Full wwPDB X-ray Structure Validation Report ⓘ

Feb 10, 2024 – 10:47 AM EST

PDB ID	:	2SCP
Title	:	STRUCTURE OF A SARCOPLASMIC CALCIUM-BINDING PROTEIN FROM NEREIS DIVERSICOLOR REFINED AT 2.0 ANGSTROMS RESOLUTION
Authors	:	Cook, W.J.; Vijay-Kumar, S.
Deposited on	:	1991-08-22
Resolution	:	2.00 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:

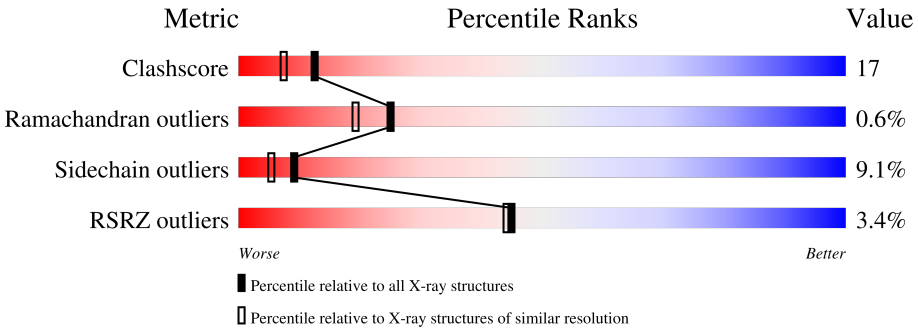
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	174	67% 29%
1	B	174	7% 64% 29% 6%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2955 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 SARCOPLASMIC CALCIUM-BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	174	Total	C	N	O	S	0	0	0
			1368	868	218	272	10			
1	B	174	Total	C	N	O	S	0	0	0
			1368	868	218	272	10			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Ca	0	0
			3	3		
2	B	3	Total	Ca	0	0
			3	3		

- Molecule 3 is water.

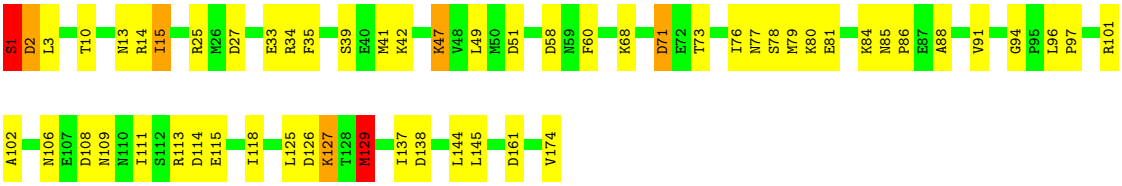
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	124	Total	O	0	0
			124	124		
3	B	89	Total	O	0	0
			89	89		

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.

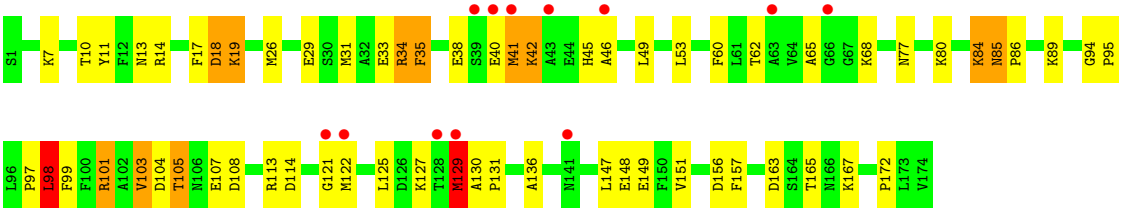
• Molecule 1: SARCOPLASMIC CALCIUM-BINDING PROTEIN

Chain A:



• Molecule 1: SARCOPLASMIC CALCIUM-BINDING PROTEIN

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	43.60Å 56.00Å 65.80Å 90.00° 92.60° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00 5.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00) 88.5 (5.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$	-	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.180 , (Not available) 0.186 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	15.7	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.68 , 114.8	EDS
L-test for twinning[1]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.042 for h,-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2955	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows:

[1]Theoretical values of $< |L| >$, $< L^2 >$ 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

