



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:19 PM UTC

PDB ID : 4FML / pdb\_00004fml  
Title : Catalytic domain of VahC from *Aeromonas hydrophila*  
Authors : Ravulapalli, R.; Kimber, M.S.; Merrill, A.R.  
Deposited on : 2012-06-18  
Resolution : 1.93 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

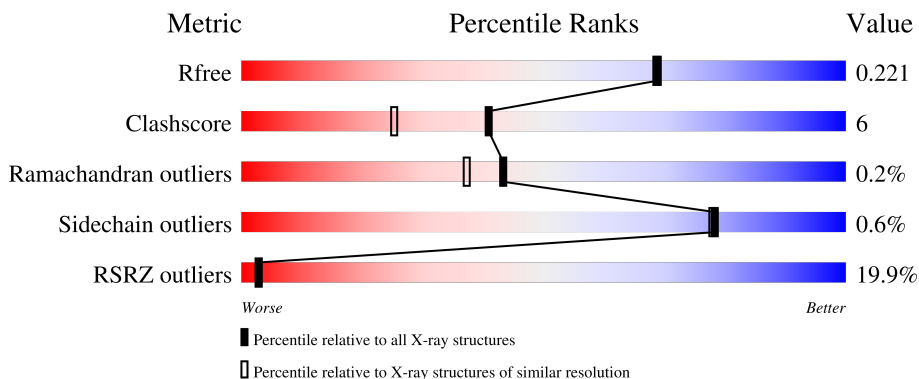
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.93 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))
$R_{free}$	180053	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	
1	B	223	
1	C	223	

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 9215 atoms, of which 4419 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 VsdC.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	204	3189	1001	1596	280	308	4	0	1	0
1	B	196	3118	979	1570	273	292	4	0	2	0
1	C	158	2496	789	1253	215	237	2	0	0	0

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	44	MET	-	expression tag	UNP Q49TP5
A	45	GLY	-	expression tag	UNP Q49TP5
A	46	SER	-	expression tag	UNP Q49TP5
A	47	SER	-	expression tag	UNP Q49TP5
A	48	HIS	-	expression tag	UNP Q49TP5
A	49	HIS	-	expression tag	UNP Q49TP5
A	50	HIS	-	expression tag	UNP Q49TP5
A	51	HIS	-	expression tag	UNP Q49TP5
A	52	HIS	-	expression tag	UNP Q49TP5
A	53	HIS	-	expression tag	UNP Q49TP5
A	54	SER	-	expression tag	UNP Q49TP5
A	55	SER	-	expression tag	UNP Q49TP5
A	56	GLY	-	expression tag	UNP Q49TP5
A	57	GLU	-	expression tag	UNP Q49TP5
A	58	ASN	-	expression tag	UNP Q49TP5
A	59	LEU	-	expression tag	UNP Q49TP5
A	60	TYR	-	expression tag	UNP Q49TP5
A	61	PHE	-	expression tag	UNP Q49TP5
A	62	GLN	-	expression tag	UNP Q49TP5
A	63	GLY	-	expression tag	UNP Q49TP5
A	64	SER	-	expression tag	UNP Q49TP5
A	65	HIS	-	expression tag	UNP Q49TP5
A	66	MET	-	expression tag	UNP Q49TP5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	44	MET	-	expression tag	UNP Q49TP5
B	45	GLY	-	expression tag	UNP Q49TP5
B	46	SER	-	expression tag	UNP Q49TP5
B	47	SER	-	expression tag	UNP Q49TP5
B	48	HIS	-	expression tag	UNP Q49TP5
B	49	HIS	-	expression tag	UNP Q49TP5
B	50	HIS	-	expression tag	UNP Q49TP5
B	51	HIS	-	expression tag	UNP Q49TP5
B	52	HIS	-	expression tag	UNP Q49TP5
B	53	HIS	-	expression tag	UNP Q49TP5
B	54	SER	-	expression tag	UNP Q49TP5
B	55	SER	-	expression tag	UNP Q49TP5
B	56	GLY	-	expression tag	UNP Q49TP5
B	57	GLU	-	expression tag	UNP Q49TP5
B	58	ASN	-	expression tag	UNP Q49TP5
B	59	LEU	-	expression tag	UNP Q49TP5
B	60	TYR	-	expression tag	UNP Q49TP5
B	61	PHE	-	expression tag	UNP Q49TP5
B	62	GLN	-	expression tag	UNP Q49TP5
B	63	GLY	-	expression tag	UNP Q49TP5
B	64	SER	-	expression tag	UNP Q49TP5
B	65	HIS	-	expression tag	UNP Q49TP5
B	66	MET	-	expression tag	UNP Q49TP5
C	44	MET	-	expression tag	UNP Q49TP5
C	45	GLY	-	expression tag	UNP Q49TP5
C	46	SER	-	expression tag	UNP Q49TP5
C	47	SER	-	expression tag	UNP Q49TP5
C	48	HIS	-	expression tag	UNP Q49TP5
C	49	HIS	-	expression tag	UNP Q49TP5
C	50	HIS	-	expression tag	UNP Q49TP5
C	51	HIS	-	expression tag	UNP Q49TP5
C	52	HIS	-	expression tag	UNP Q49TP5
C	53	HIS	-	expression tag	UNP Q49TP5
C	54	SER	-	expression tag	UNP Q49TP5
C	55	SER	-	expression tag	UNP Q49TP5
C	56	GLY	-	expression tag	UNP Q49TP5
C	57	GLU	-	expression tag	UNP Q49TP5
C	58	ASN	-	expression tag	UNP Q49TP5
C	59	LEU	-	expression tag	UNP Q49TP5
C	60	TYR	-	expression tag	UNP Q49TP5
C	61	PHE	-	expression tag	UNP Q49TP5
C	62	GLN	-	expression tag	UNP Q49TP5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	63	GLY	-	expression tag	UNP Q49TP5
C	64	SER	-	expression tag	UNP Q49TP5
C	65	HIS	-	expression tag	UNP Q49TP5
C	66	MET	-	expression tag	UNP Q49TP5

