



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 09:29 PM GMT

PDB ID : 5AMS
Title : Crystal structure of Sqt1
Authors : Frenois, F.; Legrand, P.; Fribourg, S.
Deposited on : 2015-08-31
Resolution : 3.35 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

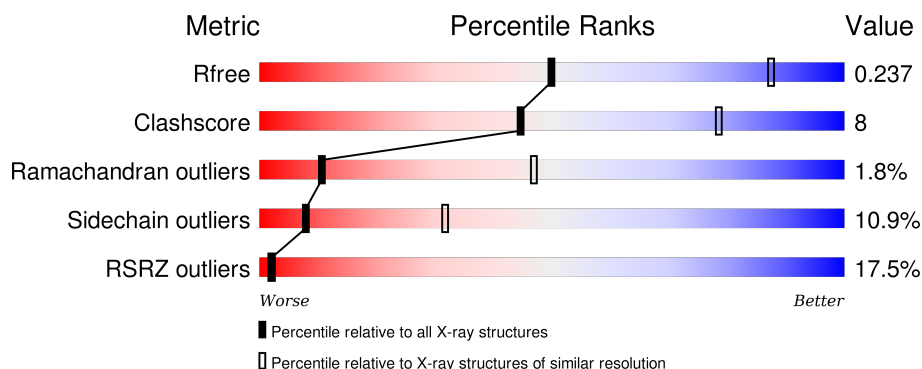
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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}	91344	1005 (3.42-3.30)
Clashscore	102246	1076 (3.42-3.30)
Ramachandran outliers	100387	1059 (3.42-3.30)
Sidechain outliers	100360	1058 (3.42-3.30)
RSRZ outliers	91569	1010 (3.42-3.30)

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. 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	431	
1	B	431	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5880 atoms, of which 0 are hydrogens and 0 are deuteriums.

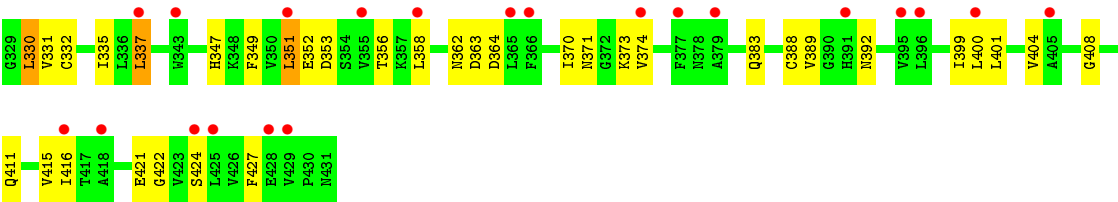
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called RIBOSOME ASSEMBLY PROTEIN SQT1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	0	0
			2990	1887	495	588	20			
1	B	379	Total	C	N	O	S	0	0	0
			2889	1826	481	562	20			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	O	0	0
			1	1		



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	166.00 Å 166.00 Å 95.35 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.37 – 3.35 83.00 – 3.35	Depositor EDS
% Data completeness (in resolution range)	99.2 (36.37-3.35) 99.1 (83.00-3.35)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 3.33 Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.171 , 0.222 0.191 , 0.237	Depositor DCC
R_{free} test set	1098 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	117.1	Xtriage
Anisotropy	0.766	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 136.0	EDS
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 21908 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5880	wwPDB-VP
Average B, all atoms (Å ²)	157.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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](#)

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	0.54	0/3051	0.85	2/4140 (0.0%)
1	B	0.49	0/2950	0.80	0/4003
All	All	0.52	0/6001	0.82	2/8143 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	30	ASP	C-N-CA	6.36	137.59	121.70
1	A	323	PHE	N-CA-C	5.24	125.14	111.00

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	2990	0	2897	40	0
1	B	2889	0	2810	52	0
2	B	1	0	0	0	0
All	All	5880	0	5707	92	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 8.

