



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 26, 2017 – 11:41 AM EDT

PDB ID : 1C1T  
Title : RECRUITING ZINC TO MEDIATE POTENT, SPECIFIC INHIBITION OF  
SERINE PROTEASES  
Authors : Katz, B.A.; Luong, C.  
Deposited on : unknown  
Resolution : 1.37 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 : 1.7.2 (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

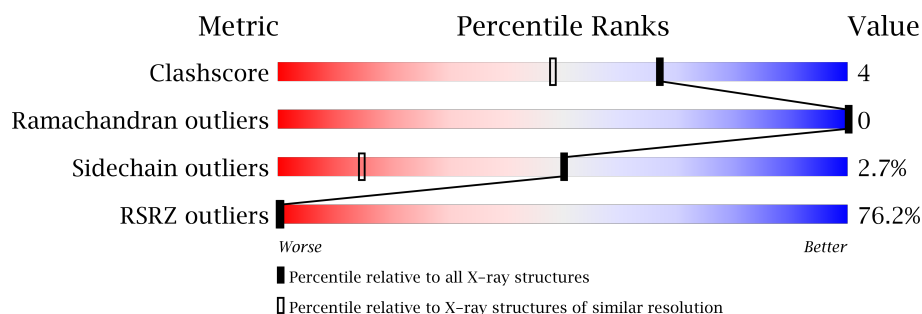
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.37 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))
Clashscore	112137	2266 (1.40-1.36)
Ramachandran outliers	110173	2215 (1.40-1.36)
Sidechain outliers	110143	2214 (1.40-1.36)
RSRZ outliers	101464	2141 (1.40-1.36)

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	223	<div> <div>76%</div> <div>85%</div> <div>13%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SO4	A	468	-	-	-	X

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4069 atoms, of which 2140 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 TRYPSIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	223	Total	C	H	N	O	S	4	11	0
			3323	1038	1658	282	330	15			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

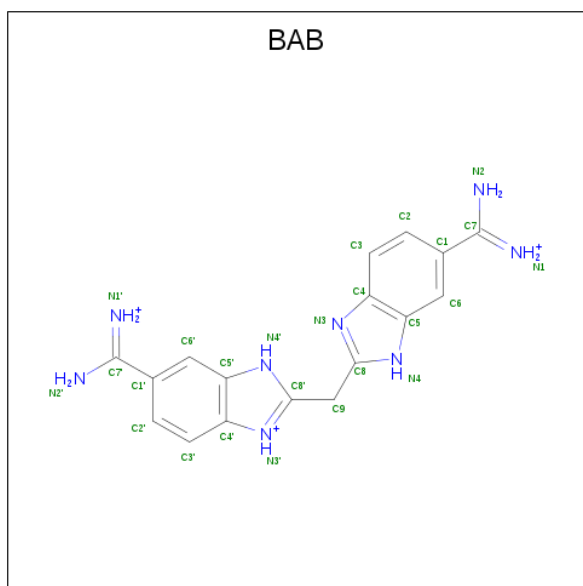
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 5 is BIS(5-AMIDINO-BENZIMIDAZOLYL)METHANE (three-letter code: BAB) (formula: C<sub>17</sub>H<sub>19</sub>N<sub>8</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	N	0	0
			43	17	18	8		

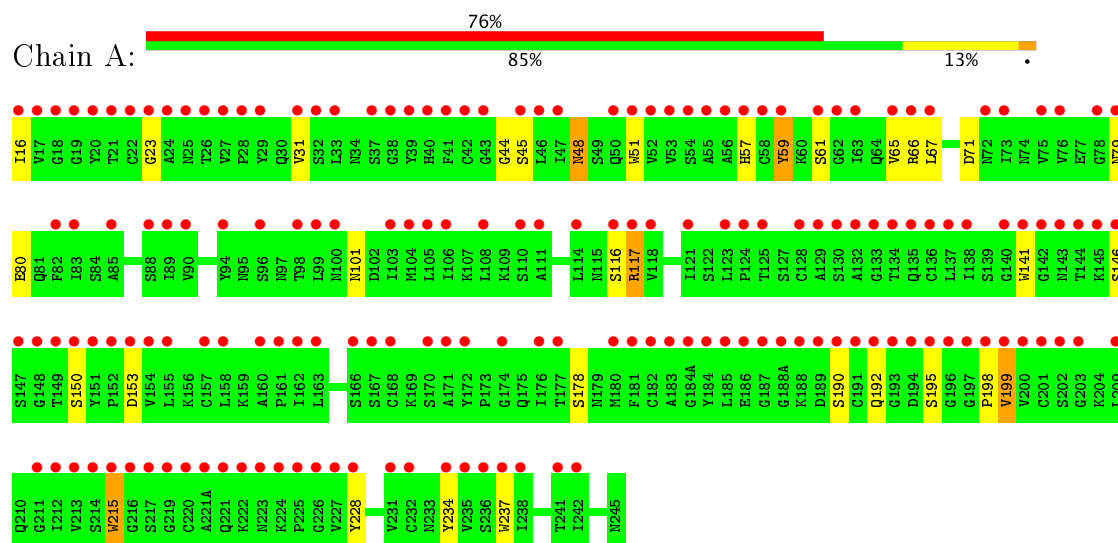
- Molecule 6 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	232	Total	H	O	0	12
			696	464	232		

