



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 02:31 pm BST

PDB ID : 6A2A
Title : Crystal structure of a synthase 2 from santalum album
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Deposited on : 2018-06-09
Resolution : 1.77 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

<https://www.wwpdb.org/validation/2017/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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

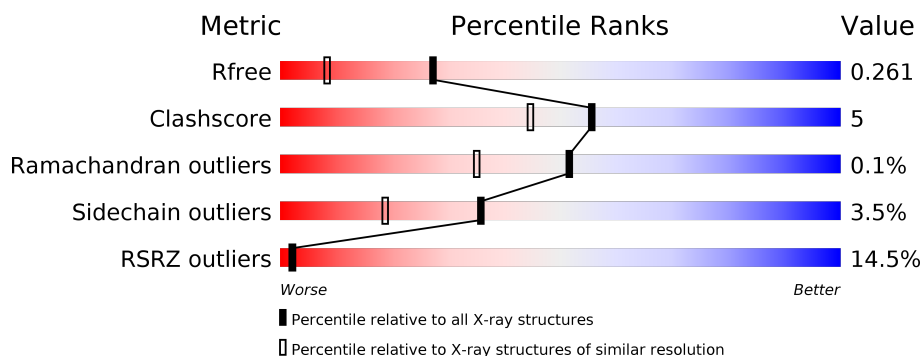
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.77 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}	130704	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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 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	566	<div> <div>5%</div> <div>86%</div> <div>7%</div> <div>7%</div> </div>
1	B	566	<div> <div>22%</div> <div>76%</div> <div>15%</div> <div>8%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9723 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 Sesquisabinene B synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	528	Total	C	N	O	S	0	0	0
			4329	2786	717	805	21			
1	B	520	Total	C	N	O	S	0	0	0
			4261	2749	703	789	20			

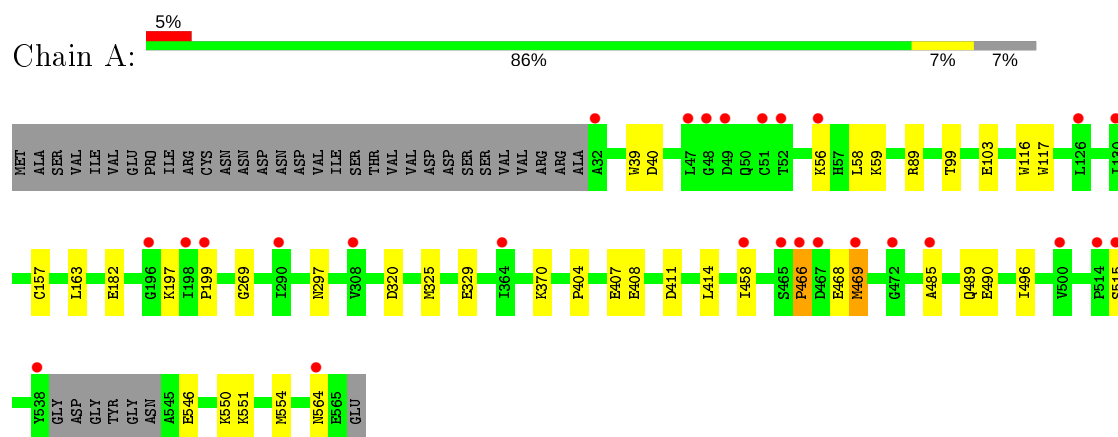
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	705	Total	O	0	0
			705	705		
2	B	428	Total	O	0	0
			428	428		

