



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 5IVL
Title : CshA Helicase
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Deposited on : 2016-03-21
Resolution : 2.30 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 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 : 2.11
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) : 2.11

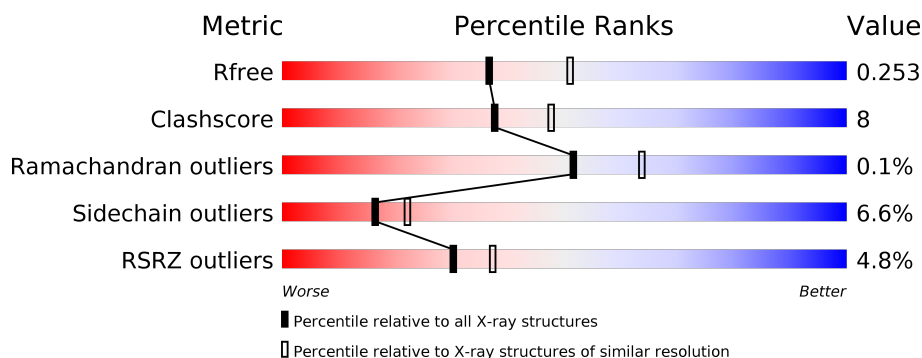
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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	429	<div> <div>3%</div> <div> <div></div> <div>79%</div> <div>11%</div> <div>6%</div> </div> </div>
1	B	429	<div> <div>6%</div> <div> <div></div> <div>74%</div> <div>19%</div> <div></div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	502	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6685 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 DEAD-box ATP-dependent RNA helicase CshA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	413	Total	C	N	O	S	0	0	0
			3262	2065	586	601	10			
1	A	404	Total	C	N	O	S	0	0	0
			3194	2019	573	591	11			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	423	GLU	-	expression tag	UNP A0A0K2H973
B	424	HIS	-	expression tag	UNP A0A0K2H973
B	425	HIS	-	expression tag	UNP A0A0K2H973
B	426	HIS	-	expression tag	UNP A0A0K2H973
B	427	HIS	-	expression tag	UNP A0A0K2H973
B	428	HIS	-	expression tag	UNP A0A0K2H973
B	429	HIS	-	expression tag	UNP A0A0K2H973
A	423	GLU	-	expression tag	UNP A0A0K2H973
A	424	HIS	-	expression tag	UNP A0A0K2H973
A	425	HIS	-	expression tag	UNP A0A0K2H973
A	426	HIS	-	expression tag	UNP A0A0K2H973
A	427	HIS	-	expression tag	UNP A0A0K2H973
A	428	HIS	-	expression tag	UNP A0A0K2H973
A	429	HIS	-	expression tag	UNP A0A0K2H973

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

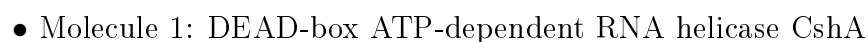


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	103	Total	O	0	0
			103	103		
3	A	106	Total	O	0	0
			106	106		

- Molecule 1: DEAD-box ATP-dependent RNA helicase CshA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.49Å 96.31Å 83.77Å 90.00° 95.21° 90.00°	Depositor
Resolution (Å)	23.52 – 2.30 23.52 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (23.52-2.30) 99.7 (23.52-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.42 (at 2.31Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, R_{free}	0.202 , 0.251 0.203 , 0.253	Depositor DCC
R_{free} test set	2057 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	35.4	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6685	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.44	0/3240	0.55	0/4370
1	B	0.45	0/3311	0.57	0/4467
All	All	0.44	0/6551	0.56	0/8837

There are no bond length outliers.

There are no bond angle outliers.

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	3194	0	3299	43	0
1	B	3262	0	3365	63	0
2	A	10	0	0	1	0
2	B	10	0	0	3	0
3	A	106	0	0	3	0
3	B	103	0	0	3	1
All	All	6685	0	6664	101	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 8.