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	1.00	1/1396 (0.1%)	1.44	14/1880 (0.7%)
1	B	0.94	0/1396	1.47	13/1880 (0.7%)
All	All	0.97	1/2792 (0.0%)	1.46	27/3760 (0.7%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	174	VAL	C-O	6.04	1.34	1.23

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	104	ASP	CB-CG-OD2	-9.28	109.95	118.30
1	B	114	ASP	CB-CG-OD1	8.31	125.78	118.30
1	B	18	ASP	CB-CG-OD2	-7.97	111.13	118.30
1	A	129	MET	CA-CB-CG	7.78	126.53	113.30
1	B	113	ARG	NE-CZ-NH2	-7.77	116.41	120.30
1	A	174	VAL	CA-C-O	-7.62	104.09	120.10
1	A	71	ASP	CB-CG-OD1	7.38	124.94	118.30
1	B	34	ARG	NE-CZ-NH1	7.22	123.91	120.30
1	A	25	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	A	51	ASP	CB-CG-OD2	-6.70	112.27	118.30
1	A	113	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	B	156	ASP	CB-CG-OD1	6.67	124.31	118.30
1	A	15	ILE	CA-CB-CG2	6.56	124.02	110.90
1	B	149	GLU	OE1-CD-OE2	-6.49	115.52	123.30
1	A	34	ARG	CD-NE-CZ	6.32	132.44	123.60
1	B	101	ARG	NE-CZ-NH2	6.31	123.46	120.30
1	B	148	GLU	CG-CD-OE1	6.29	130.88	118.30
1	A	1	SER	N-CA-CB	-6.21	101.19	110.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	98	LEU	CA-CB-CG	6.20	129.56	115.30
1	A	34	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	A	138	ASP	CB-CG-OD2	6.03	123.73	118.30
1	A	113	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	A	47	LYS	N-CA-CB	5.90	121.22	110.60
1	B	129	MET	CA-CB-CG	5.71	123.01	113.30
1	B	11	TYR	CB-CG-CD2	-5.58	117.65	121.00
1	A	115	GLU	OE1-CD-OE2	5.33	129.70	123.30
1	B	108	ASP	CB-CG-OD1	5.19	122.97	118.30

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	1368	0	1310	35	0
1	B	1368	0	1310	56	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	124	0	0	7	0
3	B	89	0	0	2	0
All	All	2955	0	2620	90	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 17.