All (92) 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:116:SER:HB3	1:B:162:THR:HG23	1.57	0.87
1:A:313:SER:HB3	1:A:331:VAL:HG23	1.64	0.80
1:A:68:VAL:HG23	1:A:422:GLY:HA2	1.64	0.79
1:A:264:GLU:CD	1:A:264:GLU:H	1.90	0.74
1:A:30:ASP:HA	1:A:31:ILE:HG23	1.68	0.72
1:A:258:SER:HB2	1:A:317:ILE:HD12	1.73	0.70
1:A:362:ASN:CG	1:A:363:ASP:H	1.94	0.69
1:B:287:ASN:HB2	1:B:295:LEU:HD11	1.74	0.68
1:A:391:HIS:CD2	1:A:425:LEU:HD12	2.31	0.65
1:B:352:GLU:HG2	1:B:371:ASN:HD22	1.64	0.63
1:A:313:SER:HB3	1:A:331:VAL:CG2	2.29	0.62
1:A:55:ASN:OD1	1:A:57:SER:HB3	1.99	0.62
1:A:374:VAL:HB	1:A:388:CYS:HB2	1.82	0.62
1:B:330:LEU:HD23	1:B:332:CYS:SG	2.43	0.58
1:B:373:LYS:HG2	1:B:389:VAL:HG12	1.85	0.57
1:B:285:VAL:HG12	1:B:295:LEU:HB2	1.88	0.56
1:B:356:THR:HG21	1:B:370:ILE:HD13	1.87	0.55
1:B:203:ASP:HB2	1:B:226:LEU:HD12	1.88	0.55
1:B:58:LEU:HD23	1:B:59:THR:HG22	1.88	0.54
1:B:183:GLN:HG3	1:B:194:LEU:HD11	1.89	0.54
1:A:219:LEU:HB2	1:A:236:PHE:CE2	2.43	0.53
1:B:287:ASN:HB3	1:B:293:ALA:HB3	1.91	0.52
1:B:261:LEU:HD11	1:B:271:SER:O	2.11	0.51
1:B:374:VAL:HB	1:B:388:CYS:HB2	1.92	0.50
1:A:162:THR:HG22	1:A:170:PHE:HB3	1.93	0.50
1:A:374:VAL:HG11	1:A:415:VAL:HG11	1.93	0.50
1:B:59:THR:HB	1:B:97:GLN:HG2	1.93	0.49
1:B:303:LEU:HD22	1:B:307:GLN:HB3	1.94	0.49
1:B:401:LEU:HD11	1:B:416:ILE:HD12	1.94	0.49
1:A:166:ILE:HG12	1:A:216:GLU:HA	1.95	0.49
1:B:275:ALA:HB2	1:B:319:TRP:CZ2	2.48	0.49
1:B:254:ALA:HA	1:B:280:ASN:HD21	1.78	0.49
1:A:211:ASN:HA	1:A:271:SER:HB2	1.95	0.49
1:B:123:PHE:HA	1:B:145:TRP:HZ3	1.77	0.49
1:A:362:ASN:CG	1:A:363:ASP:N	2.64	0.48
1:B:352:GLU:CG	1:B:371:ASN:HD22	2.26	0.48
1:B:148:ALA:HB1	1:B:189:GLY:HA3	1.94	0.48
1:B:335:ILE:HD11	1:B:351:LEU:HD11	1.95	0.48
1:A:183:GLN:HG3	1:A:194:LEU:HD11	1.95	0.48
1:A:127:ALA:HB2	1:A:160:LEU:HD13	1.94	0.48
1:B:210:ILE:HG22	1:B:261:LEU:HD13	1.97	0.47
1:A:335:ILE:HG12	1:A:358:LEU:HD21	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:ALA:HB3	1:A:273:VAL:HB	1.97	0.47
1:B:58:LEU:HG	1:B:97:GLN:HG3	1.95	0.47
1:A:352:GLU:HG2	1:A:371:ASN:HD22	1.81	0.46
1:A:92:TRP:HE3	1:A:99:PRO:HB3	1.80	0.46
1:A:328:ILE:HD11	1:A:336:LEU:HD12	1.98	0.46
1:B:123:PHE:CE2	1:B:137:MET:HG3	2.51	0.45
