Full wwPDB X-ray Structure Validation Report ⓘ

Feb 10, 2024 – 10:33 AM EST

PDB ID	:	2QCC
Title	:	Crystal structure of the orotidine-5'-monophosphate decarboxylase domain of human UMP synthase, apo form
Authors	:	Wittmann, J.; Rudolph, M.
Deposited on	:	2007-06-19
Resolution	:	1.85 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:

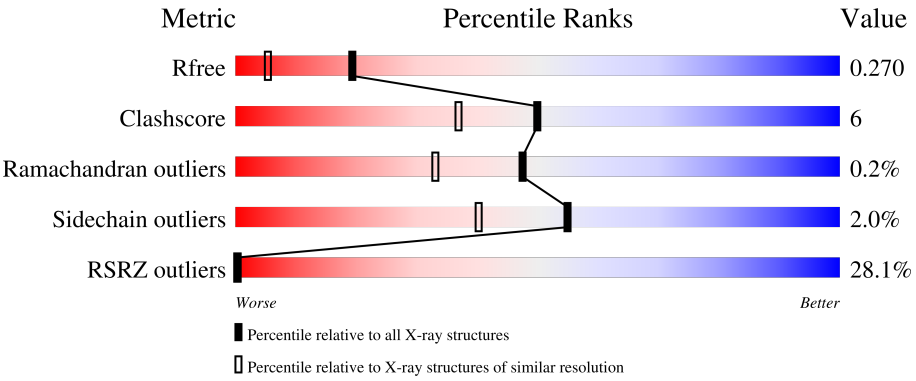
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 1.85 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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	260	27% 83% 13% 5%
1	B	260	27% 85% 12% .

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4211 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.

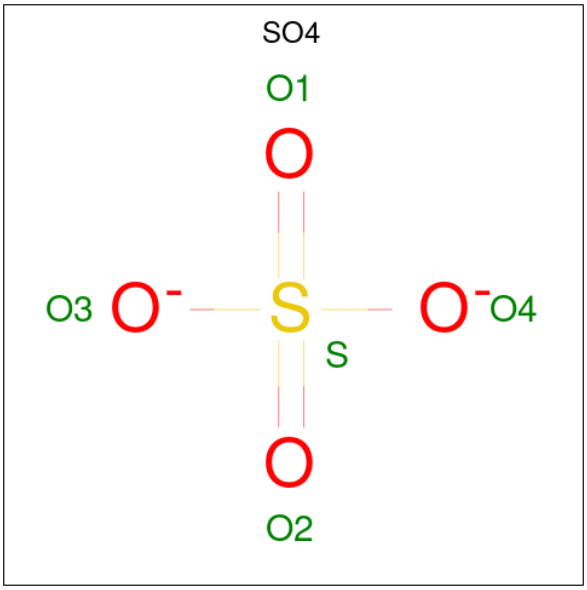
- Molecule 1 is a protein called Orotidine 5'- phosphate decarboxylase (OMPdecase).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	5	1
			1925	1228	331	354	12			
1	B	251	Total	C	N	O	S	0	9	2
			1959	1249	339	358	13			

There are 6 discrepancies between the modelled and reference sequences:

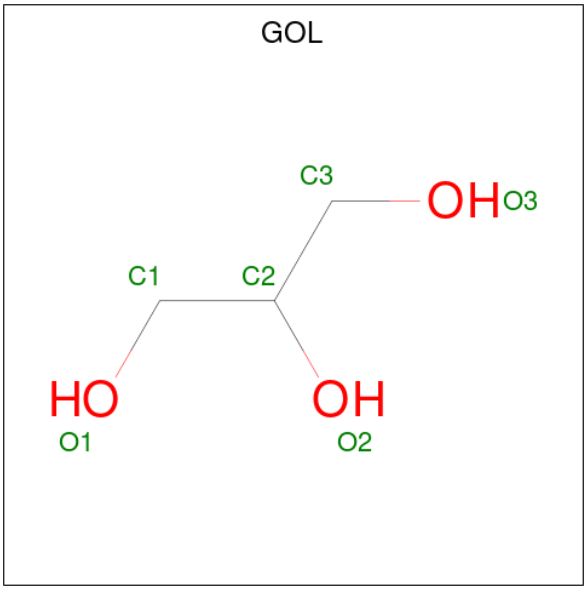
Chain	Residue	Modelled	Actual	Comment	Reference
A	221	GLY	-	expression tag	UNP P11172
A	222	ALA	-	expression tag	UNP P11172
A	223	MET	-	expression tag	UNP P11172
B	221	GLY	-	expression tag	UNP P11172
B	222	ALA	-	expression tag	UNP P11172
B	223	MET	-	expression tag	UNP P11172

