



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:27 PM UTC

PDB ID : 4ZN0 / pdb_00004zn0
Title : Structure of the NADPH-dependent thioredoxin reductase from
Methanosarcina mazei
Authors : Buey, R.M.; de Pereda, J.M.; Balsera, M.
Deposited on : 2015-05-04
Resolution : 2.60 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

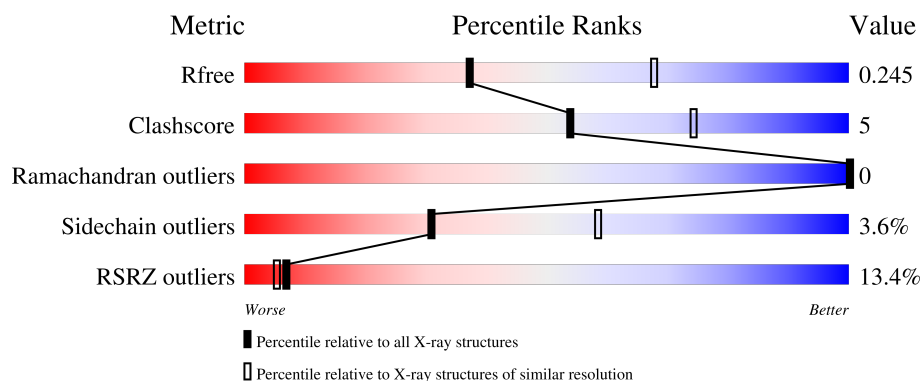
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	311	10% 81% 10% 8%
1	B	311	7% 82% 7% 10%
1	C	311	13% 82% 8% 10%
1	D	311	18% 80% 6% 13%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15485 atoms, of which 7463 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 Thioredoxin reductase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	287	Total	C	H	N	O	S	0	0	0
			4137	1326	2036	360	410	5			
1	B	279	Total	C	H	N	O	S	0	0	0
			3982	1291	1950	339	397	5			
1	C	279	Total	C	H	N	O	S	0	0	0
			3804	1252	1838	332	378	4			
1	D	270	Total	C	H	N	O	S	0	0	0
			3494	1172	1639	322	357	4			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q8PUI1
A	-1	SER	-	expression tag	UNP Q8PUI1
A	0	HIS	-	expression tag	UNP Q8PUI1
A	1	MET	-	expression tag	UNP Q8PUI1
A	2	ALA	-	expression tag	UNP Q8PUI1
A	3	SER	-	expression tag	UNP Q8PUI1
B	-2	GLY	-	expression tag	UNP Q8PUI1
B	-1	SER	-	expression tag	UNP Q8PUI1
B	0	HIS	-	expression tag	UNP Q8PUI1
B	1	MET	-	expression tag	UNP Q8PUI1
B	2	ALA	-	expression tag	UNP Q8PUI1
B	3	SER	-	expression tag	UNP Q8PUI1
C	-2	GLY	-	expression tag	UNP Q8PUI1
C	-1	SER	-	expression tag	UNP Q8PUI1
C	0	HIS	-	expression tag	UNP Q8PUI1
C	1	MET	-	expression tag	UNP Q8PUI1
C	2	ALA	-	expression tag	UNP Q8PUI1
C	3	SER	-	expression tag	UNP Q8PUI1
D	-2	GLY	-	expression tag	UNP Q8PUI1
D	-1	SER	-	expression tag	UNP Q8PUI1
D	0	HIS	-	expression tag	UNP Q8PUI1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	expression tag	UNP Q8PUI1
D	2	ALA	-	expression tag	UNP Q8PUI1
D	3	SER	-	expression tag	UNP Q8PUI1

