



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:15 PM GMT

PDB ID : 3TFX
Title : Crystal structure of Orotidine 5'-phosphate decarboxylase from *Lactobacillus acidophilus*
Authors : Satyanarayana, L.; Chamala, S.; Evans, B.; Foti, R.; Gizzi, A.; Hillerich, B.; Kar, A.; LaFleur, J.; Seidel, R.; Villigas, G.; Zencheck, W.; Almo, S.C.; Swaminathan, S.; New York Structural Genomics Research Consortium (NYSGRG)
Deposited on : 2011-08-16
Resolution : 2.19 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

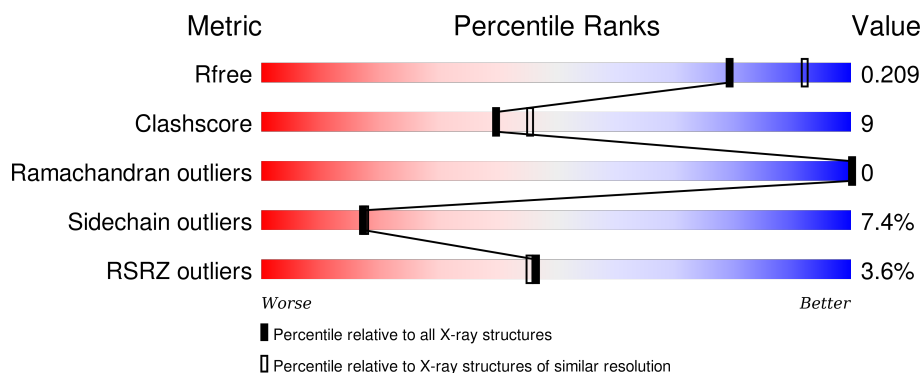
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	259	<div> <div>3%</div> <div>73%</div> <div>13%</div> <div>•</div> <div>11%</div> </div>
1	B	259	<div> <div>3%</div> <div>69%</div> <div>15%</div> <div>•</div> <div>14%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3744 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 Orotidine 5'-phosphate decarboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	231	Total	C	N	O	S	Se	0	0	0
			1762	1125	297	332	2	6			
1	B	224	Total	C	N	O	S	Se	0	0	0
			1699	1084	288	319	2	6			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	EXPRESSION TAG	UNP Q5FJB3
A	0	VAL	-	EXPRESSION TAG	UNP Q5FJB3
A	236	ALA	-	EXPRESSION TAG	UNP Q5FJB3
A	237	GLU	-	EXPRESSION TAG	UNP Q5FJB3
A	238	ASN	-	EXPRESSION TAG	UNP Q5FJB3
A	239	LEU	-	EXPRESSION TAG	UNP Q5FJB3
A	240	TYR	-	EXPRESSION TAG	UNP Q5FJB3
A	241	PHE	-	EXPRESSION TAG	UNP Q5FJB3
A	242	GLN	-	EXPRESSION TAG	UNP Q5FJB3
A	243	SER	-	EXPRESSION TAG	UNP Q5FJB3
A	244	HIS	-	EXPRESSION TAG	UNP Q5FJB3
A	245	HIS	-	EXPRESSION TAG	UNP Q5FJB3
A	246	HIS	-	EXPRESSION TAG	UNP Q5FJB3
A	247	HIS	-	EXPRESSION TAG	UNP Q5FJB3
A	248	HIS	-	EXPRESSION TAG	UNP Q5FJB3
A	249	HIS	-	EXPRESSION TAG	UNP Q5FJB3
A	250	TRP	-	EXPRESSION TAG	UNP Q5FJB3
A	251	SER	-	EXPRESSION TAG	UNP Q5FJB3
A	252	HIS	-	EXPRESSION TAG	UNP Q5FJB3
A	253	PRO	-	EXPRESSION TAG	UNP Q5FJB3
A	254	GLN	-	EXPRESSION TAG	UNP Q5FJB3
A	255	PHE	-	EXPRESSION TAG	UNP Q5FJB3
A	256	GLU	-	EXPRESSION TAG	UNP Q5FJB3
A	257	LYS	-	EXPRESSION TAG	UNP Q5FJB3
B	-1	MSE	-	EXPRESSION TAG	UNP Q5FJB3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	VAL	-	EXPRESSION TAG	UNP Q5FJB3
B	236	ALA	-	EXPRESSION TAG	UNP Q5FJB3
B	237	GLU	-	EXPRESSION TAG	UNP Q5FJB3
B	238	ASN	-	EXPRESSION TAG	UNP Q5FJB3
B	239	LEU	-	EXPRESSION TAG	UNP Q5FJB3
B	240	TYR	-	EXPRESSION TAG	UNP Q5FJB3
B	241	PHE	-	EXPRESSION TAG	UNP Q5FJB3
B	242	GLN	-	EXPRESSION TAG	UNP Q5FJB3
B	243	SER	-	EXPRESSION TAG	UNP Q5FJB3
B	244	HIS	-	EXPRESSION TAG	UNP Q5FJB3
B	245	HIS	-	EXPRESSION TAG	UNP Q5FJB3
B	246	HIS	-	EXPRESSION TAG	UNP Q5FJB3
B	247	HIS	-	EXPRESSION TAG	UNP Q5FJB3
B	248	HIS	-	EXPRESSION TAG	UNP Q5FJB3
B	249	HIS	-	EXPRESSION TAG	UNP Q5FJB3
B	250	TRP	-	EXPRESSION TAG	UNP Q5FJB3
B	251	SER	-	EXPRESSION TAG	UNP Q5FJB3
B	252	HIS	-	EXPRESSION TAG	UNP Q5FJB3
B	253	PRO	-	EXPRESSION TAG	UNP Q5FJB3
B	254	GLN	-	EXPRESSION TAG	UNP Q5FJB3
B	255	PHE	-	EXPRESSION TAG	UNP Q5FJB3
B	256	GLU	-	EXPRESSION TAG	UNP Q5FJB3
B	257	LYS	-	EXPRESSION TAG	UNP Q5FJB3