### 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 ( $\text{RSRZ} > 2$ ). 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: TRYPSIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.83Å 54.83Å 109.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	7.50 – 1.37 28.88 – 1.34	Depositor EDS
% Data completeness (in resolution range)	83.0 (7.50-1.37) 78.8 (28.88-1.34)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.52 (at 1.34Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.174 , 0.194 0.189 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	16.4	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 63.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.042 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	4069	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 8.17% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, BAB, CA, SO4

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	1.26	1/1747 (0.1%)	1.43	21/2366 (0.9%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	80	GLU	CD-OE2	-5.04	1.20	1.25

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	237	TRP	CD1-NE1-CE2	9.55	117.59	109.00
1	A	141	TRP	CD1-NE1-CE2	9.49	117.54	109.00
1	A	51	TRP	CD1-NE1-CE2	9.43	117.49	109.00
1	A	215	TRP	CD1-NE1-CE2	8.43	116.59	109.00
1	A	237	TRP	NE1-CE2-CZ2	7.77	138.95	130.40
1	A	141	TRP	NE1-CE2-CZ2	7.50	138.65	130.40
1	A	51	TRP	NE1-CE2-CZ2	7.21	138.32	130.40
1	A	237	TRP	CG-CD1-NE1	-7.18	102.92	110.10
1	A	141	TRP	CG-CD1-NE1	-6.84	103.26	110.10
1	A	215	TRP	CG-CD1-NE1	-6.38	103.72	110.10
1	A	215	TRP	NE1-CE2-CZ2	6.16	137.18	130.40
1	A	51	TRP	NE1-CE2-CD2	-6.12	101.18	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	237	TRP	NE1-CE2-CD2	-6.09	101.21	107.30
1	A	141	TRP	NE1-CE2-CD2	-6.04	101.26	107.30
1	A	199	VAL	N-CA-C	-5.80	95.33	111.00
1	A	51	TRP	CG-CD1-NE1	-5.73	104.37	110.10
1	A	117	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	A	59	TYR	CB-CG-CD1	-5.37	117.78	121.00
1	A	23	GLY	N-CA-C	-5.32	99.81	113.10
1	A	215	TRP	NE1-CE2-CD2	-5.31	101.99	107.30
1	A	71	ASP	N-CA-C	-5.27	96.77	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	66	ARG	Sidechain

## 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	1665	1658	1631	15	3
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	5	0	0	0	0
5	A	25	18	19	1	0
6	A	232	464	0	0	7
All	All	1929	2140	1650	15	8

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 (15) 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:31[A]:VAL:CG1	1:A:65:VAL:HG13	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31[B]:VAL:HG22	1:A:44:GLY:CA	2.40	0.52
1:A:31[B]:VAL:HG22	1:A:44:GLY:C	2.33	0.49
1:A:57:HIS:NE2	1:A:195:SER:HB3	2.30	0.47
1:A:48:ASN:C	1:A:48:ASN:HD22	2.19	0.45
1:A:199:VAL:HG21	1:A:228:TYR:CD1	2.53	0.44
1:A:31[A]:VAL:HG22	1:A:67[A]:LEU:CD2	2.50	0.42
1:A:79:ASN:CG	1:A:117:ARG:HD2	2.40	0.41
1:A:215:TRP:CE3	5:A:246:BAB:H6'	2.55	0.41
1:A:31[A]:VAL:HG11	1:A:65:VAL:HG13	2.02	0.41
1:A:45:SER:OG	1:A:198:PRO:HB3	2.21	0.41
1:A:101:ASN:HA	1:A:234:TYR:OH	2.21	0.41
1:A:16:ILE:HD13	1:A:190:SER:HA	2.03	0.41

