



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:19 AM GMT

PDB ID : 3LNL  
Title : Crystal structure of Staphylococcus aureus protein SA1388  
Authors : Singh, K.S.; Chruszcz, M.; Zhang, X.; Minor, W.; Zhang, H.  
Deposited on : 2010-02-02  
Resolution : 2.00 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

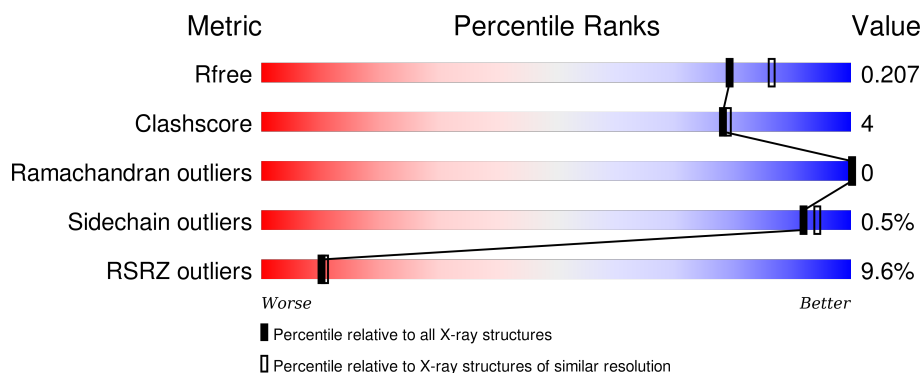
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


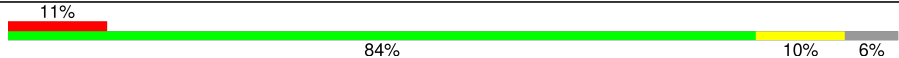
The reported resolution of this entry is 2.00 Å.

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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	370	
1	B	370	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5914 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 UPF0135 protein SA1388.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	1	0
			2400	1533	395	460	12			
1	B	349	Total	C	N	O	S	0	4	0
			2780	1775	452	538	15			

There are 14 discrepancies between the modelled and reference sequences:

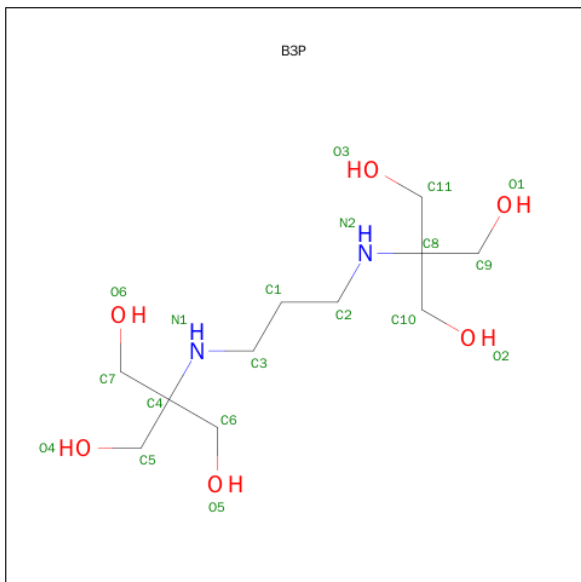
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	EXPRESSION TAG	UNP P67273
A	2	MET	-	EXPRESSION TAG	UNP P67273
A	3	ASP	-	EXPRESSION TAG	UNP P67273
A	4	PRO	-	EXPRESSION TAG	UNP P67273
A	36	GLU	GLY	ENGINEERED	UNP P67273
A	110	HIS	TYR	CONFLICT	UNP P67273
A	119	VAL	ALA	ENGINEERED	UNP P67273
B	1	ALA	-	EXPRESSION TAG	UNP P67273
B	2	MET	-	EXPRESSION TAG	UNP P67273
B	3	ASP	-	EXPRESSION TAG	UNP P67273
B	4	PRO	-	EXPRESSION TAG	UNP P67273
B	36	GLU	GLY	ENGINEERED	UNP P67273
B	110	HIS	TYR	CONFLICT	UNP P67273
B	119	VAL	ALA	ENGINEERED	UNP P67273

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is 2-[3-(2-HYDROXY-1,1-DIHYDROXYMETHYL-ETHYLAMINO)-PROPYL

AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: B3P) (formula:  $C_{11}H_{26}N_2O_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			19	11	2	6		
3	B	1	Total	C	N	O	0	0
			19	11	2	6		

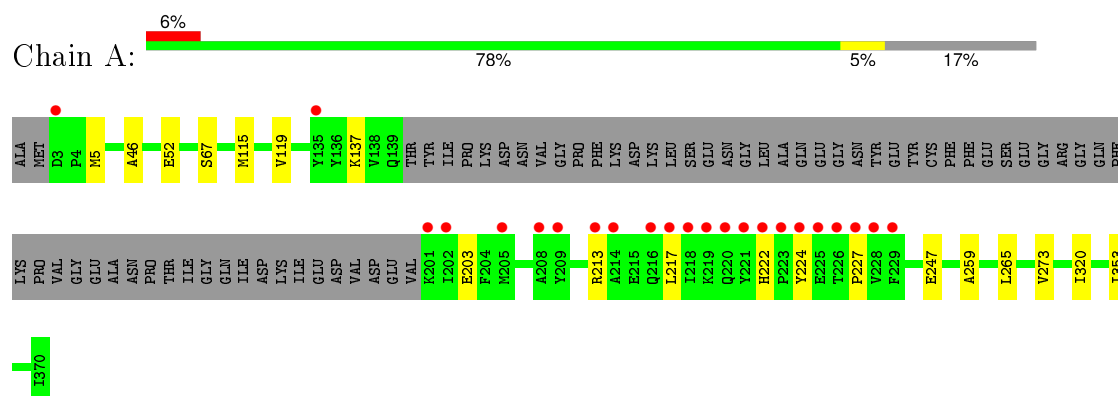
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	328	Total	O	0	0
			328	328		
4	B	364	Total	O	0	0
			364	364		

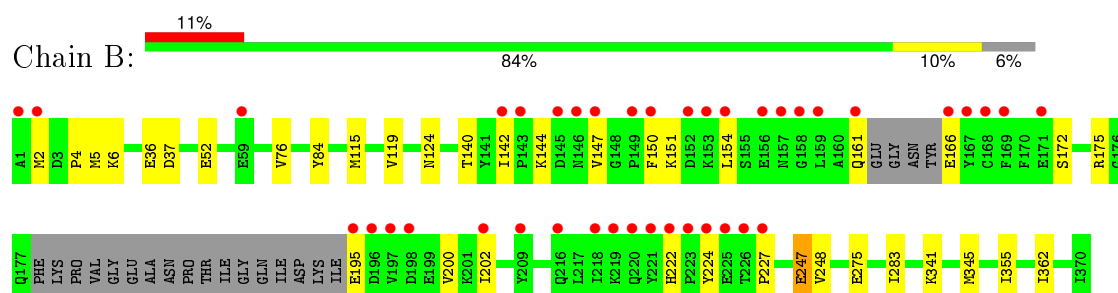
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: UPF0135 protein SA1388



- Molecule 1: UPF0135 protein SA1388



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	132.55Å 132.55Å 125.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.14 – 2.00 33.14 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.0 (33.14-2.00) 94.8 (33.14-2.00)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.149 , 0.191 0.163 , 0.207	Depositor DCC
$R_{free}$ test set	2661 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.0	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 50.1	EDS
Estimated twinning fraction	0.017 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 53095 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5914	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 4.65% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, B3P

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	0.86	3/2442 (0.1%)	0.77	0/3308
1	B	0.81	1/2831 (0.0%)	0.75	0/3829
All	All	0.83	4/5273 (0.1%)	0.76	0/7137

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	273	VAL	CB-CG1	5.32	1.64	1.52
1	B	275	GLU	CG-CD	5.29	1.59	1.51
1	A	247	GLU	CD-OE2	-5.21	1.20	1.25
1	A	259	ALA	CA-CB	5.17	1.63	1.52

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	2400	0	2377	13	0
1	B	2780	0	2736	27	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	19	0	26	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	19	0	26	0	0
4	A	328	0	0	1	0
4	B	364	0	0	1	0
All	All	5914	0	5165	37	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 4.

