



Full wwPDB X-ray Structure Validation Report

Mar 31, 2014 – 03:34 PM BST

PDB ID : 3O06
Title : Crystal Structure of yeast pyridoxal 5-phosphate synthase Snz1
Authors : Teng, Y.B.; Zhang, X.; Zhou, C.Z.; Hu, H.X.
Deposited on : 2010-07-19
Resolution : 2.35 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

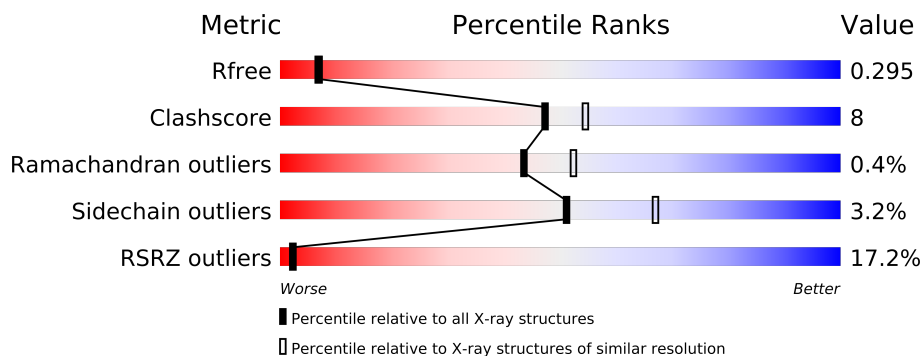
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable23004
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) : stable23004

1 Overall quality at a glance




The reported resolution of this entry is 2.35 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	3327 (2.40-2.32)
Clashscore	79885	1064 (2.38-2.34)
Ramachandran outliers	78287	1048 (2.38-2.34)
Sidechain outliers	78261	1049 (2.38-2.34)
RSRZ outliers	66119	3330 (2.40-2.32)

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 ≥ 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	291	
1	B	291	
1	C	291	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5875 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 Pyridoxine biosynthesis protein SNZ1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			1933	1214	331	373	15			
1	B	258	Total	C	N	O	S	0	0	0
			1933	1214	331	373	15			
1	C	258	Total	C	N	O	S	0	0	0
			1933	1214	331	373	15			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	EXPRESSION TAG	UNP Q03148
A	8	HIS	-	EXPRESSION TAG	UNP Q03148
A	9	HIS	-	EXPRESSION TAG	UNP Q03148
A	10	HIS	-	EXPRESSION TAG	UNP Q03148
A	11	HIS	-	EXPRESSION TAG	UNP Q03148
A	12	HIS	-	EXPRESSION TAG	UNP Q03148
A	13	HIS	-	EXPRESSION TAG	UNP Q03148
A	14	GLY	-	EXPRESSION TAG	UNP Q03148
B	7	MET	-	EXPRESSION TAG	UNP Q03148
B	8	HIS	-	EXPRESSION TAG	UNP Q03148
B	9	HIS	-	EXPRESSION TAG	UNP Q03148
B	10	HIS	-	EXPRESSION TAG	UNP Q03148
B	11	HIS	-	EXPRESSION TAG	UNP Q03148
B	12	HIS	-	EXPRESSION TAG	UNP Q03148
B	13	HIS	-	EXPRESSION TAG	UNP Q03148
B	14	GLY	-	EXPRESSION TAG	UNP Q03148
C	7	MET	-	EXPRESSION TAG	UNP Q03148
C	8	HIS	-	EXPRESSION TAG	UNP Q03148
C	9	HIS	-	EXPRESSION TAG	UNP Q03148
C	10	HIS	-	EXPRESSION TAG	UNP Q03148
C	11	HIS	-	EXPRESSION TAG	UNP Q03148
C	12	HIS	-	EXPRESSION TAG	UNP Q03148
C	13	HIS	-	EXPRESSION TAG	UNP Q03148

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Chain	Residue	Modelled	Actual	Comment	Reference
C	14	GLY	-	EXPRESSION TAG	UNP Q03148

- Molecule 2 is water.