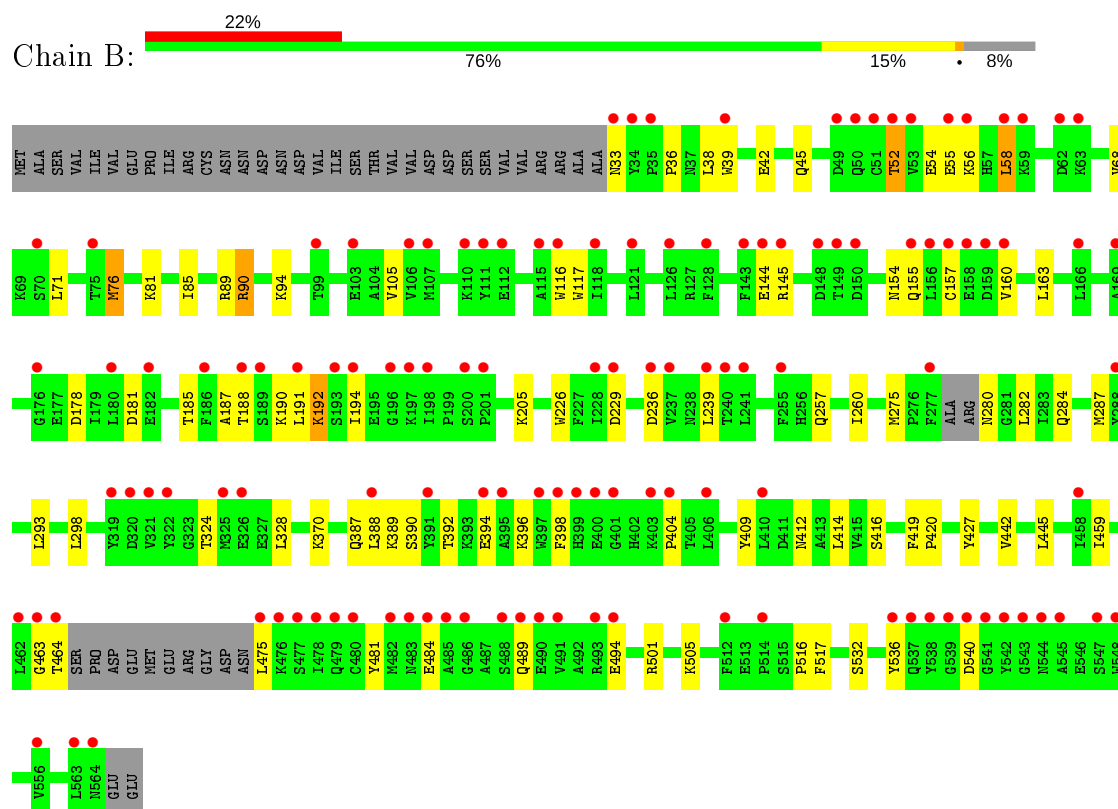
3 Residue-property plots [i](#)

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 ($RSRZ > 2$). 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: Sesquisabinene B synthase 2



• Molecule 1: Sesquisabinene B synthase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	133.01Å 133.01Å 142.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.94 – 1.77 24.92 – 1.77	Depositor EDS
% Data completeness (in resolution range)	99.9 (24.94-1.77) 100.0 (24.92-1.77)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 1.77Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.207 , 0.251 0.217 , 0.261	Depositor DCC
R_{free} test set	6235 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9723	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	0.84	0/4436	0.81	0/6007
1	B	0.65	0/4367	0.73	0/5913
All	All	0.75	0/8803	0.77	0/11920

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	4329	0	4264	23	0
1	B	4261	0	4199	65	0
2	A	705	0	0	9	0
2	B	428	0	0	18	0
All	All	9723	0	8463	87	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 5.