1:A:335:ILE:HB	1:A:349:PHE:HB2	1.98	0.45
1:A:399:ILE:HD12	1:A:401:LEU:HD21	1.97	0.45
1:B:266:LEU:HD22	1:B:324:SER:HA	1.99	0.44
1:A:264:GLU:CD	1:A:264:GLU:N	2.66	0.44
1:A:416:ILE:HG12	1:A:426:VAL:HG13	1.99	0.44
1:A:370:ILE:HG13	1:A:394:GLY:HA3	1.99	0.44
1:B:71:ILE:HD11	1:B:416:ILE:HG22	2.00	0.44
1:A:266:LEU:HD13	1:A:324:SER:HA	2.00	0.44
1:A:169:THR:HG21	1:A:219:LEU:HD11	1.99	0.43
1:A:89:ALA:HB3	1:A:105:LEU:HB2	2.00	0.43
1:A:306:GLU:HG3	1:A:306:GLU:H	1.54	0.43
1:B:325:LEU:HD13	1:B:337:LEU:HD21	2.01	0.43
1:B:256:TRP:HA	1:B:278:SER:HA	2.01	0.43
1:B:210:ILE:HA	1:B:261:LEU:HD22	2.00	0.43
1:A:300:VAL:HG11	1:A:328:ILE:HD13	2.01	0.43
1:A:343:TRP:HA	1:A:343:TRP:CE3	2.54	0.43
1:B:315:GLU:HG3	1:B:331:VAL:HG23	2.00	0.43
1:B:327:ALA:HB1	1:B:358:LEU:HD13	2.00	0.43
1:B:159:TRP:CH2	1:B:207:GLY:HA3	2.54	0.42
1:B:370:ILE:HA	1:B:370:ILE:HD12	1.82	0.42
1:A:139:GLN:HG3	1:A:146:LYS:HB2	2.02	0.42
1:A:154:VAL:HG21	1:A:174:ALA:HB2	2.01	0.42
1:B:133:VAL:HB	1:B:151:MET:HG2	2.02	0.42
1:B:68:VAL:HG23	1:B:422:GLY:HA2	2.01	0.42
1:B:134:LEU:HD23	1:B:147:LEU:HD13	2.01	0.41
1:A:323:PHE:O	1:A:324:SER:HB3	2.20	0.41
1:B:158:VAL:HG12	1:B:159:TRP:HD1	1.85	0.41
1:A:325:LEU:HD22	1:A:346:ARG:HD3	2.02	0.41
1:B:177:GLY:O	1:B:200:HIS:HB2	2.20	0.41
1:B:306:GLU:H	1:B:306:GLU:HG3	1.63	0.41
1:B:237:THR:OG1	1:B:239:GLN:HB3	2.21	0.41
1:A:228:SER:HB2	1:A:246:GLN:HG3	2.03	0.41
1:B:163:HIS:ND1	1:B:166:ILE:N	2.62	0.41
1:B:415:VAL:HB	1:B:427:PHE:HB2	2.03	0.41
1:B:243:LYS:HG2	1:B:245:THR:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:ALA:HB2	1:A:319:TRP:CZ2	2.55	0.41
1:B:160:LEU:HG	1:B:172:PHE:HB3	2.03	0.41
1:B:347:HIS:HB2	1:B:349:PHE:HE1	1.86	0.40
1:B:311:ASP:HA	1:B:331:VAL:HG12	2.03	0.40
1:B:275:ALA:HB2	1:B:319:TRP:HZ2	1.87	0.40
1:B:109:GLY:N	1:B:128:ASP:OD2	2.54	0.40
1:B:347:HIS:HB2	1:B:349:PHE:CE1	2.57	0.40
1:B:131:GLY:HA2	1:B:157:ILE:HG13	2.02	0.40
1:B:131:GLY:HA3	1:B:154:VAL:O	2.21	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	388/431 (90%)	343 (88%)	38 (10%)	7 (2%)	11	47
1	B	377/431 (88%)	336 (89%)	34 (9%)	7 (2%)	10	46
All	All	765/862 (89%)	679 (89%)	72 (9%)	14 (2%)	11	47

