



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:43 AM UTC

PDB ID : 8CEI / pdb_00008cei
Title : Succinyl-CoA Reductase from Clostridium kluyveri (SucD)
Authors : Pfister, P.; Diehl, C.; Erb, T.J.
Deposited on : 2023-02-02
Resolution : 2.20 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 types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (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

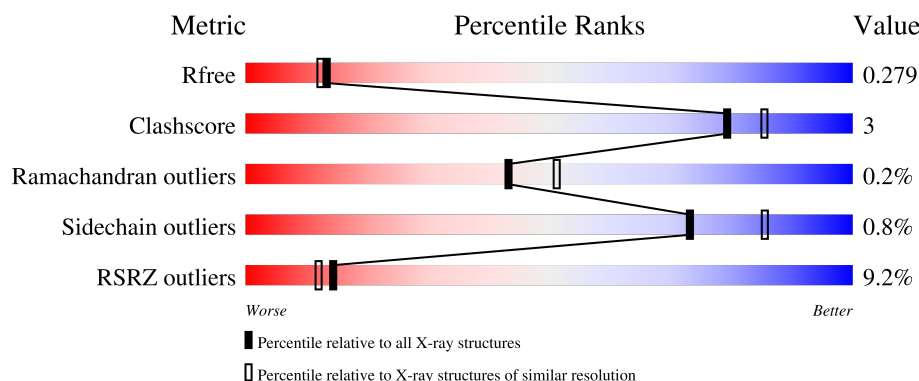
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 ≥ 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	453	9% 91% 8%
1	B	453	8% 92% 6%
1	C	453	9% 90% 9%
1	D	453	11% 91% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14600 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 Succinate-semialdehyde dehydrogenase (acetylating).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	447	Total	C	N	O	S	0	0	0
			3394	2149	573	657	15			
1	B	447	Total	C	N	O	S	0	0	0
			3394	2149	573	657	15			
1	C	447	Total	C	N	O	S	0	0	0
			3394	2149	573	657	15			
1	D	447	Total	C	N	O	S	0	0	0
			3394	2149	573	657	15			

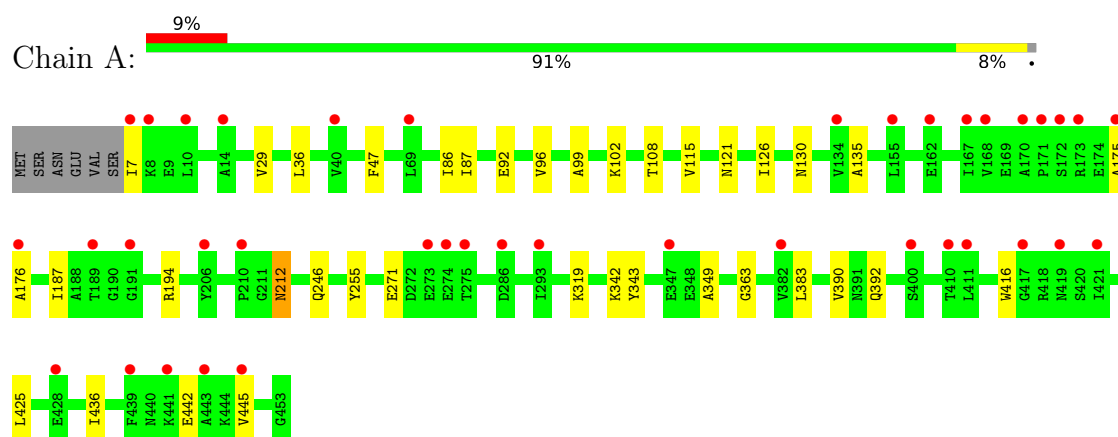
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	227	Total	O	0	0
			227	227		
2	B	259	Total	O	0	0
			259	259		
2	C	281	Total	O	0	0
			281	281		
2	D	257	Total	O	0	0
			257	257		

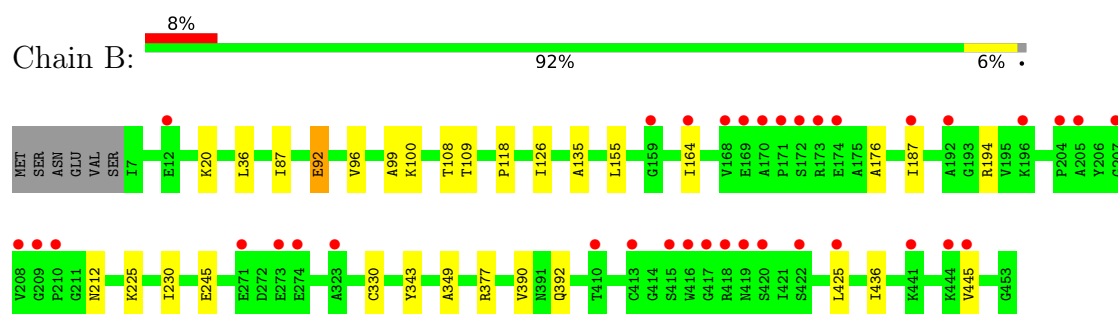
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