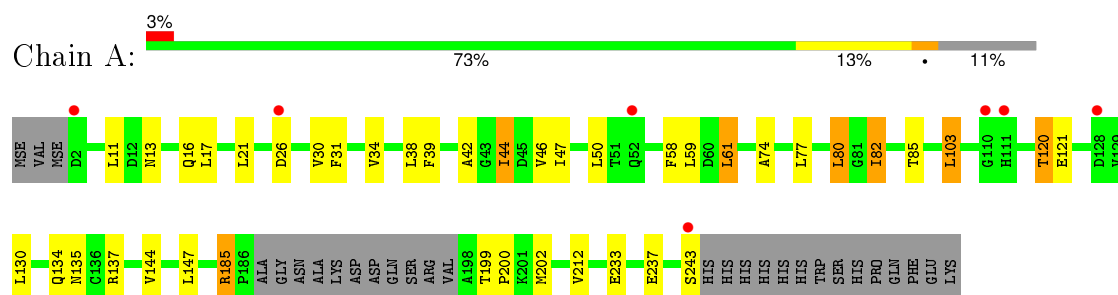
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	159	Total O 159 159	0	0
2	B	124	Total O 124 124	0	0

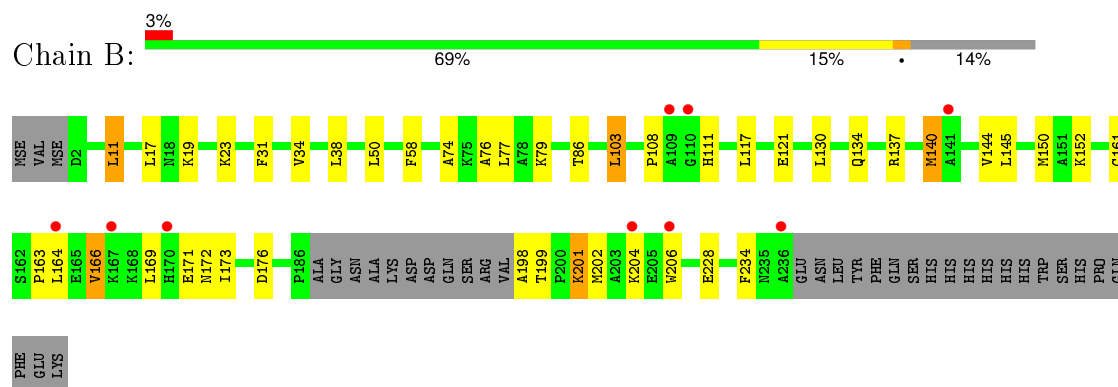
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: Orotidine 5'-phosphate decarboxylase