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	270	ASN
1	B	324	SER
1	A	31	ILE
1	A	33	GLY
1	B	323	PHE
1	B	408	GLY
1	A	55	ASN
1	A	54	SER
1	B	119	SER

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Mol	Chain	Res	Type
1	B	362	ASN
1	A	121	GLY
1	A	122	GLY
1	A	311	ASP
1	B	404	VAL

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	332/370 (90%)	300 (90%)	32 (10%)	10	38
1	B	320/370 (86%)	281 (88%)	39 (12%)	6	25
All	All	652/740 (88%)	581 (89%)	71 (11%)	8	32

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	GLU
1	A	23	VAL
1	A	25	GLN
1	A	27	VAL
1	A	31	ILE
1	A	32	GLU
1	A	34	GLU
1	A	53	MET
1	A	110	GLU
1	A	119	SER
1	A	126	THR
1	A	155	GLU
1	A	202	GLN
1	A	203	ASP
1	A	208	GLU
1	A	228	SER
1	A	258	SER
1	A	264	GLU

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Mol	Chain	Res	Type
1	A	266	LEU
1	A	302	GLU
1	A	306	GLU
1	A	309	GLU
1	A	310	LEU
1	A	311	ASP
1	A	337	LEU
1	A	353	ASP
1	A	362	ASN
1	A	370	ILE
1	A	383	GLN
1	A	400	LEU
1	A	407	THR
1	A	421	GLU
1	B	58	LEU
1	B	65	THR
1	B	97	GLN
1	B	111	SER
1	B	119	SER
1	B	126	THR
1	B	144	GLN
1	B	193	GLN
1	B	203	ASP
1	B	216	GLU
1	B	220	GLU
1	B	228	SER
1	B	233	TRP
1	B	235	CYS
1	B	239	GLN
1	B	245	THR
1	B	246	GLN
1	B	260	SER
1	B	268	LYS
1	B	276	CYS
1	B	283	LEU
1	B	306	GLU
1	B	309	GLU
1	B	311	ASP
1	B	313	SER
1	B	318	SER
1	B	330	LEU
1	B	337	LEU

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Mol	Chain	Res	Type
1	B	351	LEU
1	B	353	ASP
1	B	363	ASP
1	B	364	ASP
1	B	383	GLN
1	B	392	ASN
1	B	399	ILE
1	B	400	LEU
1	B	411	GLN
1	B	421	GLU
1	B	424	SER

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	25	GLN
1	A	246	GLN
1	B	76	ASN
1	B	187	GLN
1	B	239	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 ⓘ

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	392/431 (90%)	1.00	68 (17%) 2 2	118, 155, 198, 241	0
1	B	379/431 (87%)	1.03	67 (17%) 2 2	127, 153, 190, 238	0
All	All	771/862 (89%)	1.02	135 (17%) 2 2	118, 154, 193, 241	0