All (87) 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:287:MET:SD	2:B:949:HOH:O	2.21	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:466:PRO:HA	1:A:469:MET:HB2	1.50	0.93
1:B:459:ILE:HG22	1:B:536:TYR:HD2	1.34	0.90
1:B:532:SER:HB3	1:B:536:TYR:CE2	2.06	0.89
1:B:160:VAL:HG22	1:B:194:ILE:CD1	2.07	0.85
1:A:297:ASN:HB2	2:A:1085:HOH:O	1.80	0.81
1:B:387:GLN:O	1:B:390:SER:HB3	1.83	0.78
1:B:144:GLU:HG3	2:B:770:HOH:O	1.85	0.77
1:A:411:ASP:HB3	2:A:1087:HOH:O	1.89	0.73
1:B:257:GLN:O	1:B:260:ILE:HG22	1.91	0.70
1:B:52:THR:HA	2:B:868:HOH:O	1.93	0.67
1:B:160:VAL:HG22	1:B:194:ILE:HD12	1.76	0.67
1:B:144:GLU:CG	2:B:770:HOH:O	2.42	0.66
1:B:229:ASP:HB2	2:B:613:HOH:O	1.97	0.64
1:B:532:SER:CB	1:B:536:TYR:CE2	2.81	0.62
1:A:325:MET:O	1:A:329:GLU:HG3	1.99	0.62
1:A:197:LYS:NZ	2:A:602:HOH:O	2.32	0.62
1:B:282:LEU:C	1:B:282:LEU:HD13	2.21	0.61
1:B:459:ILE:HG22	1:B:536:TYR:CD2	2.26	0.61
1:A:485:ALA:HB2	2:A:1090:HOH:O	2.00	0.60
1:B:389:LYS:HA	1:B:392:THR:HG22	1.82	0.60
1:B:532:SER:HB3	1:B:536:TYR:HE2	1.65	0.60
1:A:550:LYS:HE3	2:A:740:HOH:O	2.00	0.59
1:A:458:ILE:HG23	1:A:496:ILE:CG2	2.34	0.58
1:B:157:CYS:HB2	1:B:190:LYS:HD2	1.84	0.58
1:B:481:TYR:HA	1:B:484:GLU:HG3	1.85	0.57
1:A:404:PRO:HB2	1:A:408:GLU:HG3	1.87	0.57
1:B:55:GLU:HA	1:B:58:LEU:HD23	1.86	0.56
1:B:459:ILE:CG2	1:B:536:TYR:HD2	2.14	0.55
1:B:501:ARG:O	1:B:505:LYS:HG3	2.06	0.55
1:B:257:GLN:HA	1:B:260:ILE:HG22	1.87	0.55
1:B:192:LYS:HE3	2:B:837:HOH:O	2.07	0.54
1:A:182:GLU:CD	2:A:628:HOH:O	2.47	0.53
1:B:389:LYS:O	1:B:392:THR:HG22	2.09	0.53
1:B:398:PHE:HD1	1:B:475:LEU:HD11	1.73	0.52
1:B:427:TYR:CD2	1:B:442:VAL:HG21	2.45	0.52
1:B:36:PRO:HD3	2:B:839:HOH:O	2.10	0.51
1:B:394:GLU:CG	1:B:412:ASN:HD22	2.22	0.51
1:B:390:SER:OG	1:B:416:SER:HB3	2.11	0.51
1:B:85:ILE:HD12	1:B:105:VAL:HG23	1.93	0.51
1:B:90:ARG:HD2	2:B:630:HOH:O	2.11	0.51
1:B:257:GLN:O	1:B:260:ILE:CG2	2.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:54:GLU:HB3	1:B:56:LYS:HG2	1.92	0.50
1:A:490:GLU:CD	1:A:490:GLU:H	2.16	0.49
1:A:269:GLY:O	1:B:370:LYS:HE2	2.12	0.49
1:B:178:ASP:OD1	2:B:601:HOH:O	2.20	0.49
1:B:404:PRO:HG2	1:B:409:TYR:HB2	1.95	0.49
1:A:404:PRO:HB2	1:A:408:GLU:CG	2.43	0.49
1:B:116:TRP:CE2	1:B:117:TRP:HD1	2.31	0.48
1:B:160:VAL:CG2	1:B:194:ILE:HD12	2.42	0.48
1:A:468:GLU:HG3	1:A:468:GLU:O	2.12	0.48
1:B:324:THR:O	1:B:328:LEU:HG	2.13	0.48
1:B:187:ALA:O	1:B:191:LEU:HG	2.14	0.48
1:B:388:LEU:C	2:B:619:HOH:O	2.53	0.48
1:A:404:PRO:CB	1:A:408:GLU:HG3	2.44	0.47
1:B:160:VAL:HG22	1:B:194:ILE:HD13	1.92	0.47
1:B:76:MET:HE1	2:B:981:HOH:O	2.14	0.47
1:A:157:CYS:HA	1:A:163:LEU:HD11	1.97	0.47
1:B:394:GLU:CG	1:B:412:ASN:ND2	2.78	0.47
1:B:68:VAL:HA	1:B:71:LEU:HD12	1.96	0.46
1:A:551:LYS:HE3	2:A:792:HOH:O	2.15	0.46
1:B:188:THR:O	1:B:192:LYS:HG3	2.16	0.46
1:B:414:LEU:C	1:B:414:LEU:HD12	2.37	0.46
1:B:205:LYS:NZ	2:B:613:HOH:O	2.50	0.45
1:B:505:LYS:NZ	2:B:618:HOH:O	2.47	0.45
1:B:94:LYS:HE2	2:B:906:HOH:O	2.18	0.44
1:B:275:MET:HA	1:B:275:MET:CE	2.48	0.44
1:A:116:TRP:CE2	1:A:117:TRP:HD1	2.35	0.44
1:B:236:ASP:OD1	1:B:236:ASP:N	2.51	0.44
1:B:445:LEU:HB2	2:B:603:HOH:O	2.17	0.44
1:A:414:LEU:C	1:A:414:LEU:HD12	2.38	0.43
1:B:45:GLN:OE1	2:B:602:HOH:O	2.21	0.43
1:A:325:MET:HE2	2:A:1201:HOH:O	2.19	0.43
1:A:99:THR:O	1:A:103:GLU:HG3	2.19	0.43
1:B:39:TRP:HB3	1:B:280:ASN:OD1	2.19	0.42
1:B:163:LEU:CB	1:B:191:LEU:HD21	2.49	0.42
1:B:463:GLY:O	1:B:464:THR:C	2.57	0.42
1:B:442:VAL:HG22	1:B:517:PHE:HE1	1.84	0.42
1:B:38:LEU:HD23	1:B:39:TRP:CZ3	2.55	0.42
1:B:516:PRO:HD2	2:B:864:HOH:O	2.20	0.42
1:B:205:LYS:HE2	1:B:226:TRP:CZ2	2.55	0.42
1:A:56:LYS:NZ	2:A:635:HOH:O	2.53	0.42
1:A:39:TRP:HE1	1:A:554:MET:HE2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:419:PHE:N	1:B:420:PRO:CD	2.83	0.41
1:B:257:GLN:C	1:B:260:ILE:HG22	2.40	0.41
1:B:293:LEU:HD12	1:B:298:LEU:HB3	2.02	0.41
1:B:76:MET:CE	2:B:981:HOH:O	2.69	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	524/566 (93%)	508 (97%)	15 (3%)	1 (0%)	47	32
1	B	514/566 (91%)	495 (96%)	19 (4%)	0	100	100
All	All	1038/1132 (92%)	1003 (97%)	34 (3%)	1 (0%)	51	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	466	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	474/507 (94%)	461 (97%)	13 (3%)	44	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	466/507 (92%)	446 (96%)	20 (4%)	29	12
All	All	940/1014 (93%)	907 (96%)	33 (4%)	36	19