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

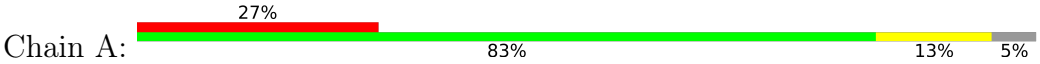
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	167	Total O 167 167	0	0
4	B	138	Total O 138 138	0	0

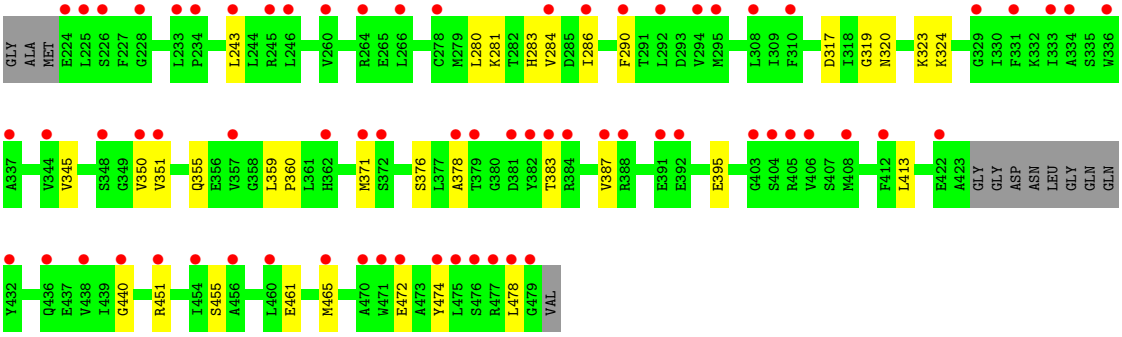
3 Residue-property plots (i)

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: Orotidine 5'- phosphate decarboxylase (OMPdecase)

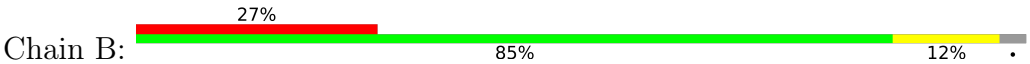
Chain A:

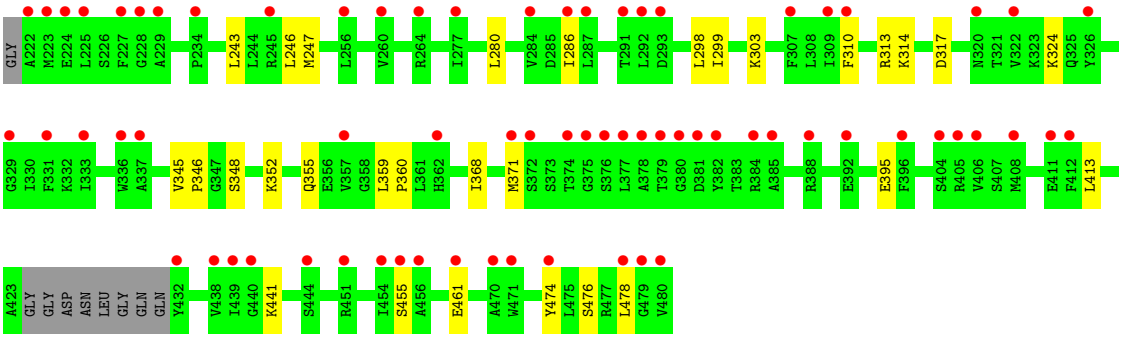




• Molecule 1: Orotidine 5'- phosphate decarboxylase (OMPdecase)

