



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2024 – 09:03 AM EST

PDB ID : 3KE6
Title : The crystal structure of the RsbU and RsbW domains of Rv1364c from Mycobacterium tuberculosis
Authors : King-Scott, J.; Panjikar, S.; Tucker, P.A.
Deposited on : 2009-10-24
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 : 4.02b-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

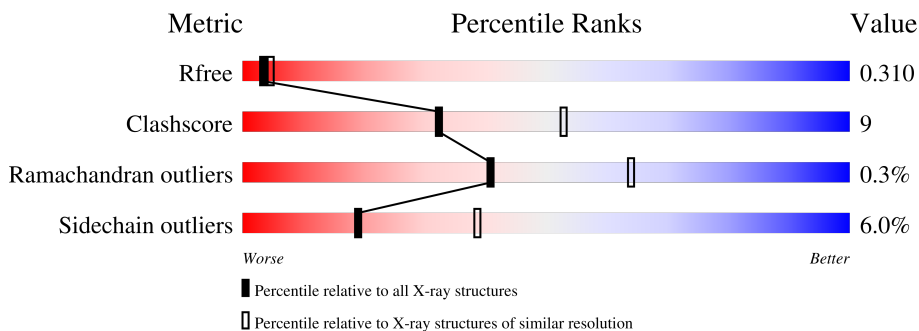
1 Overall quality at a glance

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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	399	70% 17% • 11%
1	B	399	71% 15% • 13%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 5304 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 Protein Rv1364c/MT1410.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	354	2618	1641	459	507	11	0	1	0
1	B	348	2568	1605	453	500	10	0	1	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	expression tag	UNP Q11034
A	-26	LYS	-	expression tag	UNP Q11034
A	-25	HIS	-	expression tag	UNP Q11034
A	-24	HIS	-	expression tag	UNP Q11034
A	-23	HIS	-	expression tag	UNP Q11034
A	-22	HIS	-	expression tag	UNP Q11034
A	-21	HIS	-	expression tag	UNP Q11034
A	-20	HIS	-	expression tag	UNP Q11034
A	-19	PRO	-	expression tag	UNP Q11034
A	-18	MET	-	expression tag	UNP Q11034
A	-17	SER	-	expression tag	UNP Q11034
A	-16	ASP	-	expression tag	UNP Q11034
A	-15	TYR	-	expression tag	UNP Q11034
A	-14	ASP	-	expression tag	UNP Q11034
A	-13	ILE	-	expression tag	UNP Q11034
A	-12	PRO	-	expression tag	UNP Q11034
A	-11	THR	-	expression tag	UNP Q11034
A	-10	THR	-	expression tag	UNP Q11034
A	-9	GLU	-	expression tag	UNP Q11034
A	-8	ASN	-	expression tag	UNP Q11034
A	-7	LEU	-	expression tag	UNP Q11034
A	-6	TYR	-	expression tag	UNP Q11034
A	-5	PHE	-	expression tag	UNP Q11034
A	-4	GLN	-	expression tag	UNP Q11034
A	-3	GLY	-	expression tag	UNP Q11034

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ALA	-	expression tag	UNP Q11034
A	-1	MET	-	expression tag	UNP Q11034
A	0	VAL	-	expression tag	UNP Q11034
B	-27	MET	-	expression tag	UNP Q11034
B	-26	LYS	-	expression tag	UNP Q11034
B	-25	HIS	-	expression tag	UNP Q11034
B	-24	HIS	-	expression tag	UNP Q11034
B	-23	HIS	-	expression tag	UNP Q11034
B	-22	HIS	-	expression tag	UNP Q11034
B	-21	HIS	-	expression tag	UNP Q11034
B	-20	HIS	-	expression tag	UNP Q11034
B	-19	PRO	-	expression tag	UNP Q11034
B	-18	MET	-	expression tag	UNP Q11034
B	-17	SER	-	expression tag	UNP Q11034
B	-16	ASP	-	expression tag	UNP Q11034
B	-15	TYR	-	expression tag	UNP Q11034
B	-14	ASP	-	expression tag	UNP Q11034
B	-13	ILE	-	expression tag	UNP Q11034
B	-12	PRO	-	expression tag	UNP Q11034
B	-11	THR	-	expression tag	UNP Q11034
B	-10	THR	-	expression tag	UNP Q11034
B	-9	GLU	-	expression tag	UNP Q11034
B	-8	ASN	-	expression tag	UNP Q11034
B	-7	LEU	-	expression tag	UNP Q11034
B	-6	TYR	-	expression tag	UNP Q11034
B	-5	PHE	-	expression tag	UNP Q11034
B	-4	GLN	-	expression tag	UNP Q11034
B	-3	GLY	-	expression tag	UNP Q11034
B	-2	ALA	-	expression tag	UNP Q11034
B	-1	MET	-	expression tag	UNP Q11034
B	0	VAL	-	expression tag	UNP Q11034

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



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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Mn 2 2	0	0
4	B	2	Total Mn 2 2	0	0

- Molecule 5 is water.