All (37) 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:B:147:VAL:HG22	1:B:202:ILE:HD11	1.54	0.88
1:B:5:MET:HE2	1:B:355:ILE:HD13	1.67	0.77
1:B:5:MET:CE	1:B:355:ILE:HD13	2.19	0.73
1:A:115:MET:O	1:A:119:VAL:HG23	1.92	0.69
1:B:248:VAL:HG13	1:B:283:ILE:HD11	1.79	0.63
1:B:6:LYS:NZ	1:B:37[B]:ASP:OD1	2.29	0.62
1:A:213:ARG:O	1:A:217:LEU:HD23	2.00	0.62
1:A:137:LYS:NZ	1:A:203:GLU:OE2	2.33	0.61
1:A:222:HIS:CB	1:A:227:PRO:HG3	2.33	0.59
1:B:5:MET:CE	1:B:355:ILE:CD1	2.81	0.58
1:B:150:PHE:CZ	1:B:154:LEU:HD11	2.39	0.58
1:A:224:TYR:CB	1:A:227:PRO:HA	2.34	0.58
1:B:2:MET:HE3	1:B:4:PRO:HG3	1.88	0.56
1:B:5:MET:HE2	1:B:355:ILE:CD1	2.34	0.56
1:B:161:GLN:HA	1:B:166:GLU:HA	1.88	0.55
1:A:320:ILE:HD13	1:B:84:TYR:CE2	2.41	0.55
1:B:144:LYS:HD2	1:B:200:VAL:HG21	1.92	0.52
1:A:320:ILE:CD1	1:B:84:TYR:CE2	2.93	0.51
1:B:248:VAL:HG13	1:B:283:ILE:CD1	2.44	0.48
1:B:5:MET:HE1	1:B:355:ILE:HD13	1.95	0.47
1:B:124:ASN:ND2	1:B:247:GLU:OE2	2.36	0.47
1:B:222:HIS:CG	1:B:227:PRO:HB3	2.50	0.47
1:A:119:VAL:HG11	1:A:265:LEU:HD23	1.97	0.46
1:B:142:ILE:HG23	1:B:147:VAL:HG23	1.97	0.45
1:A:137:LYS:CE	1:A:203:GLU:OE2	2.64	0.45
1:A:5:MET:CE	1:A:353:ILE:HD13	2.47	0.44
1:B:76:VAL:HG23	1:B:76:VAL:O	2.16	0.44
1:B:140:THR:HG21	1:B:222:HIS:CD2	2.52	0.44
1:B:147:VAL:HG13	1:B:151:LYS:HE2	1.99	0.43
1:A:320:ILE:HD12	1:B:84:TYR:CZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:MET:O	1:B:119:VAL:HG23	2.18	0.43
1:A:52:GLU:HG3	4:A:619:HOH:O	2.20	0.41
1:B:341:LYS:O	1:B:345[A]:MET:HG3	2.20	0.41
1:A:46:ALA:O	1:A:67:SER:HA	2.19	0.41
1:B:175:ARG:CB	1:B:195:GLU:HG2	2.51	0.40
1:B:36:GLU:OE1	4:B:466:HOH:O	2.22	0.40
1:B:52[A]:GLU:HB3	1:B:362:ILE:HD13	2.03	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	304/370 (82%)	295 (97%)	9 (3%)	0	100	100
1	B	347/370 (94%)	340 (98%)	7 (2%)	0	100	100
All	All	651/740 (88%)	635 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	262/322 (81%)	262 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	305/322 (95%)	302 (99%)	3 (1%)	82	85
All	All	567/644 (88%)	564 (100%)	3 (0%)	92	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	172	SER
1	B	224	TYR
1	B	247	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
1	B	93	GLN
1	B	177	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 ⓘ

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	B3P	A	371	-	18,18,18	2.59	4 (22%)	23,23,23	2.15	6 (26%)
3	B3P	B	371	-	18,18,18	2.22	3 (16%)	23,23,23	2.23	7 (30%)

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	B3P	A	371	-	-	0/28/28/28	0/0/0/0
3	B3P	B	371	-	-	0/28/28/28	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	371	B3P	C7-C4	-6.41	1.46	1.53
3	A	371	B3P	C5-C4	-6.14	1.46	1.53
3	B	371	B3P	C6-C4	-6.08	1.46	1.53
3	B	371	B3P	C7-C4	-5.55	1.47	1.53
3	A	371	B3P	C6-C4	-5.25	1.47	1.53
3	B	371	B3P	C9-C8	-2.71	1.50	1.53
3	A	371	B3P	C11-C8	-2.54	1.50	1.53