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ASP
1	A	58	LEU
1	A	59	LYS
1	A	89	ARG
1	A	199	PRO
1	A	320	ASP
1	A	370	LYS
1	A	407	GLU
1	A	469	MET
1	A	489	GLN
1	A	515	SER
1	A	546	GLU
1	A	564	ASN
1	B	33	ASN
1	B	42	GLU
1	B	52	THR
1	B	58	LEU
1	B	76	MET
1	B	81	LYS
1	B	89	ARG
1	B	90	ARG
1	B	145	ARG
1	B	154	ASN
1	B	155	GLN
1	B	181	ASP
1	B	185	THR
1	B	192	LYS
1	B	239	LEU
1	B	284	GLN
1	B	396	LYS
1	B	489	GLN
1	B	494	GLU
1	B	540	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	113	ASN
1	B	412	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 carbohydrates 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, 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	528/566 (93%)	0.38	27 (5%) 28 26	15, 27, 53, 94	0
1	B	520/566 (91%)	1.36	125 (24%) 0 0	20, 44, 82, 108	0
All	All	1048/1132 (92%)	0.86	152 (14%) 2 2	15, 35, 74, 108	0

All (152) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	157	CYS	7.6
1	A	466	PRO	7.5
1	B	51	CYS	7.3
1	A	472	GLY	6.7
1	B	186	PHE	6.3
1	B	538	TYR	6.2
1	A	538	TYR	6.0
1	B	111	TYR	6.0
1	B	401	GLY	5.9
1	B	485	ALA	5.8
1	A	467	ASP	5.7
1	B	486	GLY	5.6
1	B	398	PHE	5.5
1	B	464	THR	5.4
1	B	99	THR	5.4
1	B	399	HIS	5.2
1	B	50	GLN	5.2
1	B	239	LEU	5.1
1	B	52	THR	5.1
1	B	478	ILE	4.9
1	B	149	THR	4.9
1	B	75	THR	4.9
1	B	548	TRP	4.8
1	B	33	ASN	4.8