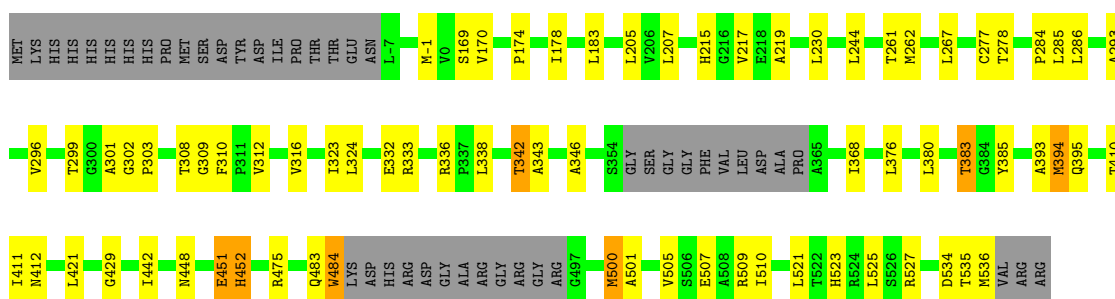
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	51	Total O 51 51	0	0
5	B	52	Total O 52 52	0	0

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. 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. 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.

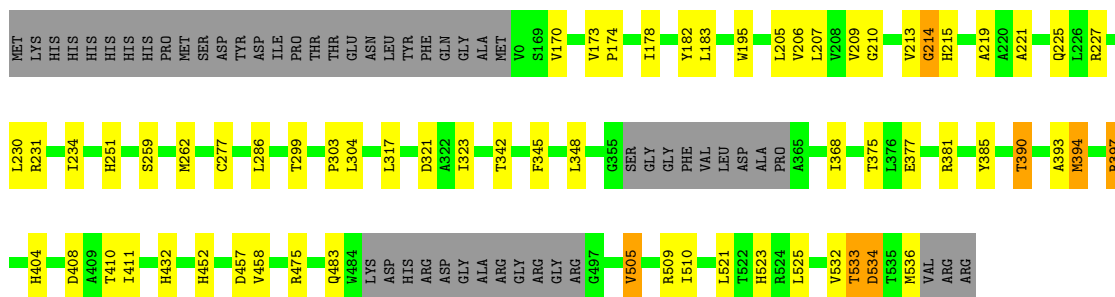
- Molecule 1: Protein Rv1364c/MT1410

Chain A:  70% 17% 11%



- Molecule 1: Protein Rv1364c/MT1410

Chain B:  71% 15% 13%



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	100.12Å 100.12Å 169.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.63 – 2.60 19.61 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.63-2.60) 99.2 (19.61-2.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 2.59Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.208 , 0.267 0.277 , 0.310	Depositor DCC
R_{free} test set	1356 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	51.6	Xtrriage
Anisotropy	0.055	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5304	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.31% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MN, 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	0.57	0/2668	0.74	2/3637 (0.1%)
1	B	0.54	0/2613	0.73	2/3563 (0.1%)
All	All	0.56	0/5281	0.74	4/7200 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	475	ARG	NE-CZ-NH2	-7.42	116.59	120.30
1	A	475	ARG	NE-CZ-NH2	-6.88	116.86	120.30
1	B	475	ARG	NE-CZ-NH1	6.86	123.73	120.30
1	A	475	ARG	NE-CZ-NH1	5.99	123.30	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	452	HIS	Peptide