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	174	Total 174	O 174	0	0
2	B	215	Total 215	O 215	0	0
2	C	23	Total 23	O 23	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.10Å 91.10Å 303.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.55 – 1.93 45.55 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.55-1.93) 99.9 (45.55-1.93)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.80 (at 1.92Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.191 , 0.217 0.197 , 0.221	Depositor DCC
$R_{free}$ test set	2852 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.4	Xtrriage
Anisotropy	0.051	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 54.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9215	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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](#)

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	1.22	5/1625 (0.3%)	0.99	1/2198 (0.0%)
1	B	1.33	3/1582 (0.2%)	1.03	1/2138 (0.0%)
1	C	0.72	0/1262	0.87	0/1706
All	All	1.15	8/4469 (0.2%)	0.97	2/6042 (0.0%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	138	PRO	C-O	-6.03	1.16	1.23
1	A	132	ALA	CA-CB	5.83	1.62	1.53
1	B	265	VAL	C-O	-5.76	1.18	1.24
1	A	158	ALA	CA-CB	-5.69	1.44	1.53
1	B	128	ALA	CA-CB	5.56	1.62	1.53
1	A	145	PHE	C-O	-5.46	1.17	1.23
1	B	106	ARG	C-O	-5.26	1.17	1.24
1	A	122	ALA	CA-CB	-5.09	1.45	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	247	SER	N-CA-C	-8.00	100.57	110.41
1	B	255	ASN	N-CA-C	-6.32	105.32	113.16

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	1593	1596	1593	9	0
1	B	1548	1570	1567	12	1
1	C	1243	1253	1252	36	3
2	A	174	0	0	1	1
2	B	215	0	0	2	2
2	C	23	0	0	6	0
All	All	4796	4419	4412	57	6

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 6.