All (8) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:315:HOH:H1	6:A:500:HOH:O[2_645]	1.31	0.29
1:A:150:SER:OG	6:A:639:HOH:H1[4_656]	1.36	0.24
1:A:178:SER:HG	6:A:859:HOH:O[4_546]	1.44	0.16
6:A:321:HOH:H2	6:A:395:HOH:O[5_565]	1.53	0.07
6:A:436:HOH:O	6:A:436:HOH:O[6_766]	2.13	0.07
1:A:59:TYR:OH	1:A:153:ASP:OD2[5_565]	2.15	0.05
6:A:314:HOH:H1	6:A:395:HOH:O[5_565]	1.56	0.04
6:A:312:HOH:H1	6:A:329:HOH:O[5_555]	1.58	0.02

## 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	233/223 (104%)	229 (98%)	4 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	196/184 (106%)	191 (97%)	5 (3%)	51 15

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	61	SER
1	A	116	SER
1	A	146	SER
1	A	192	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	48	ASN
1	A	79	ASN
1	A	97	ASN
1	A	210	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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 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	$\# Z  > 2$
5	BAB	A	246	-	22,28,28	2.22	9 (40%)	28,41,41	1.81	7 (25%)
4	SO4	A	468	-	4,4,4	0.42	0	6,6,6	0.12	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
5	BAB	A	246	-	-	0/10/12/12	0/4/4/4
4	SO4	A	468	-	-	0/0/0/0	0/0/0/0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	246	BAB	C1-C7	-5.05	1.38	1.48
5	A	246	BAB	C1'-C7'	-3.48	1.41	1.48
5	A	246	BAB	C4-N3	-2.12	1.32	1.39
5	A	246	BAB	C3'-C2'	2.00	1.40	1.36
5	A	246	BAB	C6-C1	2.38	1.41	1.37
5	A	246	BAB	C2'-C1'	2.56	1.43	1.39
5	A	246	BAB	C3-C2	2.64	1.42	1.36
5	A	246	BAB	C6'-C1'	3.14	1.42	1.37
5	A	246	BAB	C2-C1	3.78	1.45	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
5	A	246	BAB	C2-C3-C4	-3.91	116.05	120.84
5	A	246	BAB	C1-C6-C5	-2.32	117.36	121.36
5	A	246	BAB	C1'-C7'-N1'	2.12	122.68	120.12
5	A	246	BAB	C2-C1-C7	2.47	123.83	120.48
5	A	246	BAB	C5'-C4'-N3'	3.11	108.50	105.89
5	A	246	BAB	C4-C5-N4	3.20	108.57	105.89
5	A	246	BAB	C6-C5-C4	4.11	124.44	120.55

