0.60	34,34,34,34	0
3	SF8	B	501	33/33	0.10	-0.63	14,25,34,37	0
2	FE	B	500	1/1	0.11	-0.72	20,20,20,20	0
2	FE	A	500	1/1	0.10	-0.81	21,21,21,21	0
5	ACT	A	14	4/4	0.08	-0.89	30,30,31,31	0
4	ZN	A	1	1/1	0.07	-1.38	33,33,33,33	0

## 6.5 Other polymers

There are no such residues in this entry.