All (57) 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:C:228:ARG:NH1	2:C:322:HOH:O	1.99	0.86
1:C:220:THR:O	1:C:221:GLN:HG2	1.85	0.76
1:C:84:LEU:HD21	1:C:99:ALA:HA	1.71	0.73
1:C:92:ARG:HB3	1:C:93:PRO:HD2	1.73	0.69
1:B:91:ASP:OD1	2:B:462:HOH:O	2.12	0.66
1:C:71:ASP:OD1	2:C:320:HOH:O	2.16	0.63
1:C:111:ASP:O	1:C:112:GLU:C	2.44	0.58
1:C:220:THR:O	1:C:221:GLN:CG	2.50	0.58
1:A:228:ARG:NH1	1:A:262:GLU:OE2	2.36	0.57
1:C:172:VAL:HG12	1:C:223:ARG:HG2	1.86	0.57
1:C:151:ALA:C	1:C:188:ASP:OD2	2.51	0.54
1:C:106:ARG:O	1:C:107:SER:HB2	2.06	0.54
1:A:117:GLY:O	1:A:121:LYS:HB2	2.07	0.54
1:C:166:GLY:HA3	1:C:169:ASN:ND2	2.22	0.53
1:B:204:LEU:HD12	1:B:211:LYS:HE2	1.91	0.53
1:B:136:LYS:NZ	2:B:472:HOH:O	2.42	0.53
1:A:121:LYS:HA	1:A:124:LYS:HE3	1.90	0.52
1:C:221:GLN:HG3	1:C:221:GLN:O	2.10	0.52
1:A:256:ARG:HG3	2:A:356:HOH:O	2.10	0.51
1:A:147:TYR:HB3	1:A:184:ALA:HB2	1.93	0.50
1:C:127:VAL:O	1:C:128:ALA:C	2.53	0.49
1:A:148[A]:ARG:HD2	1:A:149:GLY:O	2.12	0.49
1:B:185:TRP:CE3	1:B:247:SER:CB	2.95	0.49
1:B:232:SER:HA	1:B:237:PHE:CD1	2.48	0.48
1:C:74:LEU:HD21	1:C:137:LEU:HD11	1.95	0.48
1:A:220:THR:O	1:A:221:GLN:HB2	2.14	0.48
1:C:220:THR:O	1:C:221:GLN:CB	2.61	0.48
1:C:85:LEU:HD21	1:C:127:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:89:LEU:C	1:C:91:ASP:H	2.23	0.47
1:C:84:LEU:HD21	1:C:99:ALA:CA	2.43	0.47
1:A:102:THR:O	1:A:106:ARG:HG3	2.15	0.46
1:A:150:LEU:HD23	1:A:150:LEU:N	2.31	0.46
1:B:185:TRP:CE3	1:B:247:SER:HB3	2.52	0.45
1:B:182:ASP:O	1:B:245:PRO:HG2	2.15	0.45
1:C:176:PHE:HB3	1:C:217:LEU:HD11	1.99	0.44
1:B:67:ILE:C	1:B:67:ILE:HD12	2.43	0.43
1:C:86:ASN:HD21	1:C:176:PHE:H	1.67	0.43
1:C:187:ASN:O	1:C:257:ILE:HA	2.19	0.43
1:C:69:LYS:NZ	1:C:107:SER:HB2	2.34	0.43
1:C:84:LEU:N	2:C:313:HOH:O	2.26	0.43
1:C:194:ARG:NH2	2:C:318:HOH:O	2.51	0.43
1:B:77:TYR:CE1	1:B:82:TYR:HA	2.54	0.43
1:C:150:LEU:O	1:C:151:ALA:C	2.62	0.42
1:C:74:LEU:HD12	1:C:74:LEU:O	2.19	0.42
1:C:144:SER:OG	2:C:314:HOH:O	1.96	0.42
1:C:174:PRO:O	1:C:220:THR:HB	2.20	0.41
1:C:83:THR:HB	2:C:313:HOH:O	2.21	0.41
1:C:100:ILE:O	1:C:104:LEU:HD13	2.21	0.41
1:C:221:GLN:CG	1:C:221:GLN:O	2.66	0.41
1:C:76:TYR:CD2	1:C:76:TYR:C	2.98	0.41
1:C:188:ASP:HB2	1:C:258:LYS:HE3	2.03	0.41
1:B:154:LYS:HA	1:B:155:PRO:HD3	1.86	0.40
1:C:151:ALA:HA	1:C:187:ASN:OD1	2.20	0.40
1:C:89:LEU:C	1:C:91:ASP:N	2.79	0.40
1:B:65:HIS:ND1	1:B:65:HIS:N	2.69	0.40
1:B:84:LEU:C	1:B:84:LEU:HD13	2.46	0.40
1:C:79:ALA:C	1:C:80:GLN:HG3	2.47	0.40

All (6) 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)
1:C:172:VAL:HB	1:C:172:VAL:HB[11_654]	0.65	0.95
1:B:67:ILE:HD11	1:B:67:ILE:HD11[12_564]	0.91	0.69
2:A:449:HOH:O	2:B:490:HOH:O[7_554]	1.98	0.22
2:B:446:HOH:O	2:B:451:HOH:O[12_564]	2.07	0.13
1:C:172:VAL:CB	1:C:172:VAL:HB[11_654]	1.50	0.10
1:C:170:ILE:O	1:C:221:GLN:HB2[11_654]	1.56	0.04

## 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	203/223 (91%)	201 (99%)	2 (1%)	0	100	100
1	B	194/223 (87%)	189 (97%)	4 (2%)	1 (0%)	24	15
1	C	148/223 (66%)	141 (95%)	7 (5%)	0	100	100
All	All	545/669 (82%)	531 (97%)	13 (2%)	1 (0%)	43	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	155	PRO

### 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	171/187 (91%)	170 (99%)	1 (1%)	78	78
1	B	166/187 (89%)	164 (99%)	2 (1%)	63	57
1	C	135/187 (72%)	134 (99%)	1 (1%)	76	74
All	All	472/561 (84%)	468 (99%)	4 (1%)	78	71