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	2618	0	2588	54	0
1	B	2568	0	2536	38	0
2	A	5	0	0	0	0
3	A	6	0	8	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	51	0	0	3	0
5	B	52	0	0	4	0
All	All	5304	0	5132	91	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 (91) 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:302:GLY:H	1:A:308:THR:HG21	1.31	0.91
1:B:230:LEU:HD22	1:B:262:MET:CE	2.04	0.88
1:B:206:VAL:HG11	1:B:234:ILE:HD13	1.59	0.83
1:B:214:GLY:O	1:B:219:ALA:HB2	1.82	0.80
1:B:207:LEU:HD11	1:B:394:MET:HG2	1.64	0.78
1:A:410:THR:HG22	1:A:412:ASN:H	1.49	0.77
1:A:230:LEU:HD22	1:A:262:MET:CE	2.15	0.77
1:A:285:LEU:HD21	1:A:293:ALA:HB1	1.65	0.77
1:A:302:GLY:N	1:A:308:THR:HG21	2.01	0.76
1:A:267:LEU:HD22	1:A:394:MET:CE	2.17	0.75
1:B:230:LEU:HD22	1:B:262:MET:HE3	1.74	0.70
1:B:213:VAL:HG12	5:B:30:HOH:O	1.91	0.68
1:A:183:LEU:HD11	1:A:376:LEU:HD21	1.73	0.68
1:A:505:VAL:HG22	1:A:523:HIS:ND1	2.09	0.67
1:A:207:LEU:HD11	1:A:394:MET:HG2	1.77	0.66
1:B:221:ALA:O	1:B:225:GLN:NE2	2.29	0.64
1:A:451:GLU:OE1	1:B:432:HIS:NE2	2.30	0.64
1:A:285:LEU:HD11	1:A:346:ALA:HA	1.81	0.63
1:B:214:GLY:O	1:B:219:ALA:CB	2.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:ARG:O	1:A:510:ILE:HD12	1.98	0.63
1:A:333:ARG:HD2	1:A:383:THR:HG21	1.79	0.62
1:A:267:LEU:HD22	1:A:394:MET:HE1	1.81	0.62
1:B:521:LEU:HD12	1:B:521:LEU:O	2.00	0.61
1:B:505:VAL:HG22	1:B:523:HIS:ND1	2.16	0.60
1:B:183:LEU:HD23	1:B:385:TYR:CE2	2.37	0.60
1:A:368:ILE:HD11	1:A:393:ALA:HB1	1.86	0.58
1:A:285:LEU:HD23	1:A:286:LEU:N	2.20	0.57
1:B:521:LEU:HD12	1:B:521:LEU:C	2.24	0.57
1:A:525:LEU:O	5:A:48:HOH:O	2.18	0.56
1:B:404[A]:HIS:NE2	5:B:84:HOH:O	2.27	0.56
1:B:505:VAL:HG22	1:B:523:HIS:CG	2.41	0.56
1:B:178:ILE:HD11	1:B:205:LEU:HD21	1.88	0.55
1:B:525:LEU:O	5:B:24:HOH:O	2.18	0.55
1:A:410:THR:CG2	1:A:411:ILE:N	2.72	0.53
1:A:278:THR:H	1:A:299:THR:CG2	2.23	0.51
1:B:509:ARG:O	1:B:510:ILE:HD13	2.11	0.51
1:B:390:THR:HG22	5:B:36:HOH:O	2.11	0.50
1:A:521:LEU:HD12	1:A:521:LEU:O	2.12	0.50
1:B:230:LEU:HD22	1:B:262:MET:HE2	1.89	0.50
1:A:230:LEU:HD22	1:A:262:MET:HE2	1.94	0.50
1:A:267:LEU:HD22	1:A:394:MET:HE2	1.91	0.49
1:A:308:THR:HG23	1:A:309:GLY:O	2.13	0.49
1:B:182:TYR:C	1:B:183:LEU:HD12	2.33	0.49
1:A:380:LEU:HA	1:A:383:THR:HG22	1.94	0.48
1:A:452:HIS:C	1:A:483:GLN:HB2	2.34	0.48
1:A:333:ARG:HH11	1:A:383:THR:HG21	1.79	0.48
1:A:183:LEU:N	1:A:183:LEU:HD12	2.29	0.48
1:A:174:PRO:HA	5:A:53:HOH:O	2.14	0.48
1:A:284:PRO:O	1:A:296:VAL:HG22	2.13	0.48
1:A:278:THR:H	1:A:299:THR:HG22	1.79	0.47
1:A:448:ASN:O	1:A:452:HIS:HB2	2.15	0.47
1:A:261:THR:HG22	1:A:303:PRO:HB3	1.97	0.47
1:B:195:TRP:CZ3	1:B:210:GLY:HA3	2.50	0.47
1:A:521:LEU:HD12	1:A:521:LEU:C	2.36	0.46
1:A:178:ILE:CD1	1:A:205:LEU:HD21	2.46	0.46
1:A:342:THR:HG22	1:A:343:ALA:N	2.31	0.46
1:B:377:GLU:OE2	1:B:536:MET:HE1	2.16	0.46
1:B:532:VAL:HG13	1:B:536:MET:SD	2.56	0.46
1:A:410:THR:HG22	1:A:411:ILE:N	2.31	0.46
1:A:278:THR:OG1	1:A:299:THR:HG22	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:ILE:HD11	1:A:205:LEU:HD21	1.98	0.45
1:B:206:VAL:CG1	1:B:234:ILE:HD13	2.40	0.45
1:B:227:ARG:O	1:B:231:ARG:HD2	2.17	0.45
1:A:215:HIS:HA	1:A:219:ALA:HB3	1.99	0.45
1:A:-1:MET:CG	1:A:169:SER:O	2.65	0.44
1:B:214:GLY:C	1:B:219:ALA:HB2	2.36	0.44
1:A:395:GLN:NE2	5:A:76:HOH:O	2.46	0.44
1:B:368:ILE:HD11	1:B:393:ALA:HB1	1.98	0.44
1:B:259:SER:HA	1:B:303:PRO:HB2	1.98	0.44
1:A:421:LEU:HD21	1:A:442:ILE:HD12	2.00	0.44
1:B:505:VAL:HG11	1:B:521:LEU:HB2	1.99	0.44
1:A:215:HIS:CD2	1:A:215:HIS:C	2.91	0.43
1:A:484:TRP:HA	1:A:484:TRP:CE3	2.53	0.43
1:B:215:HIS:N	1:B:219:ALA:HB2	2.33	0.43
1:B:317:LEU:HD22	1:B:321:ASP:HB3	1.99	0.43
1:B:174:PRO:O	1:B:397:ARG:HD2	2.19	0.43
1:A:484:TRP:HA	1:A:484:TRP:HE3	1.84	0.42
1:A:244:LEU:HD13	1:A:310:PHE:CD1	2.54	0.42
1:A:316:VAL:O	1:A:316:VAL:HG13	2.18	0.42
1:A:323:ILE:C	1:A:324:LEU:HD12	2.39	0.42
1:A:332:GLU:OE2	1:A:338:LEU:HD21	2.19	0.42
1:B:408:ASP:HB3	1:B:410:THR:HG23	2.02	0.42
1:A:509:ARG:C	1:A:510:ILE:HD12	2.39	0.42
1:B:277:CYS:HA	1:B:299:THR:HG21	2.02	0.42
1:A:429:GLY:O	1:A:527:ARG:NH1	2.53	0.42
1:B:452:HIS:O	1:B:483:GLN:HA	2.20	0.41
1:A:299:THR:HG23	1:A:301:ALA:H	1.85	0.41
1:A:500:MET:HE3	1:A:501:ALA:HB2	2.02	0.41
1:B:345:PHE:HE1	1:B:375:THR:HG21	1.85	0.41
1:A:277:CYS:HB2	1:A:312:VAL:HG12	2.02	0.41
1:B:533:THR:HA	1:B:534:ASP:HA	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	349/399 (88%)	338 (97%)	11 (3%)	0	100	100
1	B	343/399 (86%)	327 (95%)	14 (4%)	2 (1%)	25	47
All	All	692/798 (87%)	665 (96%)	25 (4%)	2 (0%)	41	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	214	GLY
1	B	457	ASP