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	62.02Å 75.91Å 119.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.96 – 1.85 46.96 – 1.85	Depositor EDS
% Data completeness (in resolution range)	96.0 (46.96-1.85) 96.0 (46.96-1.85)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.35 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.197 , 0.258 0.210 , 0.270	Depositor DCC
R_{free} test set	2352 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	27.2	Xtriage
Anisotropy	0.116	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 60.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4211	wwPDB-VP
Average B, all atoms (Å^2)	44.0	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 66.02 % 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 6.4597e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] 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: SO4, GOL

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	0.61	0/1971	0.66	0/2658
1	B	0.59	0/2017	0.68	2/2719 (0.1%)
All	All	0.60	0/3988	0.67	2/5377 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	313	ARG	NE-CZ-NH1	5.85	123.23	120.30
1	B	313	ARG	NE-CZ-NH2	-5.49	117.56	120.30

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	1925	0	1983	30	0
1	B	1959	0	2030	22	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	6	0	8	1	0
3	B	6	0	8	0	0
4	A	167	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	138	0	0	4	0
All	All	4211	0	4029	46	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 6.

All (46) 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:371[A]:MET:HE2	4:B:576:HOH:O	1.59	1.02
1:A:324:LYS:HB3	1:B:286[A]:ILE:HG23	1.62	0.82
1:A:371[A]:MET:HE1	4:B:507:HOH:O	1.91	0.69
1:B:474:TYR:CE1	1:B:478:LEU:HD11	2.36	0.60
1:B:474:TYR:O	1:B:478:LEU:HD13	2.02	0.60
1:A:286[A]:ILE:HG21	1:B:324:LYS:HD2	1.85	0.59
1:A:355:GLN:NE2	1:A:395:GLU:OE2	2.34	0.59
1:B:280:LEU:HD22	1:B:298:LEU:HD11	1.85	0.58
1:A:320:ASN:ND2	1:A:324:LYS:CE	2.68	0.57
1:A:324:LYS:CB	1:B:286[A]:ILE:HG23	2.35	0.57
1:A:371[B]:MET:HB2	1:A:376:SER:OG	2.08	0.54
1:A:286[A]:ILE:HG23	1:B:324:LYS:HB3	1.89	0.54
1:A:345:VAL:HG22	1:B:371:MET:CE	2.40	0.52
1:B:395:GLU:H	1:B:395:GLU:CD	2.13	0.52
1:B:455:SER:HB2	4:B:535:HOH:O	2.10	0.51
1:B:348:SER:OG	1:B:352:LYS:HE2	2.11	0.51
1:B:359:LEU:HB2	1:B:360:PRO:HD3	1.92	0.50
1:A:320:ASN:ND2	1:A:324:LYS:NZ	2.60	0.50
1:B:246:LEU:HD12	1:B:247:MET:N	2.27	0.50
1:B:345:VAL:HG12	1:B:346:PRO:HD3	1.94	0.50
1:A:472:GLU:HG2	4:A:615:HOH:O	2.13	0.49
1:B:243:LEU:HD23	1:B:413:LEU:HD13	1.95	0.49
1:A:359:LEU:HB2	1:A:360:PRO:HD3	1.95	0.48
1:A:320:ASN:HD22	1:A:324:LYS:NZ	2.11	0.48
1:A:350:VAL:HG13	1:A:351:VAL:N	2.29	0.47
1:A:345:VAL:HG22	1:B:371:MET:HE1	1.97	0.47
1:A:281:LYS:HZ1	3:A:482:GOL:C2	2.27	0.47
1:A:284[A]:VAL:CG2	1:A:290:PHE:CD1	2.99	0.46
1:A:474:TYR:CE1	1:A:478:LEU:HD11	2.51	0.46
1:B:345:VAL:N	1:B:346:PRO:CD	2.79	0.46
1:A:319:GLY:O	1:A:323:LYS:HG3	2.17	0.45
1:A:371[A]:MET:CE	4:B:576:HOH:O	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:314:LYS:HG2	1:B:368:ILE:HD11	1.98	0.45
1:A:455:SER:HB2	4:A:602:HOH:O	2.16	0.45
1:A:320:ASN:ND2	1:A:324:LYS:HE2	2.32	0.44
1:B:299:ILE:O	1:B:303:LYS:HG3	2.18	0.42
1:A:461:GLU:O	1:A:465:MET:HG3	2.18	0.42
1:A:440:GLY:HA3	4:A:583:HOH:O	2.20	0.42
1:A:243:LEU:HD23	1:A:413:LEU:HD13	2.01	0.41
1:B:243:LEU:HD23	1:B:413:LEU:CD1	2.50	0.41
1:B:246:LEU:HD12	1:B:246:LEU:C	2.41	0.41
1:A:383:THR:O	1:A:387:VAL:HG23	2.21	0.41
1:A:451:ARG:NH2	4:A:540:HOH:O	2.54	0.41
1:A:283:HIS:HD2	4:A:485:HOH:O	2.03	0.40
1:B:345:VAL:CG1	1:B:346:PRO:HD3	2.52	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	249/260 (96%)	240 (96%)	8 (3%)	1 (0%)	34 19
1	B	256/260 (98%)	251 (98%)	5 (2%)	0	100 100
All	All	505/520 (97%)	491 (97%)	13 (3%)	1 (0%)	47 33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	378	ALA