All (135) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	22	GLU	6.6
1	B	91	LEU	4.8
1	A	23	VAL	4.6
1	B	184	ILE	4.2
1	A	157	ILE	4.1
1	A	79	LEU	3.9
1	B	79	LEU	3.9
1	A	220	GLU	3.8
1	B	379	ALA	3.7
1	B	145	TRP	3.7
1	B	209	PHE	3.5
1	A	219	LEU	3.5
1	A	300	VAL	3.5
1	B	113	ILE	3.4
1	A	170	PHE	3.4
1	A	230	ILE	3.3
1	B	80	VAL	3.3
1	A	355	VAL	3.2
1	A	395	VAL	3.2
1	B	405	ALA	3.1
1	B	365	LEU	3.1
1	A	123	PHE	3.1
1	A	314	ILE	3.1
1	B	355	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	71	ILE	3.0
1	A	125	VAL	3.0
1	B	391	HIS	3.0
1	B	300	VAL	3.0
1	A	283	LEU	2.9
1	A	124	LEU	2.9
1	B	142	GLY	2.9
1	A	377	PHE	2.9
1	B	337	LEU	2.9
1	B	249	ILE	2.8
1	B	257	ILE	2.8
1	A	276	CYS	2.8
1	B	328	ILE	2.8
1	B	200	HIS	2.8
1	B	418	ALA	2.8
1	A	337	LEU	2.8
1	B	400	LEU	2.7
1	B	343	TRP	2.7
1	A	221	LEU	2.7
1	A	282	LEU	2.7
1	A	209	PHE	2.7
1	B	366	PHE	2.7
1	A	286	ILE	2.7
1	A	266	LEU	2.6
1	A	244	ILE	2.6
1	A	284	ALA	2.6
1	B	135	VAL	2.6
1	A	365	LEU	2.6
1	B	68	VAL	2.6
1	B	59	THR	2.6
1	B	124	LEU	2.6
1	B	428	GLU	2.6
1	A	336	LEU	2.6
1	B	157	ILE	2.6
1	B	219	LEU	2.6
1	A	68	VAL	2.5
1	B	112	VAL	2.5
1	A	91	LEU	2.5
1	B	81	CYS	2.5
1	A	112	VAL	2.5
1	B	266	LEU	2.5
1	A	330	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	235	CYS	2.5
1	B	210	ILE	2.5
1	A	357	LYS	2.5
1	B	77	LEU	2.5
1	A	90	HIS	2.5
1	B	221	LEU	2.5
1	B	283	LEU	2.5
1	B	424	SER	2.4
1	A	142	GLY	2.4
1	A	399	ILE	2.4
1	A	400	LEU	2.4
1	B	244	ILE	2.4
1	B	259	LEU	2.4
1	A	426	VAL	2.4
1	B	374	VAL	2.4
1	B	172	PHE	2.4
1	A	191	LEU	2.4
1	A	301	ILE	2.3
1	B	395	VAL	2.3
1	B	100	LYS	2.3
1	A	233	TRP	2.3
1	A	343	TRP	2.3
1	A	261	LEU	2.3
1	A	328	ILE	2.3
1	A	105	LEU	2.3
1	A	210	ILE	2.3
1	B	416	ILE	2.3
1	B	222	VAL	2.3
1	A	429	VAL	2.3
1	A	416	ILE	2.2
1	B	117	PHE	2.2
1	A	379	ALA	2.2
1	B	322	LYS	2.2
1	A	184	ILE	2.2
1	B	288	CYS	2.2
1	A	69	PHE	2.2
1	A	127	ALA	2.2
1	A	411	GLN	2.2
1	A	232	ALA	2.2
1	A	102	ALA	2.2
1	A	335	ILE	2.2
1	B	396	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	158	VAL	2.1
1	B	126	THR	2.1
1	B	327	ALA	2.1
1	A	222	VAL	2.1
1	B	170	PHE	2.1
1	B	89	ALA	2.1
1	B	127	ALA	2.1
1	A	114	SER	2.1
1	A	166	ILE	2.1
1	A	274	VAL	2.1
1	A	259	LEU	2.1
1	B	377	PHE	2.1
1	B	179	VAL	2.1
1	B	429	VAL	2.1
1	B	105	LEU	2.1
1	B	317	ILE	2.1
1	B	233	TRP	2.0
1	A	223	THR	2.0
1	B	230	ILE	2.0
1	A	344	ARG	2.0
1	A	285	VAL	2.0
1	B	351	LEU	2.0
1	B	425	LEU	2.0
1	A	273	VAL	2.0
1	B	358	LEU	2.0
1	A	71	ILE	2.0
1	A	415	VAL	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.