All (90) 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:A:129:MET:HB3	3:A:316:HOH:O	1.59	1.01
1:B:121:GLY:HA3	1:B:127:LYS:NZ	1.76	0.99
1:B:136:ALA:HB1	1:B:165:THR:HG22	1.46	0.97
1:B:86:PRO:O	1:B:89:LYS:HG3	1.64	0.95
1:B:45:HIS:CD2	1:B:105:THR:HG23	2.06	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:PHE:CD2	1:B:49:LEU:HD11	2.11	0.85
1:B:41:MET:HB3	1:B:105:THR:CG2	2.08	0.84
1:B:42:LYS:HE3	1:B:45:HIS:HB2	1.61	0.82
1:B:41:MET:HB3	1:B:105:THR:HG22	1.63	0.80
1:A:13:ASN:HD22	1:A:14:ARG:HE	1.27	0.80
1:B:99:PHE:O	1:B:103:VAL:HG12	1.83	0.79
1:A:78:SER:HA	1:A:81:GLU:OE1	1.82	0.79
1:B:121:GLY:HA3	1:B:127:LYS:HZ1	1.48	0.77
1:B:18:ASP:O	1:B:19:LYS:HB2	1.84	0.77
1:B:29:GLU:O	1:B:33:GLU:HG3	1.88	0.74
1:A:49:LEU:HD12	1:A:102:ALA:HB1	1.72	0.72
1:B:136:ALA:CB	1:B:165:THR:HG22	2.22	0.69
1:B:42:LYS:HD2	1:B:42:LYS:O	1.92	0.69
1:B:34:ARG:O	1:B:38:GLU:HG2	1.94	0.67
1:A:114:ASP:O	1:A:118:ILE:HD13	1.96	0.66
1:A:13:ASN:ND2	1:A:14:ARG:HE	1.92	0.66
1:A:129:MET:SD	3:A:316:HOH:O	2.53	0.65
1:B:26:MET:HG3	3:B:274:HOH:O	1.97	0.65
1:A:27:ASP:HB3	3:A:198:HOH:O	1.99	0.62
1:B:41:MET:CB	1:B:105:THR:HG22	2.30	0.62
1:B:85:ASN:ND2	1:B:85:ASN:H	1.98	0.60
1:B:41:MET:CB	1:B:105:THR:CG2	2.81	0.59
1:B:77:ASN:ND2	1:B:80:LYS:NZ	2.51	0.59
1:B:13:ASN:HD22	1:B:14:ARG:HE	1.51	0.58
1:A:88:ALA:O	1:A:91:VAL:HG13	2.04	0.58
1:B:41:MET:HB3	1:B:105:THR:HG21	1.85	0.58
1:B:163:ASP:CG	1:B:167:LYS:HZ2	2.07	0.58
1:A:49:LEU:CD1	1:A:102:ALA:HB1	2.33	0.57
1:B:41:MET:HE3	1:B:46:ALA:N	2.18	0.57
1:B:121:GLY:CA	1:B:127:LYS:NZ	2.61	0.57
1:B:121:GLY:HA3	1:B:127:LYS:HZ3	1.67	0.56
1:B:94:GLY:O	1:B:97:PRO:HD2	2.06	0.56
1:B:136:ALA:HB1	1:B:165:THR:CG2	2.28	0.56
1:B:35:PHE:HD1	1:B:35:PHE:O	1.90	0.55
1:B:84:LYS:O	1:B:86:PRO:HD3	2.06	0.55
1:B:77:ASN:HD22	1:B:80:LYS:NZ	2.05	0.54
1:A:94:GLY:O	1:A:97:PRO:HD2	2.08	0.54
1:B:65:ALA:O	1:B:68:LYS:HD3	2.08	0.53
1:B:77:ASN:ND2	1:B:80:LYS:HZ3	2.07	0.53
1:B:17:PHE:HZ	1:B:34:ARG:HD3	1.74	0.52
1:A:76:ILE:O	1:A:80:LYS:HB2	2.08	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:HIS:CD2	1:B:105:THR:CG2	2.85	0.52
1:A:126:ASP:HB3	1:A:129:MET:SD	2.49	0.52
1:B:31:MET:HG3	1:B:122:MET:SD	2.50	0.52
1:A:42:LYS:HD2	1:A:106:ASN:HA	1.92	0.51
1:A:118:ILE:HD12	1:A:127:LYS:NZ	2.25	0.51
1:A:126:ASP:O	1:A:129:MET:HG2	2.10	0.50
1:B:7:LYS:HE3	1:B:157:PHE:O	2.10	0.50
1:A:108:ASP:O	1:A:109:ASN:HB2	2.11	0.50
1:A:27:ASP:C	3:A:198:HOH:O	2.49	0.50
1:A:71:ASP:OD1	1:A:73:THR:N	2.45	0.50
1:A:60:PHE:CE1	1:A:94:GLY:HA3	2.47	0.49
1:A:1:SER:HB2	3:A:261:HOH:O	2.13	0.48
1:B:136:ALA:CB	1:B:165:THR:CG2	2.88	0.48
1:A:161:ASP:HB3	3:A:243:HOH:O	2.13	0.48
1:B:163:ASP:OD2	1:B:167:LYS:NZ	2.47	0.48
1:B:42:LYS:HD2	1:B:42:LYS:C	2.31	0.48
1:B:130:ALA:HB3	1:B:131:PRO:HD3	1.97	0.46
1:A:85:ASN:HA	1:A:86:PRO:HD2	1.80	0.45
1:A:1:SER:N	3:A:311:HOH:O	2.48	0.45
1:B:94:GLY:N	1:B:95:PRO:CD	2.80	0.45
1:B:60:PHE:CE1	1:B:94:GLY:HA3	2.52	0.44
1:A:77:ASN:O	1:A:81:GLU:HG3	2.17	0.44
1:B:41:MET:CG	1:B:105:THR:HG21	2.48	0.44
1:A:111:ILE:HB	1:A:145:LEU:HB2	2.00	0.44
1:B:95:PRO:O	1:B:98:LEU:HB2	2.18	0.44
1:A:81:GLU:O	1:A:84:LYS:HB2	2.18	0.44
1:A:13:ASN:HD22	1:A:14:ARG:NE	2.05	0.44
1:B:13:ASN:HB2	3:B:218:HOH:O	2.17	0.44
1:A:10:THR:O	1:A:14:ARG:HG2	2.18	0.43
1:B:147:LEU:O	1:B:151:VAL:HG13	2.19	0.42
1:B:31:MET:CG	1:B:122:MET:CE	2.98	0.42
1:B:42:LYS:HE3	1:B:45:HIS:CB	2.43	0.42
1:B:85:ASN:ND2	1:B:85:ASN:N	2.66	0.42
1:B:41:MET:CB	1:B:105:THR:HG21	2.47	0.42
1:B:45:HIS:HD2	1:B:105:THR:HG23	1.77	0.42
1:A:79:MET:HE2	1:A:79:MET:HB3	1.95	0.41
1:A:137:ILE:HG22	1:A:145:LEU:HD22	2.02	0.41
1:B:10:THR:O	1:B:14:ARG:HG2	2.20	0.41
1:A:96:LEU:N	1:A:97:PRO:CD	2.83	0.41
1:A:39:SER:HB3	1:A:41:MET:HE3	2.03	0.41
1:A:58:ASP:O	1:B:101:ARG:NE	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:ILE:HD12	1:A:127:LYS:HZ3	1.85	0.40
1:B:35:PHE:HB2	1:B:122:MET:HE2	2.03	0.40
1:B:129:MET:HG3	1:B:172:PRO:HG2	2.02	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	172/174 (99%)	167 (97%)	4 (2%)	1 (1%)	25	19
1	B	172/174 (99%)	164 (95%)	7 (4%)	1 (1%)	25	19
All	All	344/348 (99%)	331 (96%)	11 (3%)	2 (1%)	25	19