- Molecule 1: Orotidine 5'-phosphate decarboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	130.40Å 68.17Å 63.93Å 90.00° 106.31° 90.00°	Depositor
Resolution (Å)	50.00 – 2.19 40.23 – 2.19	Depositor EDS
% Data completeness (in resolution range)	98.4 (50.00-2.19) 98.4 (40.23-2.19)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	15.18 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.205 , 0.252 0.205 , 0.209	Depositor DCC
R_{free} test set	1378 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 27388 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3744	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.87% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.52	0/1787	0.66	0/2407
1	B	0.52	0/1722	0.64	1/2319 (0.0%)
All	All	0.52	0/3509	0.65	1/4726 (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	B	11	LEU	CA-CB-CG	5.80	128.64	115.30

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	1762	0	1808	25	0
1	B	1699	0	1754	39	0
2	A	159	0	0	2	0
2	B	124	0	0	8	0
All	All	3744	0	3562	62	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 9.

All (62) 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:121:GLU:HG3	1:B:140:MSE:HE1	1.28	1.09
1:B:34:VAL:HG21	1:B:38:LEU:HD23	1.38	1.05
1:B:150:MSE:SE	2:B:341:HOH:O	2.29	0.99
1:B:140:MSE:HE3	1:B:140:MSE:HA	1.48	0.95
1:A:120:THR:CG2	1:A:121:GLU:H	1.88	0.85
1:B:121:GLU:HG3	1:B:140:MSE:CE	2.08	0.81
1:B:140:MSE:SE	2:B:328:HOH:O	2.49	0.81
1:A:120:THR:HG22	1:A:121:GLU:H	1.44	0.79
1:B:150:MSE:HG2	2:B:341:HOH:O	1.84	0.77
1:A:74:ALA:HB1	1:A:103:LEU:HD13	1.65	0.77
1:A:199:THR:HG23	1:A:202:MSE:H	1.52	0.75
1:B:150:MSE:CG	2:B:341:HOH:O	2.35	0.74
1:B:34:VAL:HG21	1:B:38:LEU:CD2	2.16	0.73
1:B:17:LEU:HD22	1:B:38:LEU:HD21	1.71	0.72
1:B:202:MSE:HE3	1:B:206:TRP:CH2	2.24	0.72
1:B:74:ALA:HB1	1:B:103:LEU:HD13	1.73	0.70
1:B:34:VAL:CG2	1:B:38:LEU:HB3	2.22	0.69
1:A:135:ASN:O	1:B:137:ARG:HG2	1.97	0.64
1:B:140:MSE:HA	1:B:140:MSE:CE	2.23	0.64
1:A:120:THR:CG2	1:A:121:GLU:N	2.57	0.62
1:B:201:LYS:HG3	2:B:344:HOH:O	2.01	0.61
1:A:120:THR:HG21	1:A:144:VAL:HG13	1.82	0.59
1:B:140:MSE:HE2	1:B:144:VAL:HG23	1.86	0.58
1:B:152:LYS:HG2	1:B:173:ILE:HG23	1.88	0.56
1:A:137:ARG:HB3	1:B:137:ARG:HB3	1.88	0.55
1:B:150:MSE:HE3	2:B:341:HOH:O	2.08	0.54
1:A:34:VAL:HG11	1:A:38:LEU:HD23	1.90	0.53
1:A:39:PHE:CD2	1:A:61:LEU:HD21	2.43	0.53
1:B:150:MSE:CE	2:B:341:HOH:O	2.55	0.53
1:A:199:THR:CG2	1:A:202:MSE:H	2.21	0.52
1:B:19:LYS:HE2	1:B:23:LYS:HE2	1.92	0.52
1:A:26:ASP:HB3	2:A:268:HOH:O	2.11	0.51
1:A:130:LEU:O	1:A:134:GLN:O	2.31	0.49
1:A:44:ILE:HB	1:A:80:LEU:HD11	1.93	0.49
1:B:228:GLU:HG3	2:B:377:HOH:O	2.13	0.49
1:A:77:LEU:O	1:A:82:ILE:HD12	2.13	0.49
1:B:152:LYS:HE3	1:B:176:ASP:O	2.13	0.48
1:B:199:THR:OG1	1:B:201:LYS:HD2	2.13	0.48
1:B:198:ALA:HA	1:B:202:MSE:HE2	1.96	0.48
1:B:145:LEU:HD13	1:B:169:LEU:HD23	1.96	0.47
1:B:34:VAL:HG23	1:B:38:LEU:HB3	1.96	0.47
1:A:185:ARG:NH1	2:A:413:HOH:O	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:PRO:HB2	1:A:233:GLU:HG2	1.96	0.47
1:B:163:PRO:O	1:B:166:VAL:HG23	2.15	0.46
1:A:47:ILE:HD13	1:A:59:LEU:HD22	1.97	0.46
1:B:202:MSE:CE	1:B:206:TRP:CH2	2.97	0.45
1:A:120:THR:HG23	1:A:121:GLU:H	1.75	0.44
1:A:120:THR:HG23	1:A:144:VAL:HG22	1.99	0.44
1:B:204:LYS:HD2	1:B:234:PHE:O	2.17	0.44
1:B:86:THR:HA	1:B:117:LEU:O	2.16	0.44
1:A:13:ASN:ND2	1:A:16:GLN:H	2.15	0.44
1:B:34:VAL:HG21	1:B:38:LEU:HB3	1.98	0.44
1:B:152:LYS:O	1:B:152:LYS:HD2	2.18	0.43
1:B:130:LEU:O	1:B:134:GLN:O	2.36	0.43
1:B:76:ALA:O	1:B:79:LYS:HG2	2.19	0.43
1:A:120:THR:HG22	1:A:121:GLU:N	2.22	0.42
1:A:120:THR:HG23	1:A:121:GLU:N	2.34	0.42
1:A:17:LEU:HD21	1:A:50:LEU:HD11	2.02	0.42
1:B:17:LEU:HD21	1:B:50:LEU:HD11	2.03	0.41
1:A:42:ALA:HB1	1:A:46:VAL:HG21	2.03	0.41
1:B:108:PRO:O	1:B:111:HIS:HB2	2.21	0.41
1:B:161:CYS:SG	1:B:166:VAL:HG13	2.61	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	227/259 (88%)	220 (97%)	7 (3%)	0	100	100
1	B	220/259 (85%)	210 (96%)	10 (4%)	0	100	100
All	All	447/518 (86%)	430 (96%)	17 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	192/209 (92%)	175 (91%)	17 (9%)	12	11
1	B	185/209 (88%)	174 (94%)	11 (6%)	24	27
All	All	377/418 (90%)	349 (93%)	28 (7%)	17	17