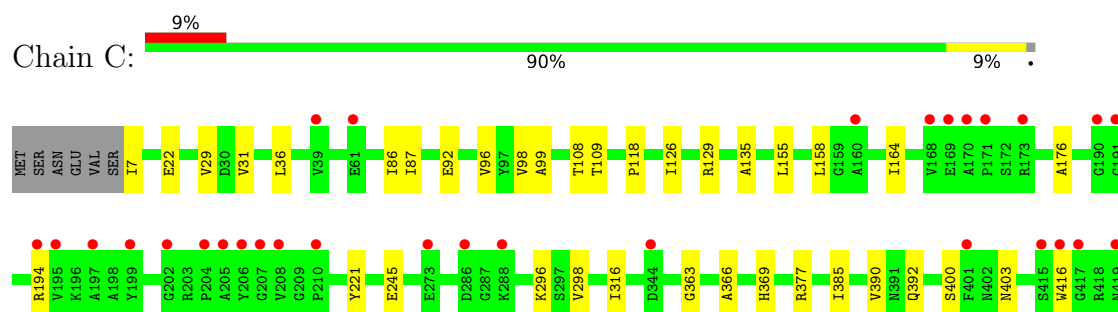
- Molecule 1: Succinate-semialdehyde dehydrogenase (acetylating)

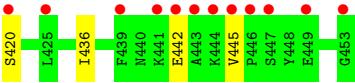


- Molecule 1: Succinate-semialdehyde dehydrogenase (acetylating)

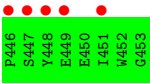
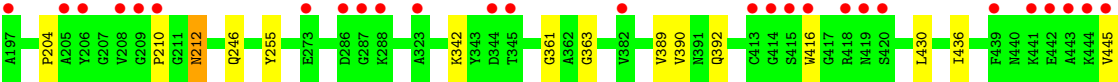
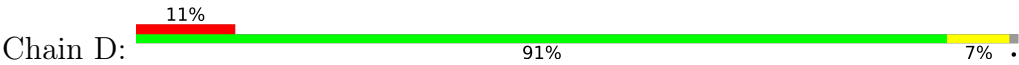


- Molecule 1: Succinate-semialdehyde dehydrogenase (acetylating)





● Molecule 1: Succinate-semialdehyde dehydrogenase (acetylating)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.23Å 89.34Å 137.32Å 90.00° 104.64° 90.00°	Depositor
Resolution (Å)	39.47 – 2.20 39.47 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.5 (39.47-2.20) 98.4 (39.47-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.20.1-4487	Depositor
R, R_{free}	0.242 , 0.267 (Not available) , 0.279	Depositor DCC
R_{free} test set	1969 reflections (1.91%)	wwPDB-VP
Wilson B-factor (Å ²)	28.5	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.58$, $\langle L^2 \rangle = 0.43$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14600	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 58.47 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0362e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [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	0.08	0/3451	0.23	0/4667
1	B	0.07	0/3451	0.22	0/4667
1	C	0.08	0/3451	0.23	0/4667
1	D	0.08	0/3451	0.23	0/4667
All	All	0.08	0/13804	0.23	0/18668

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 [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	3394	0	3441	18	0
1	B	3394	0	3441	20	0
1	C	3394	0	3441	22	0
1	D	3394	0	3441	18	0
2	A	227	0	0	1	0
2	B	259	0	0	4	0
2	C	281	0	0	3	0
2	D	257	0	0	0	0
All	All	14600	0	13764	75	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 3.