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	371	B3P	C5-C4-N1	-3.73	98.32	109.19
3	B	371	B3P	C6-C4-N1	-2.42	102.13	109.19
3	A	371	B3P	C6-C4-N1	-2.38	102.25	109.19
3	A	371	B3P	C5-C4-N1	-2.20	102.78	109.19
3	A	371	B3P	O1-C9-C8	-2.15	106.94	111.42
3	B	371	B3P	O1-C9-C8	-2.11	107.03	111.42
3	A	371	B3P	C7-C4-C5	2.21	114.75	110.14
3	B	371	B3P	C2-N2-C8	2.60	119.94	116.07
3	B	371	B3P	O6-C7-C4	3.42	118.53	111.42
3	A	371	B3P	C6-C4-C5	4.67	119.90	110.14
3	B	371	B3P	C6-C4-C5	5.07	120.74	110.14
3	B	371	B3P	C3-N1-C4	5.32	123.99	116.07
3	A	371	B3P	C3-N1-C4	6.79	126.19	116.07

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

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	307/370 (82%)	0.10	23 (7%) 17 18	9, 15, 41, 45	0
1	B	349/370 (94%)	0.14	40 (11%) 6 7	10, 16, 43, 49	0
All	All	656/740 (88%)	0.12	63 (9%) 10 11	9, 15, 42, 49	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	202	ILE	8.6
1	A	227	PRO	8.0
1	A	222	HIS	7.7
1	A	223	PRO	7.4
1	A	228	VAL	6.8
1	B	223	PRO	6.3
1	B	224	TYR	6.3
1	A	224	TYR	6.1
1	A	225	GLU	6.0
1	A	220	GLN	5.9
1	A	226	THR	5.7
1	B	150	PHE	5.5
1	B	197	VAL	5.5
1	A	221	TYR	5.4
1	A	201	LYS	5.1
1	B	167	TYR	5.1
1	B	158	GLY	4.8
1	A	219	LYS	4.7
1	A	229	PHE	4.6
1	B	221	TYR	4.5
1	A	216	GLN	4.4
1	B	146	ASN	4.4
1	B	1	ALA	4.4
1	A	209	TYR	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	220	GLN	4.3
1	B	195	GLU	4.0
1	B	166	GLU	3.9
1	B	196	ASP	3.9
1	B	145	ASP	3.8
1	A	214	ALA	3.7
1	B	159	LEU	3.7
1	B	209	TYR	3.6
1	A	217	LEU	3.6
1	A	135	TYR	3.6
1	B	147	VAL	3.6
1	B	152	ASP	3.3
1	B	142	ILE	3.2
1	B	225	GLU	3.2
1	B	143	PRO	3.1
1	B	154	LEU	3.1
1	A	3	ASP	3.0
1	A	208	ALA	3.0
1	B	168	CYS	2.9
1	B	149	PRO	2.9
1	B	226	THR	2.9
1	B	222	HIS	2.8
1	B	2	MET	2.7
1	B	169	PHE	2.7
1	B	216	GLN	2.6
1	B	161	GLN	2.6
1	A	205	MET	2.5
1	A	218	ILE	2.5
1	A	213	ARG	2.5
1	B	218	ILE	2.4
1	B	219	LYS	2.4
1	B	157	ASN	2.4
1	B	153	LYS	2.3
1	B	227	PRO	2.3
1	B	202	ILE	2.3
1	B	156	GLU	2.2
1	B	198	ASP	2.1
1	B	171	GLU	2.1
1	B	59	GLU	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](#)

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(Å <sup>2</sup> )	Q<0.9
3	B3P	A	371	19/19	0.85	0.17	1.85	19,30,49,52	0
3	B3P	B	371	19/19	0.90	0.14	0.44	19,28,51,55	0
2	ZN	A	402	1/1	0.99	0.07	-1.77	25,25,25,25	1
2	ZN	A	401	1/1	0.99	0.05	-3.73	27,27,27,27	1
2	ZN	B	401	1/1	1.00	0.07	-3.84	22,22,22,22	1
2	ZN	B	402	1/1	0.99	0.04	-4.55	23,23,23,23	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.