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	21	LEU
1	A	30	VAL
1	A	31	PHE
1	A	44	ILE
1	A	58	PHE
1	A	61	LEU
1	A	80	LEU
1	A	82	ILE
1	A	85	THR
1	A	103	LEU
1	A	120	THR
1	A	147	LEU
1	A	185	ARG
1	A	212	VAL
1	A	237	GLU
1	A	243	SER
1	B	11	LEU
1	B	31	PHE
1	B	58	PHE
1	B	77	LEU
1	B	103	LEU
1	B	140	MSE
1	B	164	LEU
1	B	166	VAL
1	B	171	GLU
1	B	172	ASN

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Mol	Chain	Res	Type
1	B	201	LYS

Some 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	16	GLN
1	A	28	HIS
1	A	135	ASN
1	B	132	ASN
1	B	135	ASN
1	B	170	HIS

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	225/259 (86%)	0.01	7 (3%) 52 51	6, 15, 27, 32	0
1	B	218/259 (84%)	0.20	9 (4%) 41 39	7, 15, 27, 32	0
All	All	443/518 (85%)	0.10	16 (3%) 46 45	6, 15, 27, 32	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	170	HIS	3.8
1	B	164	LEU	3.3
1	B	109	ALA	3.1
1	A	110	GLY	3.0
1	B	167	LYS	2.8
1	A	52	GLN	2.6
1	A	243	SER	2.5
1	A	111	HIS	2.3
1	B	236	ALA	2.3
1	B	206	TRP	2.3
1	B	141	ALA	2.2
1	B	110	GLY	2.2
1	B	204	LYS	2.1
1	A	128	ASP	2.1
1	A	26	ASP	2.1
1	A	2	ASP	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.