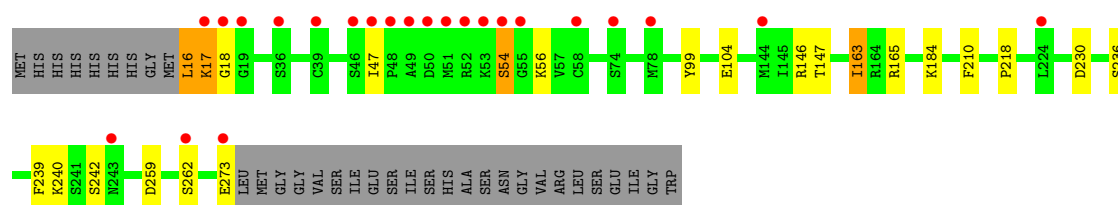
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	29	Total 29	O 29	0	0
2	B	20	Total 20	O 20	0	0
2	C	27	Total 27	O 27	0	0

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.

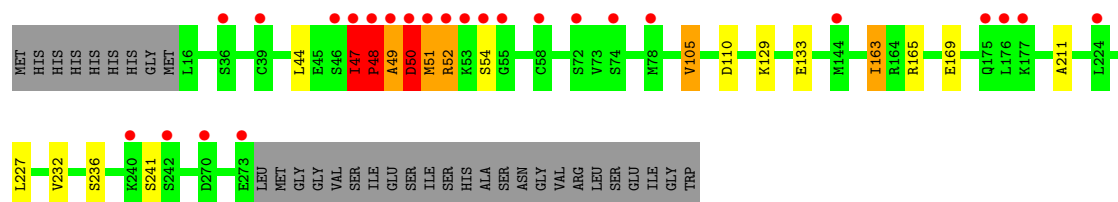
- Molecule 1: Pyridoxine biosynthesis protein SNZ1

Chain A: 



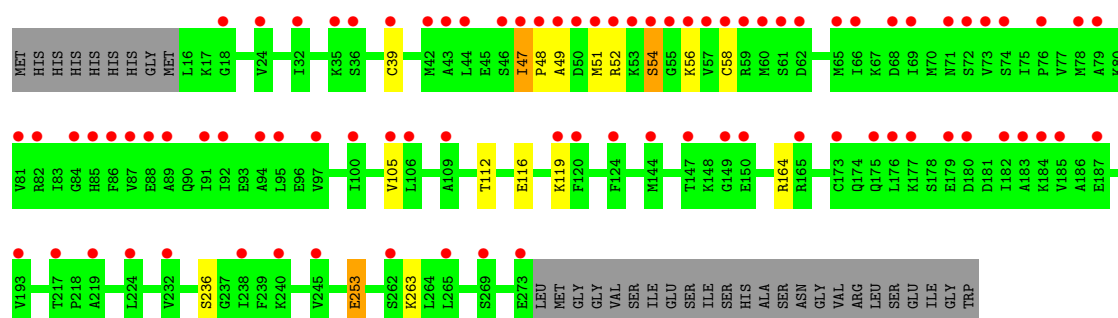
- Molecule 1: Pyridoxine biosynthesis protein SNZ1

Chain B: 



- Molecule 1: Pyridoxine biosynthesis protein SNZ1

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	59.31Å 110.38Å 156.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	110.38 – 2.35 47.14 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.5 (110.38-2.35) 99.6 (47.14-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.22 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.204 , 0.251 0.270 , 0.295	Depositor DCC
R_{free} test set	2172 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	30.8	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 16.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 43299 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	5875	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	1.05	0/1958	0.88	2/2640 (0.1%)
1	B	0.97	0/1958	0.86	3/2640 (0.1%)
1	C	1.02	3/1958 (0.2%)	0.85	0/2640
All	All	1.01	3/5874 (0.1%)	0.87	5/7920 (0.1%)