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Mol	Chain	Res	Type	RSRZ
1	B	406	LEU	4.8
1	B	176	GLY	4.7
1	B	55	GLU	4.7
1	B	56	LYS	4.7
1	A	196	GLY	4.6
1	B	191	LEU	4.5
1	B	158	GLU	4.5
1	B	462	LEU	4.4
1	B	545	ALA	4.3
1	A	465	SER	4.3
1	B	110	LYS	4.3
1	B	489	GLN	4.2
1	B	514	PRO	4.1
1	B	156	LEU	4.0
1	B	463	GLY	3.9
1	A	52	THR	3.9
1	B	540	ASP	3.9
1	B	479	GLN	3.9
1	B	49	ASP	3.9
1	B	106	VAL	3.8
1	B	395	ALA	3.8
1	B	112	GLU	3.8
1	B	322	TYR	3.7
1	B	116	TRP	3.7
1	B	541	GLY	3.7
1	B	537	GLN	3.6
1	B	62	ASP	3.6
1	B	115	ALA	3.5
1	B	277	PHE	3.5
1	B	483	ASN	3.5
1	B	107	MET	3.5
1	A	469	MET	3.5
1	B	35	PRO	3.4
1	B	155	GLN	3.4
1	B	189	SER	3.4
1	B	536	TYR	3.4
1	B	397	TRP	3.4
1	B	237	VAL	3.4
1	B	118	ILE	3.4
1	B	126	LEU	3.3
1	B	193	SER	3.3
1	B	236	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	58	LEU	3.2
1	B	70	SER	3.1
1	B	255	PHE	3.1
1	B	34	TYR	3.1
1	B	201	PRO	3.1
1	B	228	ILE	3.1
1	B	403	LYS	3.1
1	B	180	LEU	3.1
1	B	476	LYS	3.0
1	B	159	ASP	3.0
1	B	491	VAL	3.0
1	B	148	ASP	3.0
1	B	539	GLY	3.0
1	B	563	LEU	3.0
1	B	128	PHE	3.0
1	B	410	LEU	3.0
1	B	63	LYS	2.9
1	B	319	TYR	2.9
1	B	477	SER	2.9
1	A	564	ASN	2.8
1	A	32	ALA	2.8
1	B	288	TYR	2.8
1	B	512	PHE	2.8
1	A	485	ALA	2.8
1	B	182	GLU	2.7
1	B	480	CYS	2.7
1	A	48	GLY	2.7
1	B	194	ILE	2.7
1	B	404	PRO	2.7
1	B	143	PHE	2.7
1	A	51	CYS	2.7
1	B	160	VAL	2.7
1	B	488	SER	2.6
1	B	229	ASP	2.6
1	B	325	MET	2.6
1	B	145	ARG	2.6
1	A	49	ASP	2.6
1	A	515	SER	2.6
1	B	188	THR	2.5
1	B	494	GLU	2.5
1	B	321	VAL	2.5
1	B	241	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	544	ASN	2.5
1	B	144	GLU	2.5
1	A	290	ILE	2.5
1	B	39	TRP	2.5
1	B	169	ALA	2.5
1	A	364	ILE	2.5
1	B	493	ARG	2.4
1	B	198	ILE	2.4
1	B	564	ASN	2.4
1	B	543	GLY	2.4
1	A	458	ILE	2.4
1	A	199	PRO	2.4
1	A	47	LEU	2.3
1	B	542	TYR	2.3
1	B	59	LYS	2.3
1	B	53	VAL	2.3
1	B	490	GLU	2.3
1	B	166	LEU	2.3
1	A	130	ILE	2.3
1	A	514	PRO	2.3
1	B	475	LEU	2.3
1	B	394	GLU	2.3
1	A	198	ILE	2.2
1	B	482	MET	2.2
1	B	547	SER	2.2
1	A	56	LYS	2.2
1	A	308	VAL	2.2
1	B	200	SER	2.1
1	B	103	GLU	2.1
1	B	326	GLU	2.1
1	B	484	GLU	2.1
1	B	197	LYS	2.1
1	B	556	VAL	2.1
1	B	121	LEU	2.1
1	B	458	ILE	2.1
1	B	240	THR	2.1
1	A	500	VAL	2.1
1	B	400	GLU	2.1
1	B	150	ASP	2.1
1	B	320	ASP	2.0
1	A	126	LEU	2.0
1	B	388	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	391	TYR	2.0
1	B	196	GLY	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.