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	107	GLU
1	A	2	ASP

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	148/148 (100%)	135 (91%)	13 (9%)	10	6

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	148/148 (100%)	134 (90%)	14 (10%)	8 5
All	All	296/296 (100%)	269 (91%)	27 (9%)	9 5

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	SER
1	A	2	ASP
1	A	3	LEU
1	A	15	ILE
1	A	33	GLU
1	A	35	PHE
1	A	47	LYS
1	A	68	LYS
1	A	101	ARG
1	A	125	LEU
1	A	127	LYS
1	A	129	MET
1	A	144	LEU
1	B	19	LYS
1	B	35	PHE
1	B	40	GLU
1	B	41	MET
1	B	42	LYS
1	B	53	LEU
1	B	62	THR
1	B	84	LYS
1	B	85	ASN
1	B	98	LEU
1	B	103	VAL
1	B	105	THR
1	B	125	LEU
1	B	129	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	109	ASN
1	A	110	ASN
1	B	13	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	45	HIS
1	B	77	ASN
1	B	85	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 95^{th} 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	174/174 (100%)	-0.36	0 100 100	8, 16, 30, 34	0
1	B	174/174 (100%)	0.22	12 (6%) 16 16	11, 26, 31, 32	0
All	All	348/348 (100%)	-0.07	12 (3%) 45 44	8, 20, 31, 34	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	40	GLU	3.8
1	B	43	ALA	2.7
1	B	66	GLY	2.6
1	B	128	THR	2.6
1	B	141	ASN	2.5
1	B	63	ALA	2.5
1	B	122	MET	2.4
1	B	41	MET	2.4
1	B	121	GLY	2.2
1	B	46	ALA	2.1
1	B	39	SER	2.1
1	B	129	MET	2.1

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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CA	B	194	1/1	0.96	0.23	9,9,9,9	0
2	CA	A	192	1/1	0.98	0.16	2,2,2,2	0
2	CA	B	193	1/1	0.99	0.22	2,2,2,2	0
2	CA	A	191	1/1	0.99	0.15	2,2,2,2	0
2	CA	B	195	1/1	0.99	0.28	2,2,2,2	0
2	CA	A	190	1/1	1.00	0.20	2,2,2,2	0

6.5 Other polymers (i)

There are no such residues in this entry.