All (101) 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:251:ARG:NH1	1:B:255:GLU:OE1	2.04	0.90
1:A:108:GLN:O	1:A:130:ARG:NH2	2.13	0.81
1:B:114:ILE:HD12	1:B:139:THR:HG21	1.72	0.71
1:A:367:LYS:HD3	1:A:368:PRO:HD2	1.75	0.68
1:B:100:ARG:NH1	1:B:119:LYS:O	2.27	0.68
1:A:357:ARG:NH1	3:A:606:HOH:O	2.26	0.67
1:B:268:GLU:HG3	1:B:291:ILE:HG21	1.78	0.65
1:A:284:ARG:NH1	1:A:288:GLU:OE1	2.31	0.63
1:B:212:VAL:N	3:B:602:HOH:O	2.34	0.61
1:B:61:VAL:HG13	1:B:99:VAL:HG21	1.82	0.61
1:B:17:ILE:HG23	1:B:22:PHE:HB2	1.84	0.60
1:B:383:ILE:HD11	1:A:401:ALA:HB1	1.83	0.59
1:A:102:LEU:HD12	1:A:103:PRO:HD2	1.83	0.59
1:B:379:GLN:NE2	1:B:423:GLU:OE2	2.37	0.58
1:B:405:LEU:HD21	1:A:386:LEU:HD23	1.87	0.57
1:A:242:LEU:HD22	1:A:286:PHE:CE1	2.40	0.56
1:B:108:GLN:O	1:B:130:ARG:NH2	2.29	0.56
1:B:134:HIS:HB3	1:B:140:LEU:HB2	1.88	0.56
1:A:314:ASN:HB2	1:A:342:THR:HA	1.87	0.55
1:A:221:GLU:OE1	1:A:365:ARG:NH2	2.31	0.54
1:B:380:ARG:HD3	1:B:381:ILE:HG13	1.90	0.54
1:A:406:LEU:HD23	1:A:414:ILE:HG13	1.90	0.54
1:B:17:ILE:HD11	1:B:58:ILE:HD11	1.89	0.53
1:A:396:SER:HA	1:A:399:LYS:HD3	1.89	0.52
1:B:17:ILE:HG12	1:B:22:PHE:HD1	1.73	0.52
1:A:248:ARG:NH2	1:A:317:ILE:O	2.41	0.52
1:B:12:GLU:N	1:B:12:GLU:OE1	2.40	0.51
1:B:154:ASP:HA	1:B:157:LEU:HD22	1.91	0.51
1:A:12:GLU:CD	1:A:12:GLU:H	2.15	0.50
1:A:225:LYS:HD3	1:A:225:LYS:H	1.76	0.50
1:B:75:VAL:HB	1:B:125:VAL:HB	1.92	0.50
1:B:214:ASN:ND2	1:B:336:LYS:O	2.44	0.50
1:A:241:GLU:CD	1:A:241:GLU:H	2.10	0.49
1:B:185:MET:SD	1:B:189:ILE:HG21	2.54	0.48
1:B:250:LYS:HG2	2:B:501:SO4:O2	2.13	0.48
1:A:103:PRO:O	1:A:104:ILE:HG13	2.14	0.48
1:A:274:LEU:HD12	1:A:274:LEU:HA	1.72	0.48
1:A:304:LEU:HD12	1:A:330:ARG:HD2	1.95	0.48
1:A:173:PRO:O	1:A:176:ARG:HD2	2.14	0.47
1:B:339:VAL:HG12	1:B:341:MET:HE2	1.96	0.47
1:A:255:GLU:OE2	3:A:601:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:383:ILE:HG23	1:A:405:LEU:HD11	1.97	0.47
1:B:15:LYS:CE	1:B:15:LYS:HA	2.45	0.47
1:B:17:ILE:HA	1:B:20:MET:CE	2.44	0.47
1:B:15:LYS:HE3	1:B:15:LYS:HA	1.97	0.47
1:B:17:ILE:HA	1:B:20:MET:HE3	1.96	0.47
1:A:250:LYS:HE2	2:A:502:SO4:O2	2.15	0.47
1:B:306:ILE:HD11	1:B:309:VAL:HG23	1.96	0.47
1:A:79:THR:HG21	1:A:319:GLN:HB2	1.97	0.46
1:B:271:HIS:CE1	1:B:273:ASP:HB2	2.50	0.46
1:B:347:ARG:H	1:B:347:ARG:CD	2.29	0.46