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	208/210 (99%)	206 (99%)	2 (1%)	76 69
1	B	213/210 (101%)	207 (97%)	6 (3%)	43 27
All	All	421/420 (100%)	413 (98%)	8 (2%)	55 43

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	280	LEU
1	A	317	ASP
1	B	310	PHE
1	B	317	ASP
1	B	355	GLN
1	B	441	LYS
1	B	461	GLU
1	B	476	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	283	HIS
1	A	320	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GOL	A	482	-	5,5,5	0.38	0	5,5,5	0.17	0
3	GOL	B	482	-	5,5,5	0.41	0	5,5,5	0.80	0
2	SO4	B	481	-	4,4,4	0.20	0	6,6,6	0.37	0
2	SO4	A	481	-	4,4,4	0.17	0	6,6,6	0.26	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	482	-	-	0/4/4/4	-
3	GOL	A	482	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	482	GOL	C1-C2-C3-O3
3	A	482	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	482	GOL	1	0

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	248/260 (95%)	1.62	70 (28%)	0	0	39, 43, 50, 54	0
1	B	251/260 (96%)	1.73	70 (27%)	0	0	39, 43, 51, 67	0
All	All	499/520 (95%)	1.68	140 (28%)	0	0	39, 43, 50, 67	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	223	MET	12.6
1	B	222	ALA	10.7
1	B	480	VAL	8.0
1	A	479	GLY	7.7
1	A	478	LEU	7.0
1	B	379	THR	6.8
1	B	408	MET	6.1
1	A	387	VAL	5.6
1	B	470	ALA	5.1
1	B	388	ARG	4.9
1	B	406	VAL	4.8
1	A	404	SER	4.6
1	B	381	ASP	4.5
1	A	408	MET	4.5
1	B	385	ALA	4.4
1	A	379	THR	4.4
1	B	474	TYR	4.1
1	A	436	GLN	4.1
1	B	382	TYR	3.9
1	A	391	GLU	3.8
1	B	432	TYR	3.8
1	A	264	ARG	3.8
1	B	471	TRP	3.7
1	A	440	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	284[A]	VAL	3.7
1	A	438	VAL	3.7
1	B	404	SER	3.6
1	A	388	ARG	3.6
1	B	392	GLU	3.6
1	A	474	TYR	3.5
1	A	432	TYR	3.5
1	A	286[A]	ILE	3.5
1	B	384	ARG	3.5
1	B	478	LEU	3.4
1	A	476	SER	3.4
1	B	378	ALA	3.4
1	A	384	ARG	3.4
1	B	375	GLY	3.4
1	B	439	ILE	3.4
1	B	451[A]	ARG	3.3
1	B	229	ALA	3.3
1	A	381	ASP	3.3
1	A	378	ALA	3.3
1	B	286[A]	ILE	3.2
1	B	412	PHE	3.2
1	A	246	LEU	3.2
1	B	456	ALA	3.2