All (75) 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:330:CYS:SG	2:B:501:HOH:O	2.43	0.76
1:C:36:LEU:HD11	1:C:126:ILE:HD12	1.79	0.64
1:D:36:LEU:HD11	1:D:126:ILE:HD12	1.79	0.64
1:B:36:LEU:HD11	1:B:126:ILE:HD12	1.86	0.57
1:C:296:LYS:NZ	2:C:506:HOH:O	2.38	0.57
1:C:108:THR:HG21	1:C:194:ARG:HH21	1.70	0.56
1:D:87:ILE:HD13	1:D:99:ALA:HB2	1.87	0.56
1:C:22:GLU:HA	1:C:129:ARG:HD2	1.88	0.56
1:D:96:VAL:HB	1:D:436:ILE:HB	1.88	0.54
1:A:36:LEU:HD11	1:A:126:ILE:HD12	1.89	0.54
1:B:225:LYS:NZ	2:B:517:HOH:O	2.40	0.54
1:C:87:ILE:HD13	1:C:99:ALA:HB2	1.90	0.53
1:A:271:GLU:HG3	1:A:319:LYS:HD2	1.91	0.52
1:B:20:LYS:NZ	2:B:522:HOH:O	2.43	0.51
1:A:383:LEU:O	1:B:100:LYS:HE2	2.11	0.51
1:B:194:ARG:NH1	2:B:527:HOH:O	2.45	0.50
1:C:176:ALA:HB1	1:C:194:ARG:HH22	1.76	0.49
1:B:109:THR:HG21	1:B:118:PRO:HG3	1.94	0.49
1:A:86:ILE:HD13	1:B:377:ARG:HH11	1.78	0.49
1:A:108:THR:HG22	1:A:135:ALA:HB3	1.95	0.49
1:C:7:ILE:N	2:C:516:HOH:O	2.46	0.48
1:C:363:GLY:HA3	1:C:416:TRP:HB2	1.94	0.48
1:B:108:THR:HG21	1:B:194:ARG:HH21	1.79	0.48
1:D:155:LEU:HD13	1:D:164:ILE:HD11	1.95	0.47
1:C:109:THR:HG21	1:C:118:PRO:HG3	1.96	0.47
1:A:87:ILE:HD13	1:A:99:ALA:HB2	1.97	0.47
1:A:96:VAL:HB	1:A:436:ILE:HB	1.96	0.47
1:C:31:VAL:HG12	1:C:158:LEU:HD13	1.97	0.47
1:B:87:ILE:HD13	1:B:99:ALA:HB2	1.96	0.47
1:A:343:TYR:CG	1:A:349:ALA:HB2	2.50	0.46
1:C:86:ILE:HG12	1:C:98:VAL:HG22	1.98	0.46
1:C:366:ALA:HB3	1:C:385:ILE:HD13	1.98	0.46
1:D:390:VAL:O	1:D:392:GLN:HG2	2.15	0.45
1:A:187:ILE:HD13	1:A:425:LEU:HD21	1.99	0.45
1:B:176:ALA:HB1	1:B:194:ARG:HH22	1.82	0.45
1:C:108:THR:HG22	1:C:135:ALA:HB3	1.98	0.45
1:B:92:GLU:H	1:B:92:GLU:CD	2.25	0.44
1:D:31:VAL:HG12	1:D:158:LEU:HD13	2.00	0.44
1:D:389:VAL:CG1	1:D:392:GLN:HG3	2.48	0.44
1:B:108:THR:HG22	1:B:135:ALA:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:187:ILE:HD11	1:D:430:LEU:HD21	2.00	0.44
1:C:96:VAL:HB	1:C:436:ILE:HB	1.98	0.44
1:C:155:LEU:HD13	1:C:164:ILE:HD11	2.00	0.44
1:B:230:ILE:HG23	1:B:245:GLU:HG2	1.99	0.44
1:D:255:TYR:CD1	1:D:342:LYS:HG2	2.53	0.44
1:B:96:VAL:HB	1:B:436:ILE:HB	1.99	0.44
1:A:102:LYS:N	1:A:130:ASN:OD1	2.47	0.44
1:A:176:ALA:HB1	1:A:194:ARG:HH22	1.83	0.44
1:A:121:ASN:ND2	2:A:517:HOH:O	2.48	0.43
1:D:22:GLU:HA	1:D:129:ARG:HD2	2.01	0.43
1:D:363:GLY:HA3	1:D:416:TRP:HB2	2.00	0.43
1:D:389:VAL:HG12	1:D:392:GLN:HG3	2.01	0.43
1:C:298:VAL:HG13	1:C:316:ILE:HD11	2.00	0.43
1:B:155:LEU:HD13	1:B:164:ILE:HD11	2.00	0.43
1:B:187:ILE:HD13	1:B:425:LEU:HD21	2.01	0.42
1:B:390:VAL:O	1:B:392:GLN:HG2	2.19	0.42
1:C:377:ARG:NH1	2:C:520:HOH:O	2.49	0.42
1:C:245:GLU:OE1	1:C:245:GLU:N	2.52	0.42
1:B:343:TYR:CG	1:B:349:ALA:HB2	2.55	0.42
1:C:390:VAL:O	1:C:392:GLN:HG2	2.19	0.42
1:A:7:ILE:HD11	1:A:175:ALA:HB1	2.02	0.41
1:A:47:PHE:HB3	1:A:115:VAL:HG21	2.02	0.41
1:A:212:ASN:HA	1:A:246:GLN:HG3	2.02	0.41
1:D:108:THR:HG22	1:D:135:ALA:HB3	2.01	0.41
1:A:390:VAL:O	1:A:392:GLN:HG2	2.19	0.41
1:B:245:GLU:OE1	1:B:245:GLU:N	2.46	0.41
1:C:400:SER:HB3	1:C:403:ASN:ND2	2.36	0.41
1:D:109:THR:HG21	1:D:118:PRO:HG3	2.02	0.41
1:D:212:ASN:HA	1:D:246:GLN:HG3	2.02	0.41
1:A:255:TYR:CD1	1:A:342:LYS:HG2	2.56	0.41
1:C:221:TYR:CE2	1:C:369:HIS:HB3	2.56	0.41
1:A:363:GLY:HA3	1:A:416:TRP:HB2	2.03	0.41
1:C:420:SER:HA	1:D:204:PRO:HB3	2.03	0.41
1:D:136:PRO:HG3	1:D:167:ILE:HD11	2.03	0.41
1:D:210:PRO:O	1:D:361:GLY:HA2	2.20	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	445/453 (98%)	437 (98%)	7 (2%)	1 (0%)	43	51
1	B	445/453 (98%)	437 (98%)	7 (2%)	1 (0%)	43	51
1	C	445/453 (98%)	437 (98%)	8 (2%)	0	100	100
1	D	445/453 (98%)	439 (99%)	5 (1%)	1 (0%)	43	51
All	All	1780/1812 (98%)	1750 (98%)	27 (2%)	3 (0%)	43	51