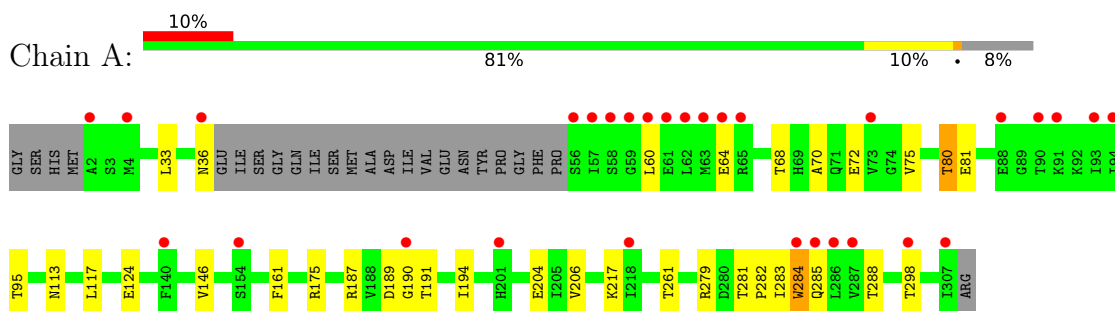
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	22	Total 22	O 22	0	0
2	B	23	Total 23	O 23	0	0
2	C	9	Total 9	O 9	0	0
2	D	14	Total 14	O 14	0	0

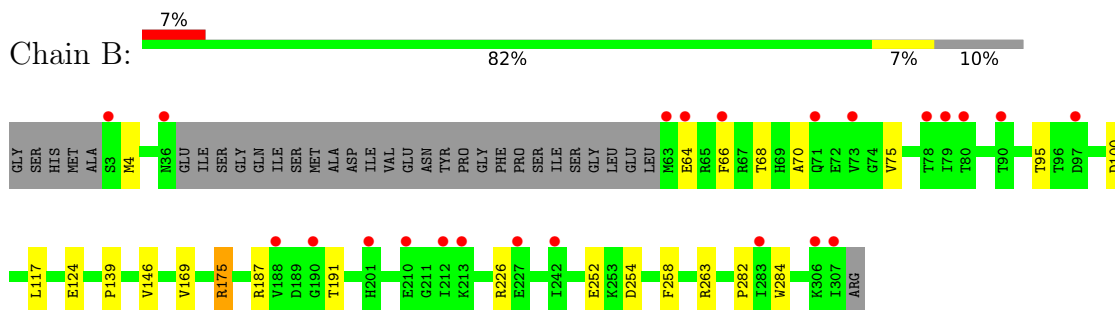
3 Residue-property plots [i](#)

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.

