



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:03 PM GMT

PDB ID : 1WD9  
Title : Calcium bound form of human peptidylarginine deiminase type4 (PAD4)  
Authors : Arita, K.; Hashimoto, H.; Shimizu, T.; Nakashima, K.; Yamada, M.; Sato, M.  
Deposited on : 2004-05-12  
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](mailto: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.

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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

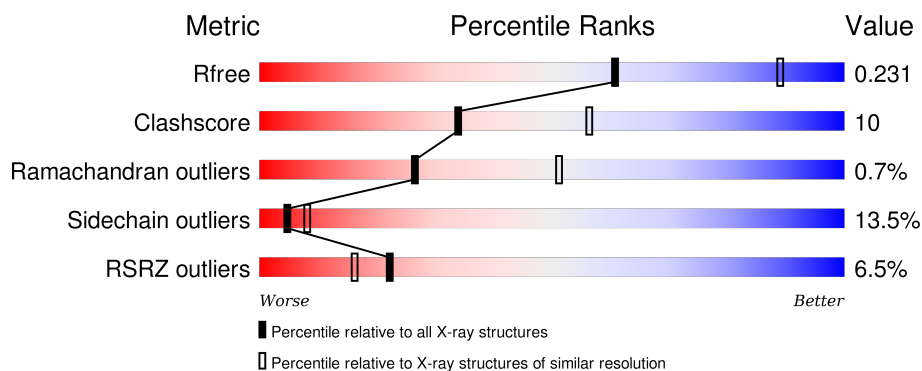
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	670	

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
3	SO4	A	906	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4829 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-arginine deiminase type IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	603	4745	3035	797	880	33	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	EXPRESSION TAG	UNP Q9UM07
A	-5	PRO	-	EXPRESSION TAG	UNP Q9UM07
A	-4	LEU	-	EXPRESSION TAG	UNP Q9UM07
A	-3	GLY	-	EXPRESSION TAG	UNP Q9UM07
A	-2	SER	-	EXPRESSION TAG	UNP Q9UM07
A	-1	PRO	-	EXPRESSION TAG	UNP Q9UM07
A	0	GLN	-	EXPRESSION TAG	UNP Q9UM07
A	645	ALA	CYS	ENGINEERED	UNP Q9UM07

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	Ca	0	0
			5	5		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

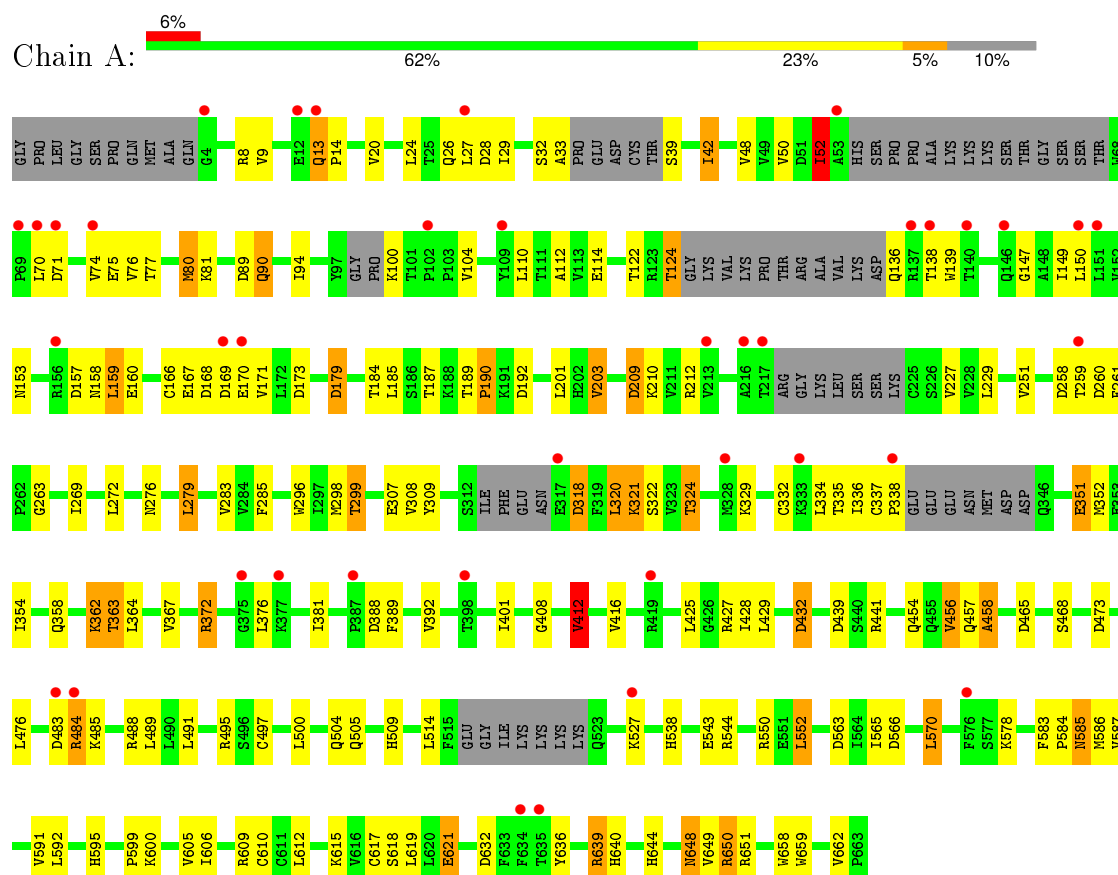
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	64	Total	O	0	0
			64	64		