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	ASN
1	D	212	ASN
1	B	212	ASN

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	360/366 (98%)	356 (99%)	4 (1%)	65	79
1	B	360/366 (98%)	358 (99%)	2 (1%)	78	89
1	C	360/366 (98%)	356 (99%)	4 (1%)	65	79
1	D	360/366 (98%)	358 (99%)	2 (1%)	78	89
All	All	1440/1464 (98%)	1428 (99%)	12 (1%)	73	85

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	VAL
1	A	92	GLU
1	A	442	GLU
1	A	445	VAL
1	B	92	GLU
1	B	445	VAL
1	C	29	VAL
1	C	92	GLU
1	C	442	GLU
1	C	445	VAL
1	D	92	GLU
1	D	445	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	HIS
1	B	163	ASN
1	C	402	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 ⓘ

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	447/453 (98%)	0.85	39 (8%) 16 13	22, 32, 53, 103	0
1	B	447/453 (98%)	0.69	36 (8%) 18 15	21, 30, 46, 112	0
1	C	447/453 (98%)	0.91	42 (9%) 14 11	21, 30, 52, 102	0
1	D	447/453 (98%)	0.73	48 (10%) 11 8	20, 31, 50, 120	0
All	All	1788/1812 (98%)	0.80	165 (9%) 14 12	20, 30, 52, 120	0