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	B	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	39	CYS	CB-SG	5.27	1.91	1.82
1	C	253	GLU	CB-CG	5.21	1.62	1.52
1	C	58	CYS	CB-SG	5.17	1.91	1.82

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	47	ILE	C-N-CD	-6.30	106.73	120.60
1	A	147	THR	CB-CA-C	5.82	127.30	111.60
1	A	163	ILE	CG1-CB-CG2	-5.70	98.86	111.40
1	B	163	ILE	CG1-CB-CG2	-5.44	99.43	111.40
1	B	48	PRO	C-N-CA	5.19	134.67	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	47	ILE	Mainchain,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	1933	0	98	12	0
1	B	1933	0	98	24	0
1	C	1933	0	98	14	0
2	A	29	0	0	0	0
2	B	20	0	0	0	0
2	C	27	0	0	0	0
All	All	5875	0	294	49	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 8.

All (49) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:48:PRO:HG2	1:B:105:VAL:CG1	1.71	1.21
1:C:47:ILE:HD12	1:C:236:SER:CB	1.72	1.17
1:C:47:ILE:CD1	1:C:236:SER:CB	2.30	1.10
1:B:48:PRO:CG	1:B:105:VAL:CG1	2.38	1.01
1:B:47:ILE:HG21	1:B:236:SER:OG	1.64	0.97
1:C:48:PRO:HG2	1:C:105:VAL:CG1	1.96	0.95
1:A:16:LEU:HB3	1:A:99:TYR:OH	1.72	0.90
1:A:16:LEU:HD23	1:A:16:LEU:N	1.91	0.86
1:A:242:SER:OG	1:A:273:GLU:HB3	1.78	0.82
1:B:47:ILE:CG2	1:B:236:SER:OG	2.26	0.82
1:C:47:ILE:HD12	1:C:236:SER:OG	1.80	0.81
1:C:47:ILE:HD11	1:C:236:SER:CB	2.20	0.71
1:B:47:ILE:O	1:B:48:PRO:C	2.30	0.68
1:B:47:ILE:O	1:B:49:ALA:N	2.26	0.68
1:A:47:ILE:HD13	1:A:240:LYS:NZ	2.08	0.68
1:B:47:ILE:HG21	1:B:236:SER:CB	2.25	0.67
1:B:48:PRO:HG3	1:B:105:VAL:CG1	2.24	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:49:ALA:O	1:B:52:ARG:N	2.28	0.66
1:B:49:ALA:O	1:B:51:MET:N	2.30	0.64
1:A:17:LYS:O	1:A:210:PHE:CZ	2.51	0.64
1:B:165:ARG:NE	1:B:169:GLU:OE2	2.30	0.64
1:C:47:ILE:CD1	1:C:236:SER:OG	2.41	0.63
1:B:165:ARG:NH2	1:B:169:GLU:OE2	2.33	0.62
1:A:16:LEU:CD2	1:A:16:LEU:N	2.63	0.61
1:A:54:SER:HB2	1:A:56:LYS:CG	2.33	0.58
1:C:48:PRO:CG	1:C:105:VAL:CG1	2.78	0.57
1:C:47:ILE:HG22	1:C:49:ALA:H	1.69	0.57
1:B:47:ILE:HG12	1:B:47:ILE:O	2.07	0.55
1:A:17:LYS:O	1:A:210:PHE:CE2	2.60	0.55
1:B:165:ARG:CZ	1:B:169:GLU:OE2	2.57	0.53
1:C:116:GLU:OE1	1:C:119:LYS:NZ	2.42	0.53
1:C:51:MET:O	1:C:54:SER:N	2.42	0.53
1:B:49:ALA:C	1:B:51:MET:N	2.64	0.50
1:C:253:GLU:OE1	1:C:263:LYS:NZ	2.44	0.50
1:C:47:ILE:CG2	1:C:49:ALA:HB3	2.41	0.49
1:A:104:GLU:OE2	1:A:146:ARG:NH1	2.46	0.49
1:B:50:ASP:O	1:B:54:SER:OG	2.23	0.49
1:B:129:LYS:N	1:B:133:GLU:OE1	2.47	0.48
1:B:163:ILE:CD1	1:B:227:LEU:CB	2.91	0.48
1:C:47:ILE:HD11	1:C:236:SER:N	2.30	0.47
1:A:47:ILE:HG12	1:A:236:SER:CB	2.45	0.47
1:B:44:LEU:CD2	1:B:44:LEU:N	2.80	0.44
1:A:236:SER:O	1:A:239:PHE:N	2.51	0.44
1:B:49:ALA:O	1:B:50:ASP:C	2.56	0.43
1:B:49:ALA:C	1:B:51:MET:H	2.23	0.41
1:B:110:ASP:OD2	1:C:164:ARG:NE	2.53	0.41
1:B:48:PRO:HB2	1:B:49:ALA:H	1.61	0.41
1:B:211:ALA:CB	1:B:232:VAL:CG2	2.99	0.41
1:A:18:GLY:CA	1:A:230:ASP:O	2.70	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	256/291 (88%)	243 (95%)	13 (5%)	0	100	100
1	B	256/291 (88%)	245 (96%)	8 (3%)	3 (1%)	19	19
1	C	256/291 (88%)	249 (97%)	7 (3%)	0	100	100
All	All	768/873 (88%)	737 (96%)	28 (4%)	3 (0%)	43	52