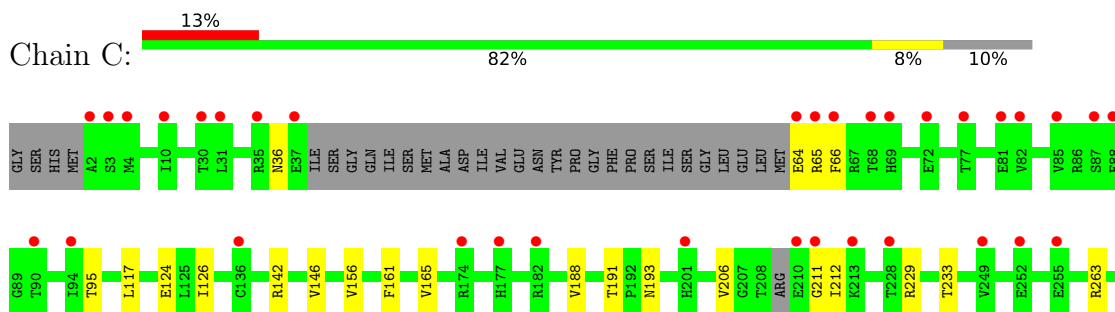
- Molecule 1: Thioredoxin reductase



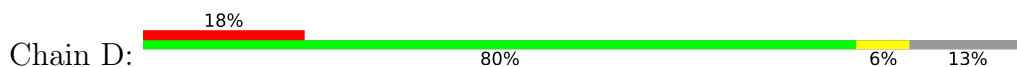
- Molecule 1: Thioredoxin reductase

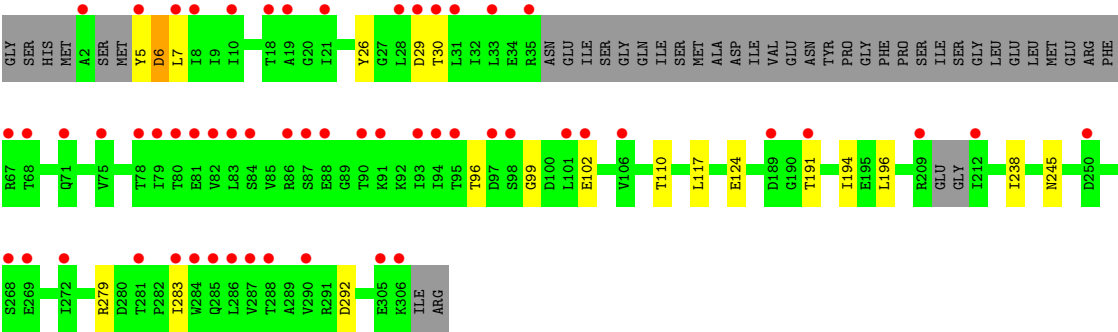


- Molecule 1: Thioredoxin reductase



- Molecule 1: Thioredoxin reductase





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	117.14Å 182.50Å 152.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.89 – 2.60 46.89 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.89-2.60) 100.0 (46.89-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.61Å)	Xtriage
Refinement program	PHENIX dev_1839	Depositor
R, R_{free}	0.217 , 0.241 0.227 , 0.245	Depositor DCC
R_{free} test set	2412 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	61.0	Xtriage
Anisotropy	0.432	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 65.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15485	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% 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 [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	0.33	0/2132	0.69	0/2899
1	B	0.32	0/2063	0.65	0/2813
1	C	0.33	0/1996	0.68	0/2728
1	D	0.34	0/1882	0.74	1/2564 (0.0%)
All	All	0.33	0/8073	0.69	1/11004 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	283	ILE	N-CA-C	6.16	117.64	110.62

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	2101	2036	2030	32	0
1	B	2032	1950	1947	18	0
1	C	1966	1838	1836	12	0
1	D	1855	1639	1635	24	0
2	A	22	0	0	0	0
2	B	23	0	0	2	0
2	C	9	0	0	0	0
2	D	14	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8022	7463	7448	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 5.

