



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 13, 2023 – 10:19 AM JST

PDB ID : 5WVA
Title : Serratia marcescens short-chain dehydrogenase/reductase F98Y/F202Y mutant
Authors : Liu, J.S.; Tsou, Y.; Wang, W.C.
Deposited on : 2016-12-23
Resolution : 1.47 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

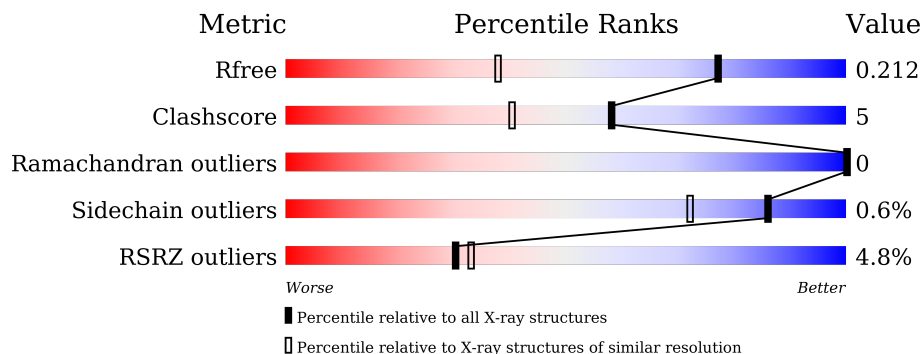
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.47 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	4690 (1.50-1.46)
Clashscore	141614	4955 (1.50-1.46)
Ramachandran outliers	138981	4846 (1.50-1.46)
Sidechain outliers	138945	4844 (1.50-1.46)
RSRZ outliers	127900	4614 (1.50-1.46)

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	287	 4% (red), 75% (green), 10% (yellow), 15% (grey)
1	B	287	 4% (red), 67% (green), 8% (yellow), 24% (grey)

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3666 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 Short-chain dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	245	1760	1094	316	344	6	0	0	0
1	B	218	1561	977	282	297	5	0	0	0