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	48	PRO
1	B	49	ALA
1	B	50	ASP

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	211/238 (89%)	202 (96%)	9 (4%)	40	51
1	B	211/238 (89%)	205 (97%)	6 (3%)	56	73
1	C	211/238 (89%)	206 (98%)	5 (2%)	61	78
All	All	633/714 (89%)	613 (97%)	20 (3%)	51	67

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

Mol	Chain	Res	Type
1	A	16	LEU
1	A	17	LYS
1	A	54	SER
1	A	163	ILE
1	A	165	ARG
1	A	184	LYS
1	A	218	PRO
1	A	259	ASP
1	A	262	SER

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Mol	Chain	Res	Type
1	B	47	ILE
1	B	50	ASP
1	B	51	MET
1	B	52	ARG
1	B	105	VAL
1	B	241	SER
1	C	47	ILE
1	C	52	ARG
1	C	54	SER
1	C	56	LYS
1	C	112	THR

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 ⓘ

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, 95th 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 ²)	Q<0.9
1	A	258/291 (88%)	0.24	23 (8%) 10 11	10, 25, 57, 99	15 (5%)
1	B	258/291 (88%)	0.43	25 (9%) 8 10	9, 27, 60, 99	15 (5%)
1	C	258/291 (88%)	1.89	85 (32%) 1 1	31, 60, 96, 123	15 (5%)
All	All	774/873 (88%)	0.85	133 (17%) 2 2	9, 35, 87, 123	45 (5%)

All (133) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	51	MET	14.8
1	C	47	ILE	14.4
1	C	51	MET	14.3
1	C	49	ALA	14.0
1	B	47	ILE	12.8
1	B	48	PRO	12.5
1	C	48	PRO	11.5
1	C	58	CYS	9.4
1	B	49	ALA	9.1
1	C	52	ARG	8.9
1	B	54	SER	8.7
1	A	48	PRO	8.5
1	B	46	SER	8.2
1	B	51	MET	8.1
1	C	50	ASP	7.8
1	C	46	SER	7.7
1	A	47	ILE	7.6
1	A	49	ALA	7.0
1	A	52	ARG	6.8
1	B	50	ASP	6.7
1	B	52	ARG	6.7
1	C	262	SER	5.8
1	C	39	CYS	5.7