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:D:96:THR:HG22	1:D:99:GLY:O	1.35	1.22
1:D:96:THR:HG23	1:D:99:GLY:H	1.27	0.99
1:C:279:ARG:NH1	1:C:292:ASP:OD2	1.96	0.98
1:A:282:PRO:HG3	1:B:252:GLU:OE1	1.66	0.94
1:D:6:ASP:HB2	1:D:29:ASP:O	1.75	0.85
1:D:96:THR:CG2	1:D:99:GLY:O	2.21	0.85
1:D:5:TYR:HB2	1:D:102:GLU:O	1.78	0.83
1:A:206:VAL:CG1	1:A:217:LYS:HB2	2.09	0.83
1:A:191:THR:HG21	1:A:194:ILE:HD12	1.61	0.81
1:D:6:ASP:CB	1:D:29:ASP:O	2.29	0.80
1:B:95:THR:HG22	1:B:100:ASP:OD1	1.84	0.78
1:A:68:THR:O	1:A:72:GLU:HG3	1.84	0.77
1:A:282:PRO:O	1:A:284:TRP:CZ3	2.39	0.76
1:A:282:PRO:CG	1:B:252:GLU:OE1	2.36	0.74
1:A:281:THR:O	1:A:284:TRP:HZ3	1.71	0.72
1:B:146:VAL:CG1	1:B:169:VAL:HG22	2.23	0.68
1:A:204:GLU:OE1	1:B:226:ARG:NH1	2.28	0.67
1:A:283:ILE:HG22	1:A:285:GLN:H	1.61	0.66
1:A:298:THR:HG21	1:C:161:PHE:CE1	2.31	0.65
1:A:64:GLU:O	1:A:68:THR:HG23	1.95	0.65
1:D:96:THR:CG2	1:D:99:GLY:H	2.06	0.63
1:B:175:ARG:NH1	2:B:401:HOH:O	2.33	0.61
1:A:282:PRO:C	1:A:284:TRP:CZ3	2.79	0.60
1:A:187:ARG:NH1	1:C:263:ARG:HE	1.98	0.60
1:D:6:ASP:HB2	1:D:29:ASP:CA	2.32	0.60
1:D:6:ASP:HB2	1:D:29:ASP:N	2.16	0.60
1:A:191:THR:HG21	1:A:194:ILE:CD1	2.31	0.59
1:A:283:ILE:C	1:A:284:TRP:CE3	2.82	0.58
1:A:187:ARG:HH12	1:C:263:ARG:HE	1.51	0.58
1:D:6:ASP:HB2	1:D:29:ASP:C	2.28	0.57
1:A:281:THR:O	1:A:284:TRP:CZ3	2.56	0.57
1:A:284:TRP:CE3	1:A:284:TRP:N	2.73	0.56
1:A:206:VAL:HG12	1:A:217:LYS:HB2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:PRO:HA	1:D:26:TYR:HE1	1.71	0.55
1:D:279:ARG:NH1	1:D:292:ASP:OD2	2.39	0.55
1:D:124:GLU:OE1	1:D:124:GLU:N	2.40	0.54
1:B:263:ARG:NH2	2:B:403:HOH:O	2.41	0.54
1:C:124:GLU:N	1:C:124:GLU:OE1	2.39	0.54
1:D:124:GLU:OE2	2:D:401:HOH:O	2.18	0.53
1:D:124:GLU:CD	2:D:401:HOH:O	2.51	0.53
1:A:124:GLU:N	1:A:124:GLU:OE1	2.41	0.53
1:A:190:GLY:HA2	1:A:191:THR:C	2.34	0.53
1:B:124:GLU:OE1	1:B:124:GLU:N	2.42	0.52
1:D:6:ASP:HB2	1:D:29:ASP:CB	2.40	0.51
1:D:110:THR:HB	1:D:245:ASN:HB2	1.92	0.51
1:A:284:TRP:N	1:A:284:TRP:CD2	2.79	0.51
1:C:64:GLU:HG2	1:C:65:ARG:H	1.76	0.51
1:B:282:PRO:O	1:B:284:TRP:N	2.43	0.51
1:A:282:PRO:O	1:A:284:TRP:CH2	2.64	0.50
1:B:187:ARG:O	1:B:191:THR:OG1	2.29	0.50
1:A:261:THR:OG1	1:A:279:ARG:HD2	2.13	0.49
1:D:6:ASP:CB	1:D:29:ASP:N	2.76	0.49
1:B:64:GLU:O	1:B:68:THR:HG23	2.13	0.49
1:B:70:ALA:HB1	1:B:75:VAL:HG21	1.94	0.48
1:C:156:VAL:HG13	1:C:188:VAL:HG21	1.95	0.48
1:B:139:PRO:HA	1:D:26:TYR:CE1	2.49	0.47
1:D:6:ASP:CB	1:D:29:ASP:H	2.28	0.47
1:A:80:THR:OG1	1:A:81:GLU:N	2.48	0.46
1:D:117:LEU:HD11	1:D:238:ILE:HG12	1.96	0.46
1:C:191:THR:HG22	1:C:193:ASN:OD1	2.15	0.45
1:B:254:ASP:OD1	1:B:258:PHE:N	2.46	0.45
1:C:142:ARG:HA	1:C:165:VAL:HG22	1.99	0.45
1:D:6:ASP:HB2	1:D:29:ASP:H	1.83	0.44
1:A:70:ALA:HB1	1:A:75:VAL:CG2	2.48	0.43
1:B:95:THR:HG22	1:B:100:ASP:CG	2.43	0.43
1:C:211:GLY:HA2	1:C:212:ILE:C	2.44	0.43
1:D:7:LEU:O	1:D:30:THR:HA	2.19	0.43
1:D:191:THR:OG1	1:D:194:ILE:HD12	2.18	0.43
1:A:70:ALA:HB1	1:A:75:VAL:HG21	2.01	0.42
1:A:161:PHE:CE1	1:C:298:THR:HG21	2.54	0.42
1:A:282:PRO:HB3	1:B:252:GLU:HG3	2.02	0.41
1:A:285:GLN:O	1:A:288:THR:OG1	2.36	0.41
1:B:75:VAL:O	1:B:75:VAL:HG23	2.20	0.41
1:A:161:PHE:CZ	1:C:298:THR:HG21	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:ILE:C	1:A:284:TRP:HE3	2.28	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	283/311 (91%)	267 (94%)	16 (6%)	0	100	100
1	B	275/311 (88%)	264 (96%)	11 (4%)	0	100	100
1	C	273/311 (88%)	258 (94%)	15 (6%)	0	100	100
1	D	263/311 (85%)	253 (96%)	10 (4%)	0	100	100
All	All	1094/1244 (88%)	1042 (95%)	52 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	209/255 (82%)	198 (95%)	11 (5%)	20	43
1	B	200/255 (78%)	196 (98%)	4 (2%)	48	74
1	C	182/255 (71%)	172 (94%)	10 (6%)	19	41
1	D	152/255 (60%)	150 (99%)	2 (1%)	61	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	743/1020 (73%)	716 (96%)	27 (4%)	31 58