All (165) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	344	ASP	5.8
1	C	170	ALA	5.7
1	D	170	ALA	5.6
1	C	171	PRO	5.1
1	D	171	PRO	5.1
1	A	275	THR	5.0
1	D	169	GLU	5.0
1	C	443	ALA	4.3
1	C	206	TYR	4.3
1	A	170	ALA	4.2
1	B	170	ALA	4.2
1	C	344	ASP	4.1
1	C	419	ASN	4.1
1	B	417	GLY	4.0
1	C	208	VAL	3.8
1	A	441	LYS	3.8
1	A	443	ALA	3.8
1	D	168	VAL	3.7
1	B	171	PRO	3.7
1	A	171	PRO	3.6
1	D	445	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	441	LYS	3.5
1	B	209	GLY	3.5
1	A	173	ARG	3.5
1	A	7	ILE	3.4
1	D	446	PRO	3.4
1	A	175	ALA	3.4
1	D	382	VAL	3.2
1	D	413	CYS	3.1
1	A	176	ALA	3.1
1	B	208	VAL	3.1
1	D	197	ALA	3.1
1	D	443	ALA	3.1
1	D	447	SER	3.1
1	C	194	ARG	3.0
1	C	415	SER	3.0
1	C	441	LYS	3.0
1	D	209	GLY	3.0
1	C	169	GLU	3.0
1	A	274	GLU	3.0
1	D	273	GLU	3.0
1	C	39	VAL	2.9
1	C	168	VAL	2.9
1	D	414	GLY	2.9
1	A	172	SER	2.9
1	B	273	GLU	2.9
1	B	323	ALA	2.9
1	D	442	GLU	2.9
1	C	420	SER	2.8
1	C	205	ALA	2.8
1	C	447	SER	2.8
1	C	202	GLY	2.8
1	C	204	PRO	2.8
1	A	206	TYR	2.8
1	A	168	VAL	2.8
1	C	173	ARG	2.8
1	D	194	ARG	2.8
1	A	428	GLU	2.8
1	D	206	TYR	2.8
1	D	418	ARG	2.8
1	C	210	PRO	2.7
1	D	167	ILE	2.7
1	D	420	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	439	PHE	2.7
1	A	410	THR	2.7
1	C	207	GLY	2.7
1	B	173	ARG	2.7
1	D	173	ARG	2.7
1	B	441	LYS	2.6
1	D	191	GLY	2.6
1	D	416	TRP	2.6
1	B	12	GLU	2.6
1	C	61	GLU	2.6
1	C	286	ASP	2.6
1	A	445	VAL	2.6
1	B	196	LYS	2.6
1	D	288	LYS	2.6
1	C	425	LEU	2.5
1	D	449	GLU	2.5
1	D	419	ASN	2.5
1	A	189	THR	2.5
1	D	208	VAL	2.5
1	B	274	GLU	2.5
1	C	288	LYS	2.5
1	D	287	GLY	2.5
1	D	345	THR	2.5
1	C	417	GLY	2.5
1	B	271	GLU	2.5
1	C	273	GLU	2.5
1	D	23	ALA	2.5
1	C	191	GLY	2.5
1	B	422	SER	2.4
1	A	191	GLY	2.4
1	D	323	ALA	2.4
1	A	8	LYS	2.4
1	B	445	VAL	2.4
1	D	192	ALA	2.4
1	B	410	THR	2.4
1	B	420	SER	2.4
1	A	382	VAL	2.4
1	C	442	GLU	2.4
1	B	419	ASN	2.3
1	D	286	ASP	2.3
1	D	190	GLY	2.3
1	D	444	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	453	GLY	2.3
1	D	205	ALA	2.3
1	C	449	GLU	2.3
1	B	416	TRP	2.3
1	B	174	GLU	2.3
1	C	445	VAL	2.3
1	C	444	LYS	2.3
1	C	199	TYR	2.3
1	C	160	ALA	2.3
1	C	197	ALA	2.3
1	C	195	VAL	2.3
1	B	207	GLY	2.2
1	C	190	GLY	2.2
1	A	419	ASN	2.2
1	C	446	PRO	2.2
1	D	210	PRO	2.2
1	B	415	SER	2.2
1	A	293	ILE	2.2
1	A	411	LEU	2.2
1	A	347	GLU	2.2
1	A	155	LEU	2.2
1	B	418	ARG	2.2
1	A	286	ASP	2.2
1	B	169	GLU	2.2
1	D	61	GLU	2.2
1	B	413	CYS	2.2
1	A	400	SER	2.2
1	B	187	ILE	2.1
1	D	7	ILE	2.1
1	D	451	ILE	2.1
1	C	416	TRP	2.1
1	B	204	PRO	2.1
1	A	14	ALA	2.1
1	D	415	SER	2.1
1	C	439	PHE	2.1
1	B	172	SER	2.1
1	A	69	LEU	2.1
1	B	168	VAL	2.1
1	B	159	GLY	2.1
1	B	192	ALA	2.1
1	B	205	ALA	2.1
1	B	425	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	155	LEU	2.1
1	A	167	ILE	2.1
1	B	164	ILE	2.1
1	B	210	PRO	2.1
1	A	134	VAL	2.1
1	D	172	SER	2.0
1	D	448	TYR	2.0
1	A	40	VAL	2.0
1	A	417	GLY	2.0
1	C	401	PHE	2.0
1	D	439	PHE	2.0
1	A	162	GLU	2.0
1	A	273	GLU	2.0
1	A	10	LEU	2.0
1	A	210	PRO	2.0
1	A	421	ILE	2.0
1	B	444	LYS	2.0
1	D	196	LYS	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.