1:B:225:LYS:HG2	3:B:652:HOH:O	2.16	0.46
1:B:102:LEU:HD23	1:B:117:LEU:HD13	1.98	0.45
1:A:274:LEU:HB3	1:A:275:SER:H	1.52	0.45
1:B:190:ARG:NE	1:B:194:GLU:OE2	2.49	0.45
1:B:49:GLY:HA2	2:B:502:SO4:O4	2.17	0.45
1:B:226:LYS:HD2	3:B:696:HOH:O	2.17	0.44
1:A:175:GLU:OE2	3:A:602:HOH:O	2.21	0.44
1:B:66:VAL:HA	1:B:122:HIS:CE1	2.52	0.44
1:B:74:LEU:HD11	1:B:131:ILE:HD13	1.99	0.44
1:A:245:VAL:HG22	1:A:313:TYR:HB2	2.00	0.44
1:B:410:ASP:OD1	1:B:412:VAL:HG12	2.16	0.44
1:A:219:TYR:CZ	1:A:365:ARG:HB2	2.52	0.44
1:B:278:LYS:HA	1:B:278:LYS:HD2	1.82	0.44
1:A:67:LYS:HE2	1:A:67:LYS:HB2	1.85	0.43
1:B:186:PRO:HD2	1:B:189:ILE:HG12	1.99	0.43
1:B:108:GLN:OE1	1:B:113:GLN:NE2	2.43	0.43
1:A:104:ILE:HD12	1:A:124:ILE:HD12	2.00	0.43
1:A:175:GLU:H	1:A:175:GLU:CD	2.21	0.43
1:B:367:LYS:HD3	1:B:367:LYS:HA	1.79	0.43
1:B:48:THR:OG1	2:B:502:SO4:O3	2.33	0.43
1:B:71:ILE:HD13	1:B:124:ILE:HG13	2.01	0.43
1:B:58:ILE:HB	1:B:59:PRO:HD3	2.01	0.43
1:B:250:LYS:HG2	1:B:250:LYS:H	1.48	0.42
1:B:169:LEU:O	1:B:172:VAL:HG12	2.18	0.42
1:A:252:ARG:O	1:A:256:LEU:HB2	2.19	0.42
1:A:284:ARG:HG3	1:A:285:LYS:N	2.34	0.42
1:B:387:LEU:HD21	1:A:408:GLU:OE1	2.19	0.42
1:B:251:ARG:HH21	1:B:252:ARG:HG2	1.83	0.42
1:B:29:GLN:O	1:B:33:ILE:HG13	2.20	0.42
1:B:268:GLU:HG3	1:B:291:ILE:HD13	2.02	0.42
1:A:103:PRO:HA	1:A:125:VAL:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:LEU:HD13	1:B:117:LEU:HA	1.93	0.41
1:B:347:ARG:H	1:B:347:ARG:HD3	1.85	0.41
1:A:88:GLU:HG3	1:A:92:LYS:HE2	2.02	0.41
1:B:150:LEU:HD12	1:B:180:LEU:HD12	2.03	0.41
1:B:409:HIS:HB2	1:B:414:ILE:HD11	2.02	0.41
1:A:45:GLN:HA	1:A:182:SER:O	2.21	0.41
1:B:132:ILE:HD12	1:B:132:ILE:HA	1.94	0.41
1:A:42:VAL:HB	1:A:179:LEU:HD12	2.03	0.41
1:A:268:GLU:HG3	1:A:291:ILE:HG21	2.02	0.41
1:A:225:LYS:HE2	1:A:225:LYS:HB2	1.95	0.40
1:B:186:PRO:HD2	1:B:189:ILE:CG1	2.51	0.40
1:B:387:LEU:O	1:B:390:VAL:HG13	2.21	0.40
1:B:368:PRO:HA	1:B:369:PRO:HD3	1.94	0.40
1:A:387:LEU:HD12	1:A:387:LEU:HA	1.93	0.40
1:B:87:SER:HB3	1:B:125:VAL:HG13	2.03	0.40
1:A:410:ASP:OD2	1:A:413:THR:OG1	2.25	0.40
1:B:149:VAL:HG22	1:B:179:LEU:HB2	2.04	0.40
1:B:169:LEU:HA	1:B:172:VAL:HG12	2.04	0.40
1:B:386:LEU:HD23	1:A:405:LEU:HD21	2.04	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)
3:B:691:HOH:O	3:B:695:HOH:O[2_756]	2.19	0.01