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

Mol	Chain	Res	Type
1	A	33	LEU
1	A	36	ASN
1	A	60	LEU
1	A	80	THR
1	A	95	THR
1	A	113	ASN
1	A	117	LEU
1	A	146	VAL
1	A	175	ARG
1	A	189	ASP
1	A	284	TRP
1	B	4	MET
1	B	66	PHE
1	B	117	LEU
1	B	175	ARG
1	C	36	ASN
1	C	66	PHE
1	C	95	THR
1	C	117	LEU
1	C	126	ILE
1	C	146	VAL
1	C	206	VAL
1	C	229	ARG
1	C	233	THR
1	C	298	THR
1	D	6	ASP
1	D	196	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	167	GLN
1	B	245	ASN
1	D	113	ASN
1	D	199	ASN
1	D	245	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 [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	287/311 (92%)	0.65	30 (10%) 11 9	45, 65, 115, 143	0
1	B	279/311 (89%)	0.61	23 (8%) 17 14	49, 69, 104, 132	0
1	C	279/311 (89%)	0.85	40 (14%) 6 5	59, 79, 114, 137	0
1	D	270/311 (86%)	1.11	56 (20%) 2 2	49, 83, 118, 143	0
All	All	1115/1244 (89%)	0.80	149 (13%) 7 5	45, 72, 113, 143	0

All (149) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	2	ALA	8.3
1	B	36	ASN	6.5
1	A	2	ALA	6.0
1	A	307	ILE	5.6
1	D	30	THR	5.3
1	B	283	ILE	5.3
1	D	212	ILE	5.2
1	C	3	SER	5.1
1	D	98	SER	5.1
1	D	102	GLU	5.0
1	D	285	GLN	5.0
1	B	307	ILE	5.0
1	C	210	GLU	5.0
1	D	90	THR	5.0
1	C	64	GLU	5.0
1	B	78	THR	4.9
1	C	90	THR	4.8
1	D	97	ASP	4.7
1	D	87	SER	4.6
1	A	88	GLU	4.6
1	B	63	MET	4.6