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-37	MET	-	expression tag	UNP A0A192ICX3
A	-36	HIS	-	expression tag	UNP A0A192ICX3
A	-35	HIS	-	expression tag	UNP A0A192ICX3
A	-34	HIS	-	expression tag	UNP A0A192ICX3
A	-33	HIS	-	expression tag	UNP A0A192ICX3
A	-32	HIS	-	expression tag	UNP A0A192ICX3
A	-31	HIS	-	expression tag	UNP A0A192ICX3
A	-30	SER	-	expression tag	UNP A0A192ICX3
A	-29	SER	-	expression tag	UNP A0A192ICX3
A	-28	GLY	-	expression tag	UNP A0A192ICX3
A	-27	LEU	-	expression tag	UNP A0A192ICX3
A	-26	VAL	-	expression tag	UNP A0A192ICX3
A	-25	PRO	-	expression tag	UNP A0A192ICX3
A	-24	ARG	-	expression tag	UNP A0A192ICX3
A	-23	GLY	-	expression tag	UNP A0A192ICX3
A	-22	SER	-	expression tag	UNP A0A192ICX3
A	-21	GLY	-	expression tag	UNP A0A192ICX3
A	-20	MET	-	expression tag	UNP A0A192ICX3
A	-19	LYS	-	expression tag	UNP A0A192ICX3
A	-18	GLU	-	expression tag	UNP A0A192ICX3
A	-17	THR	-	expression tag	UNP A0A192ICX3
A	-16	ALA	-	expression tag	UNP A0A192ICX3
A	-15	ALA	-	expression tag	UNP A0A192ICX3
A	-14	ALA	-	expression tag	UNP A0A192ICX3
A	-13	LYS	-	expression tag	UNP A0A192ICX3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	PHE	-	expression tag	UNP A0A192ICX3
A	-11	GLU	-	expression tag	UNP A0A192ICX3
A	-10	ARG	-	expression tag	UNP A0A192ICX3
A	-9	GLN	-	expression tag	UNP A0A192ICX3
A	-8	HIS	-	expression tag	UNP A0A192ICX3
A	-7	MET	-	expression tag	UNP A0A192ICX3
A	-6	ASP	-	expression tag	UNP A0A192ICX3
A	-5	SER	-	expression tag	UNP A0A192ICX3
A	-4	PRO	-	expression tag	UNP A0A192ICX3
A	-3	ASP	-	expression tag	UNP A0A192ICX3
A	-2	LEU	-	expression tag	UNP A0A192ICX3
A	-1	GLY	-	expression tag	UNP A0A192ICX3
A	0	THR	-	expression tag	UNP A0A192ICX3
A	98	TYR	PHE	engineered mutation	UNP A0A192ICX3
A	202	TYR	PHE	engineered mutation	UNP A0A192ICX3
B	-37	MET	-	expression tag	UNP A0A192ICX3
B	-36	HIS	-	expression tag	UNP A0A192ICX3
B	-35	HIS	-	expression tag	UNP A0A192ICX3
B	-34	HIS	-	expression tag	UNP A0A192ICX3
B	-33	HIS	-	expression tag	UNP A0A192ICX3
B	-32	HIS	-	expression tag	UNP A0A192ICX3
B	-31	HIS	-	expression tag	UNP A0A192ICX3
B	-30	SER	-	expression tag	UNP A0A192ICX3
B	-29	SER	-	expression tag	UNP A0A192ICX3
B	-28	GLY	-	expression tag	UNP A0A192ICX3
B	-27	LEU	-	expression tag	UNP A0A192ICX3
B	-26	VAL	-	expression tag	UNP A0A192ICX3
B	-25	PRO	-	expression tag	UNP A0A192ICX3
B	-24	ARG	-	expression tag	UNP A0A192ICX3
B	-23	GLY	-	expression tag	UNP A0A192ICX3
B	-22	SER	-	expression tag	UNP A0A192ICX3
B	-21	GLY	-	expression tag	UNP A0A192ICX3
B	-20	MET	-	expression tag	UNP A0A192ICX3
B	-19	LYS	-	expression tag	UNP A0A192ICX3
B	-18	GLU	-	expression tag	UNP A0A192ICX3
B	-17	THR	-	expression tag	UNP A0A192ICX3
B	-16	ALA	-	expression tag	UNP A0A192ICX3
B	-15	ALA	-	expression tag	UNP A0A192ICX3
B	-14	ALA	-	expression tag	UNP A0A192ICX3
B	-13	LYS	-	expression tag	UNP A0A192ICX3
B	-12	PHE	-	expression tag	UNP A0A192ICX3
B	-11	GLU	-	expression tag	UNP A0A192ICX3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	ARG	-	expression tag	UNP A0A192ICX3
B	-9	GLN	-	expression tag	UNP A0A192ICX3
B	-8	HIS	-	expression tag	UNP A0A192ICX3
B	-7	MET	-	expression tag	UNP A0A192ICX3
B	-6	ASP	-	expression tag	UNP A0A192ICX3
B	-5	SER	-	expression tag	UNP A0A192ICX3
B	-4	PRO	-	expression tag	UNP A0A192ICX3
B	-3	ASP	-	expression tag	UNP A0A192ICX3
B	-2	LEU	-	expression tag	UNP A0A192ICX3
B	-1	GLY	-	expression tag	UNP A0A192ICX3
B	0	THR	-	expression tag	UNP A0A192ICX3
B	98	TYR	PHE	engineered mutation	UNP A0A192ICX3
B	202	TYR	PHE	engineered mutation	UNP A0A192ICX3


- Molecule 2 is water.

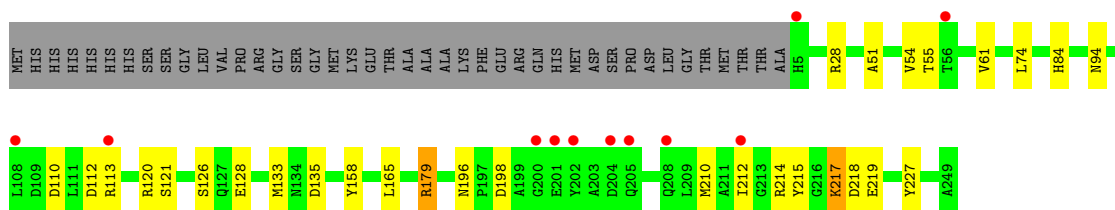
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	190	Total O 190 190	0	0
2	B	155	Total O 155 155	0	0

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.