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	268/304 (88%)	254 (95%)	14 (5%)	23	46
1	B	263/304 (86%)	245 (93%)	18 (7%)	16	32
All	All	531/608 (87%)	499 (94%)	32 (6%)	19	39

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	170	VAL
1	A	217	VAL
1	A	336	ARG
1	A	342	THR
1	A	383	THR
1	A	385	TYR
1	A	394	MET
1	A	451	GLU
1	A	484	TRP
1	A	500	MET
1	A	507	GLU

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Mol	Chain	Res	Type
1	A	534	ASP
1	A	535	THR
1	A	536	MET
1	B	170	VAL
1	B	173	VAL
1	B	209	VAL
1	B	251	HIS
1	B	286	LEU
1	B	304	LEU
1	B	323	ILE
1	B	342	THR
1	B	348	LEU
1	B	381	ARG
1	B	390	THR
1	B	394	MET
1	B	397	ARG
1	B	411	ILE
1	B	458	VAL
1	B	505	VAL
1	B	533	THR
1	B	534	ASP

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	253	GLN
1	A	395	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](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	1	-	4,4,4	0.42	0	6,6,6	0.27	0
3	GOL	A	540	-	5,5,5	0.64	0	5,5,5	0.63	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	A	540	-	-	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	540	GOL	O1-C1-C2-C3
3	A	540	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.