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
5	A	246	BAB	1	0

## 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 ⓘ

### 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	223/223 (100%)	3.09	170 (76%) 0 0	10, 16, 26, 35	20 (8%)

All (170) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	172	TYR	7.5
1	A	148	GLY	7.4
1	A	147	SER	7.4
1	A	149	THR	6.9
1	A	39	TYR	6.6
1	A	185	LEU	6.1
1	A	17	VAL	6.1
1	A	146	SER	6.0
1	A	191	CYS	5.9
1	A	221(A)	ALA	5.5
1	A	220	CYS	5.4
1	A	53[A]	VAL	5.4
1	A	183	ALA	5.4
1	A	76	VAL	5.3
1	A	223	ASN	5.1
1	A	42	CYS	5.1
1	A	144	THR	5.0
1	A	226	GLY	5.0
1	A	200	VAL	5.0
1	A	20	TYR	4.9
1	A	85	ALA	4.7
1	A	151	TYR	4.7
1	A	182	CYS	4.6
1	A	31[A]	VAL	4.6
1	A	158	LEU	4.5
1	A	22	CYS	4.5
1	A	168	CYS	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	16	ILE	4.5
1	A	63	ILE	4.5
1	A	73	ILE	4.5
1	A	193	GLY	4.5
1	A	170[A]	SER	4.4
1	A	198	PRO	4.4
1	A	89	ILE	4.4
1	A	213	VAL	4.4
1	A	27	VAL	4.3
1	A	209	LEU	4.3
1	A	118	VAL	4.3
1	A	67[A]	LEU	4.3
1	A	29	TYR	4.3
1	A	116	SER	4.2
1	A	108	LEU	4.2
1	A	134	THR	4.2
1	A	157	CYS	4.2
1	A	181	PHE	4.2
1	A	121	ILE	4.2
1	A	212	ILE	4.2
1	A	215	TRP	4.1
1	A	138	ILE	4.1
1	A	117	ARG	4.1
1	A	65	VAL	4.1
1	A	227	VAL	4.1
1	A	222	LYS	4.1
1	A	216	GLY	4.0
1	A	33	LEU	4.0
1	A	142	GLY	4.0
1	A	114	LEU	3.9
1	A	106	ILE	3.8
1	A	58	CYS	3.8
1	A	137	LEU	3.8
1	A	150	SER	3.8
1	A	160	ALA	3.8
1	A	41	PHE	3.8
1	A	225	PRO	3.8
1	A	176	ILE	3.8
1	A	145	LYS	3.8
1	A	155	LEU	3.7
1	A	141	TRP	3.7
1	A	237	TRP	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	228	TYR	3.7
1	A	221	GLN	3.6
1	A	199	VAL	3.6
1	A	197	GLY	3.6
1	A	143	ASN	3.6
1	A	18	GLY	3.6
1	A	94	TYR	3.5
1	A	184	TYR	3.5
1	A	61	SER	3.5
1	A	192	GLN	3.5
1	A	174	GLY	3.5
1	A	124	PRO	3.5
1	A	104[A]	MET	3.4
1	A	75	VAL	3.4
1	A	162	ILE	3.4
1	A	190	SER	3.4
1	A	99	LEU	3.4
1	A	26	THR	3.4
1	A	82	PHE	3.4
1	A	98	THR	3.4
1	A	136	CYS	3.3
1	A	47	ILE	3.3
1	A	103	ILE	3.3
1	A	163	LEU	3.3
1	A	90	VAL	3.3
1	A	234	TYR	3.3
1	A	37	SER	3.2
1	A	24	ALA	3.2
1	A	43	GLY	3.2
1	A	79	ASN	3.2
1	A	217	SER	3.2
1	A	23	GLY	3.2
1	A	214	SER	3.1
1	A	110[A]	SER	3.1
1	A	123	LEU	3.1
1	A	177	THR	3.1
1	A	186	GLU	3.0
1	A	242	ILE	3.0
1	A	19	GLY	3.0
1	A	201	CYS	3.0
1	A	232	CYS	3.0
1	A	161	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	59	TYR	2.9
1	A	38	GLY	2.9
1	A	51	TRP	2.9
1	A	195	SER	2.9
1	A	231	VAL	2.9
1	A	238	ILE	2.9
1	A	140	GLY	2.8
1	A	152	PRO	2.8
1	A	235	VAL	2.8
1	A	224[A]	LYS	2.8
1	A	105	LEU	2.8
1	A	154	VAL	2.8
1	A	129	ALA	2.8
1	A	187	GLY	2.7
1	A	219	GLY	2.7
1	A	52	VAL	2.7
1	A	25	ASN	2.7
1	A	40	HIS	2.6
1	A	21	THR	2.6
1	A	236[A]	SER	2.6
1	A	83	ILE	2.6
1	A	46	LEU	2.6
1	A	132	ALA	2.6
1	A	62	GLY	2.6
1	A	211	GLY	2.6
1	A	57	HIS	2.6
1	A	135	GLN	2.6
1	A	78	GLY	2.5
1	A	188(A)	GLY	2.5
1	A	55	ALA	2.5
1	A	96	SER	2.5
1	A	28	PRO	2.5
1	A	184(A)	GLY	2.5
1	A	203	GLY	2.5
1	A	241	THR	2.4
1	A	133	GLY	2.4
1	A	56	ALA	2.4
1	A	50[A]	GLN	2.4
1	A	128	CYS	2.4
1	A	171	ALA	2.3
1	A	194	ASP	2.3
1	A	196	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	188	LYS	2.3
1	A	54	SER	2.3
1	A	180	MET	2.3
1	A	32	SER	2.2
1	A	100	ASN	2.2
1	A	111	ALA	2.2
1	A	125	THR	2.2
1	A	130	SER	2.2
1	A	45	SER	2.2
1	A	202	SER	2.2
1	A	153	ASP	2.2
1	A	167	SER	2.1
1	A	88	SER	2.1
1	A	189	ASP	2.1
1	A	166	SER	2.1
1	A	72	ASN	2.0
1	A	66	ARG	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(Å <sup>2</sup> )	Q<0.9
4	SO4	A	468	5/5	0.51	0.49	5.87	58,58,59,59	5
5	BAB	A	246	25/25	0.66	0.26	1.07	17,29,34,35	0
3	MG	A	263	1/1	0.64	0.23	0.86	21,21,21,21	0
2	CA	A	247	1/1	0.91	0.12	-3.45	23,23,23,23	0

## 6.5 Other polymers

There are no such residues in this entry.