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	ILE
1	B	148[A]	ARG

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Mol	Chain	Res	Type
1	B	148[B]	ARG
1	C	112	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	209	HIS
1	A	255	ASN
1	C	80	GLN
1	C	86	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 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	204/223 (91%)	0.33	19 (9%) 14 16	20, 43, 104, 146	1 (0%)
1	B	196/223 (87%)	-0.07	7 (3%) 46 52	20, 33, 82, 118	2 (1%)
1	C	158/223 (70%)	2.28	85 (53%) 0 0	64, 114, 165, 242	0
All	All	558/669 (83%)	0.74	111 (19%) 3 3	20, 53, 140, 242	3 (0%)

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	89	LEU	8.0
1	C	88	TYR	6.7
1	C	174	PRO	5.1
1	C	185	TRP	5.1
1	C	84	LEU	5.0
1	C	127	VAL	4.9
1	C	126	TYR	4.9
1	C	99	ALA	4.8
1	C	172	VAL	4.7
1	C	104	LEU	4.4
1	C	204	LEU	4.3
1	C	164	PHE	4.2
1	C	100	ILE	4.2
1	C	85	LEU	3.8
1	B	208	ALA	3.7
1	C	229	VAL	3.7
1	B	65	HIS	3.6
1	A	182	ASP	3.6
1	C	246	THR	3.5
1	C	170	ILE	3.5
1	C	171	VAL	3.5
1	C	186	VAL	3.5
1	B	207	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	217	LEU	3.5
1	C	103	LEU	3.4
1	A	79	ALA	3.3
1	C	125	ALA	3.3
1	C	193	ILE	3.2
1	A	84	LEU	3.2
1	A	148[A]	ARG	3.2
1	C	167	VAL	3.2
1	C	237	PHE	3.2
1	C	90	ARG	3.2
1	B	247	SER	3.1
1	C	184	ALA	3.1
1	C	108	TYR	3.1
1	A	109	LEU	3.1
1	A	87	ASN	3.1
1	C	191	LEU	3.0
1	C	226	VAL	3.0
1	C	220	THR	3.0
1	C	197	ALA	3.0
1	A	115	SER	3.0
1	C	93	PRO	3.0
1	A	250	ALA	3.0
1	C	130	VAL	2.9
1	C	128	ALA	2.9
1	C	74	LEU	2.9
1	C	82	TYR	2.9
1	C	83	THR	2.8
1	C	111	ASP	2.8
1	C	190	LEU	2.7
1	C	165	THR	2.7
1	C	132	ALA	2.7
1	C	235	GLY	2.6
1	C	94	TYR	2.6
1	C	96	GLN	2.6
1	C	225	ARG	2.6
1	C	231	SER	2.6
1	C	221	GLN	2.6
1	C	168	GLY	2.6
1	C	263	VAL	2.6
1	A	76	TYR	2.5
1	B	206	ASP	2.5
1	C	218	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	109	LEU	2.5
1	C	137	LEU	2.5
1	B	157	LEU	2.4
1	C	214	ALA	2.4
1	C	149	GLY	2.4
1	C	232	SER	2.4
1	C	241	LEU	2.4
1	A	117	GLY	2.4
1	C	260	LEU	2.4
1	C	92	ARG	2.4
1	C	259	ARG	2.4
1	C	138	PRO	2.4
1	C	219	PRO	2.4
1	C	224	LEU	2.3
1	C	135	ALA	2.3
1	A	228	ARG	2.3
1	C	91	ASP	2.3
1	C	240	LEU	2.3
1	C	151	ALA	2.3
1	A	93	PRO	2.3
1	C	68	SER	2.3
1	C	169	ASN	2.3
1	C	243	THR	2.3
1	C	73	ALA	2.3
1	A	100	ILE	2.3
1	B	209	HIS	2.3
1	C	95	LYS	2.3
1	C	195	LEU	2.3
1	C	203	LEU	2.3
1	C	234	SER	2.2
1	C	261	ILE	2.2
1	A	102	THR	2.2
1	C	86	ASN	2.2
1	C	230	VAL	2.2
1	A	116	ALA	2.2
1	C	257	ILE	2.2
1	C	198	GLY	2.1
1	C	134	LEU	2.1
1	C	148	ARG	2.1
1	C	79	ALA	2.1
1	C	147	TYR	2.1
1	C	213	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	75	ARG	2.1
1	A	91	ASP	2.1
1	A	95	LYS	2.0
1	A	113	PRO	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 oligosaccharides 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.