1	B	333	ILE	3.2
1	A	383	THR	3.1
1	B	440	GLY	3.0
1	B	377	LEU	3.0
1	B	455	SER	2.9
1	A	228	GLY	2.9
1	B	331	PHE	2.9
1	A	224	GLU	2.8
1	B	438	VAL	2.8
1	A	470	ALA	2.8
1	A	278	CYS	2.8
1	A	472	GLU	2.8
1	A	456	ALA	2.7
1	A	372	SER	2.7
1	B	461	GLU	2.7
1	A	290	PHE	2.7
1	A	403	GLY	2.7
1	A	334	ALA	2.7
1	A	266	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	333	ILE	2.7
1	B	374	THR	2.7
1	A	245	ARG	2.7
1	B	293	ASP	2.6
1	B	405	ARG	2.6
1	A	331	PHE	2.6
1	B	320[A]	ASN	2.6
1	B	284	VAL	2.6
1	A	362	HIS	2.5
1	A	260	VAL	2.5
1	B	292	LEU	2.5
1	B	371	MET	2.5
1	A	329	GLY	2.5
1	A	412	PHE	2.5
1	B	227	PHE	2.5
1	B	329	GLY	2.5
1	B	372	SER	2.5
1	A	451	ARG	2.5
1	A	357	VAL	2.4
1	B	224	GLU	2.4
1	B	234	PRO	2.4
1	A	225	LEU	2.3
1	A	295	MET	2.3
1	A	371[A]	MET	2.3
1	B	260	VAL	2.3
1	B	357	VAL	2.3
1	A	475	LEU	2.3
1	B	225	LEU	2.3
1	B	337	ALA	2.3
1	B	362	HIS	2.3
1	A	336	TRP	2.3
1	A	234	PRO	2.3
1	A	406	VAL	2.3
1	A	460	LEU	2.3
1	B	307	PHE	2.2
1	B	277	ILE	2.2
1	A	477	ARG	2.2
1	A	350	VAL	2.2
1	B	454	ILE	2.2
1	A	308	LEU	2.2
1	A	465	MET	2.2
1	B	376	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	226	SER	2.2
1	A	348	SER	2.2
1	A	337	ALA	2.2
1	A	405	ARG	2.2
1	A	471	TRP	2.2
1	B	336	TRP	2.2
1	A	422	GLU	2.1
1	B	291	THR	2.1
1	B	479	GLY	2.1
1	A	294	VAL	2.1
1	B	264	ARG	2.1
1	B	411	GLU	2.1
1	A	243	LEU	2.1
1	B	287	LEU	2.1
1	B	380	GLY	2.1
1	A	344	VAL	2.1
1	A	454	ILE	2.1
1	B	228	GLY	2.1
1	A	310	PHE	2.1
1	B	396	PHE	2.1
1	A	233	LEU	2.1
1	A	382	TYR	2.0
1	B	444	SER	2.0
1	A	292	LEU	2.0
1	B	256	LEU	2.0
1	B	326	TYR	2.0
1	A	351	VAL	2.0
1	B	245	ARG	2.0
1	B	322	VAL	2.0
1	A	392	GLU	2.0
1	B	310	PHE	2.0
1	B	309	ILE	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

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
3	GOL	B	482	6/6	0.66	0.29	47,53,53,54	0
3	GOL	A	482	6/6	0.87	0.22	47,51,52,52	0
2	SO4	A	481	5/5	0.93	0.23	57,58,58,59	0
2	SO4	B	481	5/5	0.94	0.25	54,55,57,58	0

6.5 Other polymers

There are no such residues in this entry.