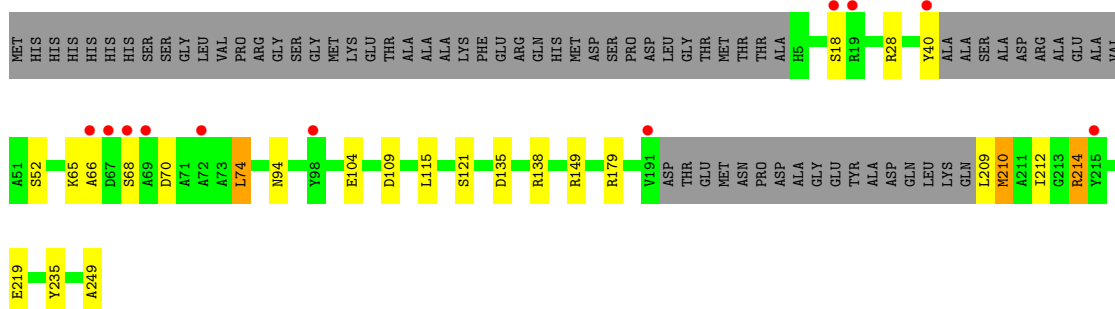
- Molecule 1: Short-chain dehydrogenase

Chain A: 



- Molecule 1: Short-chain dehydrogenase

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	83.92Å 83.92Å 115.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	67.55 – 1.47 23.72 – 1.47	Depositor EDS
% Data completeness (in resolution range)	98.6 (67.55-1.47) 98.6 (23.72-1.47)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	15.41 (at 1.47Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.175 , 0.207 0.182 , 0.212	Depositor DCC
R_{free} test set	3391 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	13.2	Xtrriage
Anisotropy	0.025	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3666	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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	1.31	2/1784 (0.1%)	1.43	19/2416 (0.8%)
1	B	1.30	3/1581 (0.2%)	1.27	11/2137 (0.5%)
All	All	1.31	5/3365 (0.1%)	1.35	30/4553 (0.7%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	128	GLU	CD-OE1	-6.11	1.19	1.25
1	B	235	TYR	CE1-CZ	-6.00	1.30	1.38
1	A	126	SER	CB-OG	5.48	1.49	1.42
1	B	52	SER	CB-OG	-5.30	1.35	1.42
1	B	66	ALA	N-CA	-5.27	1.35	1.46

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	28	ARG	NE-CZ-NH2	-16.71	111.94	120.30
1	A	112	ASP	C-N-CA	11.51	150.47	121.70
1	A	218	ASP	CB-CG-OD1	10.04	127.33	118.30
1	B	70	ASP	CB-CG-OD1	9.59	126.93	118.30
1	A	120	ARG	NE-CZ-NH2	-8.94	115.83	120.30
1	B	74	LEU	CB-CG-CD2	8.79	125.95	111.00
1	A	135	ASP	CB-CG-OD1	8.72	126.14	118.30
1	A	120	ARG	NE-CZ-NH1	8.61	124.60	120.30
1	B	135	ASP	CB-CG-OD1	8.21	125.69	118.30
1	A	218	ASP	CB-CG-OD2	-7.05	111.96	118.30
1	B	210	MET	O-C-N	-6.69	112.00	122.70
1	A	112	ASP	O-C-N	-6.61	112.13	122.70
1	A	179	ARG	NE-CZ-NH2	-6.22	117.19	120.30
1	B	28	ARG	NE-CZ-NH2	-5.94	117.33	120.30
1	A	28	ARG	NH1-CZ-NH2	5.85	125.83	119.40
1	B	109	ASP	CB-CG-OD1	5.84	123.56	118.30
1	B	138	ARG	NE-CZ-NH2	-5.83	117.39	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	214	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	A	210	MET	CA-CB-CG	-5.73	103.56	113.30
1	B	70	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	A	28	ARG	CG-CD-NE	-5.61	100.03	111.80
1	A	158	TYR	CB-CG-CD2	5.54	124.33	121.00
1	B	249	ALA	CA-C-O	-5.47	108.61	120.10
1	A	112	ASP	CA-C-N	5.41	129.10	117.20
1	A	217	LYS	CD-CE-NZ	5.31	123.92	111.70
1	A	227	TYR	CZ-CE2-CD2	-5.21	115.11	119.80
1	A	165	LEU	CB-CG-CD2	5.14	119.74	111.00
1	A	110	ASP	CB-CG-OD2	-5.13	113.69	118.30
1	B	210	MET	CA-C-N	5.12	128.46	117.20
1	A	227	TYR	CB-CG-CD2	-5.01	118.00	121.00

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	1760	0	1748	13	0
1	B	1561	0	1570	19	1
2	A	190	0	0	6	0
2	B	155	0	0	0	0
All	All	3666	0	3318	32	1