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Mol	Chain	Res	Type	RSRZ
1	A	50	ASP	5.6
1	C	224	LEU	5.4
1	A	54	SER	5.3
1	C	55	GLY	5.2
1	C	53	LYS	5.2
1	C	78	MET	5.2
1	B	39	CYS	5.0
1	C	36	SER	5.0
1	C	72	SER	4.9
1	A	53	LYS	4.9
1	A	262	SER	4.8
1	B	58	CYS	4.8
1	C	54	SER	4.4
1	A	224	LEU	4.3
1	C	144	MET	4.3
1	A	39	CYS	3.9
1	B	53	LYS	3.9
1	B	78	MET	3.9
1	C	18	GLY	3.8
1	C	74	SER	3.8
1	B	175	GLN	3.7
1	C	89	ALA	3.6
1	A	36	SER	3.6
1	B	36	SER	3.6
1	C	87	VAL	3.6
1	B	273	GLU	3.6
1	B	55	GLY	3.5
1	C	240	LYS	3.5
1	C	193	VAL	3.5
1	B	177	LYS	3.5
1	B	242	SER	3.4
1	A	19	GLY	3.3
1	C	232	VAL	3.3
1	C	176	LEU	3.2
1	A	58	CYS	3.2
1	A	46	SER	3.2
1	C	109	ALA	3.2
1	C	57	VAL	3.2
1	C	43	ALA	3.2
1	C	185	VAL	3.1
1	B	144	MET	3.1
1	C	238	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	150	GLU	3.1
1	C	65	MET	3.1
1	C	44	LEU	3.0
1	C	177	LYS	3.0
1	B	224	LEU	3.0
1	C	60	MET	2.8
1	C	97	VAL	2.8
1	C	92	ILE	2.8
1	C	85	HIS	2.8
1	C	91	ILE	2.8
1	A	78	MET	2.7
1	C	56	LYS	2.7
1	B	72	SER	2.7
1	C	62	ASP	2.7
1	A	243	ASN	2.7
1	C	94	ALA	2.7
1	C	61	SER	2.6
1	A	74	SER	2.6
1	C	59	ARG	2.6
1	C	24	VAL	2.6
1	A	144	MET	2.6
1	A	273	GLU	2.6
1	C	32	ILE	2.6
1	A	18	GLY	2.5
1	B	176	LEU	2.5
1	C	79	ALA	2.5
1	C	105	VAL	2.5
1	C	149	GLY	2.5
1	C	265	LEU	2.5
1	C	86	PHE	2.5
1	C	165	ARG	2.5
1	C	73	VAL	2.5
1	C	100	ILE	2.4
1	A	17	LYS	2.4
1	C	269	SER	2.4
1	C	217	THR	2.4
1	C	187	GLU	2.4
1	C	175	GLN	2.4
1	C	68	ASP	2.3
1	C	245	VAL	2.3
1	C	71	ASN	2.3
1	B	240	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	74	SER	2.3
1	A	55	GLY	2.3
1	C	273	GLU	2.2
1	C	35	LYS	2.2
1	C	182	ILE	2.2
1	C	180	ASP	2.2
1	C	184	LYS	2.2
1	C	219	ALA	2.2
1	C	84	GLY	2.2
1	C	66	ILE	2.2
1	C	124	PHE	2.2
1	B	270	ASP	2.2
1	C	42	MET	2.2
1	C	81	VAL	2.1
1	C	88	GLU	2.1
1	C	76	PRO	2.1
1	C	183	ALA	2.1
1	C	82	ARG	2.1
1	C	173	CYS	2.1
1	C	147	THR	2.1
1	C	95	LEU	2.1
1	C	69	ILE	2.1
1	C	119	LYS	2.0
1	C	120	PHE	2.0
1	C	106	LEU	2.0
1	C	179	GLU	2.0

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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.