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Mol	Chain	Res	Type	RSRZ
1	D	268	SER	4.6
1	D	209	ARG	4.5
1	A	60	LEU	4.5
1	A	94	ILE	4.4
1	D	80	THR	4.4
1	C	37	GLU	4.4
1	D	283	ILE	4.4
1	A	73	VAL	4.3
1	A	57	ILE	4.1
1	C	94	ILE	4.1
1	A	284	TRP	4.1
1	D	95	THR	4.1
1	D	31	LEU	4.0
1	C	307	ILE	4.0
1	B	227	GLU	4.0
1	A	59	GLY	4.0
1	D	29	ASP	3.9
1	A	61	GLU	3.8
1	B	210	GLU	3.8
1	D	68	THR	3.8
1	C	2	ALA	3.8
1	D	88	GLU	3.7
1	A	65	ARG	3.7
1	C	87	SER	3.6
1	A	4	MET	3.6
1	C	82	VAL	3.6
1	A	63	MET	3.6
1	D	101	LEU	3.6
1	D	94	ILE	3.6
1	C	287	VAL	3.6
1	D	35	ARG	3.5
1	D	75	VAL	3.5
1	C	174	ARG	3.5
1	C	65	ARG	3.4
1	D	7	LEU	3.4
1	C	68	THR	3.4
1	C	201	HIS	3.4
1	A	58	SER	3.3
1	A	93	ILE	3.3
1	C	30	THR	3.2
1	C	255	GLU	3.2
1	D	287	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	250	ASP	3.2
1	B	79	ILE	3.2
1	D	290	VAL	3.2
1	A	64	GLU	3.1
1	D	93	ILE	3.1
1	D	189	ASP	3.1
1	C	77	THR	3.1
1	D	288	THR	3.0
1	D	21	ILE	3.0
1	D	84	SER	3.0
1	A	36	ASN	3.0
1	D	284	TRP	3.0
1	D	81	GLU	3.0
1	D	86	ARG	3.0
1	D	67	ARG	2.9
1	B	90	THR	2.9
1	D	306	LYS	2.9
1	C	283	ILE	2.9
1	D	8	ILE	2.8
1	D	281	THR	2.8
1	B	212	ILE	2.8
1	B	80	THR	2.8
1	D	71	GLN	2.7
1	C	10	ILE	2.7
1	C	31	LEU	2.7
1	D	10	ILE	2.7
1	A	286	LEU	2.7
1	C	72	GLU	2.7
1	B	3	SER	2.7
1	A	56	SER	2.7
1	C	66	PHE	2.6
1	D	272	ILE	2.6
1	A	190	GLY	2.6
1	D	79	ILE	2.6
1	D	33	LEU	2.6
1	D	286	LEU	2.6
1	C	35	ARG	2.6
1	D	78	THR	2.5
1	A	90	THR	2.5
1	A	62	LEU	2.5
1	B	213	LYS	2.5
1	A	285	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	5	TYR	2.5
1	D	106	VAL	2.5
1	B	306	LYS	2.4
1	B	64	GLU	2.4
1	D	82	VAL	2.4
1	D	18	THR	2.4
1	B	97	ASP	2.3
1	D	19	ALA	2.3
1	D	28	LEU	2.3
1	D	83	LEU	2.3
1	D	269	GLU	2.3
1	C	284	TRP	2.3
1	C	249	VAL	2.3
1	C	4	MET	2.3
1	B	242	ILE	2.2
1	A	91	LYS	2.2
1	C	213	LYS	2.2
1	D	191	THR	2.2
1	C	81	GLU	2.2
1	C	85	VAL	2.2
1	A	218	ILE	2.2
1	A	298	THR	2.2
1	C	285	GLN	2.2
1	A	154	SER	2.2
1	B	190	GLY	2.2
1	C	88	GLU	2.2
1	C	286	LEU	2.2
1	B	66	PHE	2.2
1	C	182	ARG	2.1
1	C	136	CYS	2.1
1	C	211	GLY	2.1
1	A	287	VAL	2.1
1	C	177	HIS	2.1
1	A	140	PHE	2.1
1	B	73	VAL	2.1
1	D	91	LYS	2.1
1	B	201	HIS	2.1
1	C	69	HIS	2.1
1	D	305	GLU	2.0
1	A	201	HIS	2.0
1	B	188	VAL	2.0
1	C	252	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	228	THR	2.0
1	B	71	GLN	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.