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 (32) 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:40:TYR:OH	1:B:65:LYS:HE3	1.54	1.06
1:A:196:ASN:HB2	2:A:457:HOH:O	1.56	1.05
1:B:40:TYR:CZ	1:B:65:LYS:HE3	2.09	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:SER:HB3	1:B:40:TYR:HB2	1.57	0.86
1:B:18:SER:HB3	1:B:40:TYR:CB	2.11	0.79
1:A:219:GLU:HB3	2:A:465:HOH:O	1.85	0.77
1:B:40:TYR:CZ	1:B:65:LYS:HG3	2.23	0.72
1:B:18:SER:CB	1:B:40:TYR:HB2	2.18	0.72
1:B:40:TYR:CE1	1:B:65:LYS:HG3	2.35	0.61
1:A:113:ARG:HD3	2:A:475:HOH:O	2.02	0.59
1:B:68:SER:O	1:B:121:SER:OG	2.10	0.59
1:B:40:TYR:CZ	1:B:65:LYS:CE	2.84	0.58
1:B:40:TYR:CE2	1:B:65:LYS:CE	2.88	0.56
1:B:40:TYR:CZ	1:B:65:LYS:CG	2.88	0.56
1:A:212:ILE:HG22	1:A:214:ARG:HG2	1.88	0.56
1:B:40:TYR:CE2	1:B:65:LYS:HE2	2.42	0.55
1:A:51:ALA:O	1:A:55:THR:HG23	2.07	0.54
1:B:212:ILE:HD12	1:B:214:ARG:HG2	1.91	0.53
1:A:84:HIS:HE1	2:A:414:HOH:O	1.91	0.53
1:B:40:TYR:CE2	1:B:65:LYS:HE3	2.46	0.49
1:B:94:ASN:O	1:B:94:ASN:CG	2.48	0.49
1:A:217:LYS:HE3	2:A:409:HOH:O	2.13	0.47
1:A:198:ASP:OD2	1:A:215:TYR:HB2	2.14	0.47
1:A:133:MET:O	1:A:179:ARG:NH2	2.50	0.45
1:B:18:SER:OG	1:B:40:TYR:HB2	2.17	0.45
1:A:121:SER:HB2	2:A:307:HOH:O	2.18	0.42
1:A:74:LEU:CD1	1:A:121:SER:HB3	2.50	0.42
1:A:54:VAL:HG11	1:A:61:VAL:HB	2.02	0.41
1:B:149:ARG:HH21	1:B:209:LEU:HD22	1.86	0.40
1:B:210:MET:HB3	1:B:210:MET:HE3	1.98	0.40
1:A:94:ASN:CG	1:A:94:ASN:O	2.59	0.40
1:B:115:LEU:HD23	1:B:115:LEU:HA	1.95	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:GLU:OE2	1:B:179:ARG:NH1[7_555]	1.58	0.62

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	243/287 (85%)	237 (98%)	6 (2%)	0	100	100
1	B	212/287 (74%)	206 (97%)	6 (3%)	0	100	100
All	All	455/574 (79%)	443 (97%)	12 (3%)	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	171/205 (83%)	171 (100%)	0	100	100
1	B	152/205 (74%)	150 (99%)	2 (1%)	69	42
All	All	323/410 (79%)	321 (99%)	2 (1%)	86	72

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	74	LEU
1	B	219	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	84	HIS
1	A	187	GLN
1	B	8	GLN
1	B	15	GLN
1	B	187	GLN

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 monosaccharides 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	245/287 (85%)	-0.01	11 (4%) 33 36	8, 14, 27, 46	0
1	B	218/287 (75%)	0.02	11 (5%) 28 31	8, 13, 28, 52	0
All	All	463/574 (80%)	0.00	22 (4%) 30 33	8, 14, 28, 52	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	67	ASP	6.2
1	B	40	TYR	4.1
1	A	201	GLU	3.9
1	B	215	TYR	3.7
1	B	98	TYR	3.5
1	B	191	VAL	3.3
1	B	72	ALA	3.3
1	B	66	ALA	3.2
1	A	202	TYR	3.0
1	A	205	GLN	2.9
1	A	200	GLY	2.8
1	A	204	ASP	2.6
1	A	5	HIS	2.5
1	A	108	LEU	2.4
1	B	69	ALA	2.3
1	B	19	ARG	2.3
1	A	212	ILE	2.3
1	A	113	ARG	2.3
1	B	68	SER	2.3
1	A	208	GLN	2.2
1	B	18	SER	2.2
1	A	56	THR	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 monosaccharides 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.