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	396/429 (92%)	386 (98%)	9 (2%)	1 (0%)	41 50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	405/429 (94%)	394 (97%)	11 (3%)	0	100	100
All	All	801/858 (93%)	780 (97%)	20 (2%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	274	LEU

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	345/366 (94%)	327 (95%)	18 (5%)	23	32
1	B	350/366 (96%)	322 (92%)	28 (8%)	12	15
All	All	695/732 (95%)	649 (93%)	46 (7%)	16	22

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	4	PHE
1	B	5	GLN
1	B	6	GLU
1	B	7	LEU
1	B	11	GLN
1	B	15	LYS
1	B	17	ILE
1	B	23	GLU
1	B	48	THR
1	B	52	LYS
1	B	117	LEU
1	B	125	VAL
1	B	127	THR
1	B	157	LEU
1	B	190	ARG

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Mol	Chain	Res	Type
1	B	279	ARG
1	B	304	LEU
1	B	306	ILE
1	B	347	ARG
1	B	375	LEU
1	B	379	GLN
1	B	380	ARG
1	B	387	LEU
1	B	390	VAL
1	B	391	GLU
1	B	404	GLU
1	B	410	ASP
1	B	420	LYS
1	A	12	GLU
1	A	118	LYS
1	A	130	ARG
1	A	175	GLU
1	A	176	ARG
1	A	179	LEU
1	A	195	ARG
1	A	241	GLU
1	A	242	LEU
1	A	248	ARG
1	A	256	LEU
1	A	274	LEU
1	A	284	ARG
1	A	304	LEU
1	A	330	ARG
1	A	345	THR
1	A	387	LEU
1	A	405	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 [i](#)

There are no carbohydrates 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	$\# Z > 2$
2	SO4	A	501	-	4,4,4	0.20	0	6,6,6	0.32	0
2	SO4	B	502	-	4,4,4	0.11	0	6,6,6	0.49	0
2	SO4	B	501	-	4,4,4	0.22	0	6,6,6	0.26	0
2	SO4	A	502	-	4,4,4	0.20	0	6,6,6	0.20	0

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.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	502	SO4	2	0
2	B	501	SO4	1	0
2	A	502	SO4	1	0

5.7 Other polymers [i](#)

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, 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	404/429 (94%)	0.15	14 (3%) 44 51	27, 45, 67, 91	0
1	B	413/429 (96%)	0.26	25 (6%) 21 27	26, 44, 72, 92	0
All	All	817/858 (95%)	0.21	39 (4%) 30 37	26, 45, 69, 92	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	397	PHE	5.3
1	A	424	HIS	4.5
1	B	335	GLY	4.4
1	A	214	ASN	4.3
1	B	212	VAL	3.9
1	B	67	LYS	3.6
1	B	334	ALA	3.4
1	B	245	VAL	3.3
1	B	207	ALA	3.3
1	A	245	VAL	3.3
1	A	415	VAL	3.0
1	B	389	VAL	3.0
1	B	388	ASN	3.0
1	B	398	TYR	2.8
1	B	244	ILE	2.8
1	A	305	ASP	2.8
1	A	410	ASP	2.8
1	B	206	LYS	2.6
1	B	15	LYS	2.5
1	B	399	LYS	2.5
1	B	392	THR	2.5
1	B	149	VAL	2.5
1	A	342	THR	2.4
1	A	98	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	312	VAL	2.4
1	B	415	VAL	2.3
1	B	390	VAL	2.3
1	B	296	ALA	2.2
1	A	399	LYS	2.2
1	B	340	ALA	2.2
1	A	23	GLU	2.2
1	B	56	PHE	2.1
1	A	75	VAL	2.1
1	A	175	GLU	2.1
1	A	149	VAL	2.1
1	B	23	GLU	2.0
1	A	111	GLU	2.0
1	B	418	CYS	2.0
1	B	76	VAL	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](#)

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, 95th 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(\AA^2)	Q<0.9
2	SO4	A	502	5/5	0.97	0.13	46,50,52,55	0
2	SO4	B	502	5/5	0.99	0.07	36,40,44,48	0
2	SO4	B	501	5/5	0.99	0.11	40,42,44,44	0
2	SO4	A	501	5/5	0.99	0.14	40,45,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.