### 3 Residue-property plots

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 ( $RSRZ > 2$ ). 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: Protein-arginine deiminase type IV



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	146.39Å 60.09Å 115.34Å 90.00° 124.37° 90.00°	Depositor
Resolution (Å)	22.80 – 2.60 22.80 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.1 (22.80-2.60) 96.3 (22.80-2.60)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.05 (at 2.60Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.224 , 0.269 0.229 , 0.231	Depositor DCC
$R_{free}$ test set	2474 reflections (11.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	58.8	Xtriage
Anisotropy	0.663	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 61.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 24775 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4829	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0.74	1/4857 (0.0%)	0.93	19/6590 (0.3%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	416	VAL	CB-CG2	-5.22	1.41	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	563	ASP	CB-CG-OD2	7.27	124.84	118.30
1	A	566	ASP	CB-CG-OD2	7.21	124.79	118.30
1	A	412	VAL	CB-CA-C	-6.84	98.40	111.40
1	A	192	ASP	CB-CG-OD2	6.50	124.15	118.30
1	A	260	ASP	CB-CG-OD2	6.43	124.09	118.30
1	A	483	ASP	CB-CG-OD2	6.35	124.01	118.30
1	A	209	ASP	CB-CG-OD2	6.24	123.92	118.30
1	A	168	ASP	CB-CG-OD2	6.05	123.74	118.30
1	A	367	VAL	CB-CA-C	-5.85	100.28	111.40
1	A	157	ASP	CB-CG-OD2	5.79	123.51	118.30
1	A	318	ASP	CB-CG-OD2	5.53	123.27	118.30
1	A	432	ASP	CB-CG-OD2	5.40	123.16	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	427	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	A	179	ASP	CB-CG-OD2	5.30	123.07	118.30
1	A	173	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	388	ASP	CB-CG-OD2	5.17	122.96	118.30
1	A	465	ASP	CB-CG-OD2	5.16	122.95	118.30
1	A	203	VAL	CB-CA-C	-5.11	101.69	111.40
1	A	71	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	454	GLN	Peptide

## 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	4745	0	4709	96	0
2	A	5	0	0	0	0
3	A	15	0	0	1	0
4	A	64	0	0	6	0
All	All	4829	0	4709	96	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 10.

All (96) 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:354:ILE:HG21	1:A:650:ARG:HG2	1.52	0.92
1:A:136:GLN:N	4:A:970:HOH:O	2.13	0.80
1:A:39:SER:N	4:A:927:HOH:O	2.14	0.78
1:A:425:LEU:HD12	1:A:456:VAL:HG13	1.66	0.78
1:A:42:ILE:HG21	1:A:50:VAL:HG11	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:LEU:HD21	1:A:251:VAL:HG12	1.67	0.76
1:A:299:THR:O	1:A:299:THR:CG2	2.36	0.72
1:A:425:LEU:HD12	1:A:456:VAL:CG1	2.25	0.67
1:A:362:LYS:NZ	1:A:364:LEU:HD22	2.11	0.66
1:A:320:LEU:HD11	1:A:336:ILE:CD1	2.28	0.64
1:A:320:LEU:HD11	1:A:336:ILE:HD13	1.80	0.64
1:A:412:VAL:HG13	1:A:428:ILE:HD13	1.81	0.63
1:A:585:ASN:ND2	1:A:587:VAL:HG12	2.13	0.63
1:A:362:LYS:HZ3	1:A:364:LEU:HD22	1.64	0.63
1:A:13:GLN:HB2	1:A:14:PRO:HD2	1.80	0.62
1:A:509:HIS:CD2	1:A:606:ILE:HD12	2.34	0.62
1:A:8:ARG:HG2	1:A:28:ASP:HB3	1.82	0.61
1:A:24:LEU:HD21	1:A:77:THR:HG21	1.81	0.61
1:A:153:ASN:HB3	1:A:166:CYS:HB3	1.83	0.61
1:A:296:TRP:CH2	1:A:298:MET:HG3	2.36	0.60
1:A:441:ARG:HH11	1:A:441:ARG:HG3	1.67	0.59
1:A:299:THR:O	1:A:299:THR:HG23	2.04	0.58
1:A:33:ALA:C	4:A:928:HOH:O	2.43	0.57
1:A:48:VAL:HG23	1:A:90:GLN:HG3	1.86	0.57
1:A:20:VAL:HG21	1:A:285:PHE:CG	2.40	0.56
1:A:362:LYS:HB3	1:A:362:LYS:HZ2	1.71	0.56
1:A:648:ASN:HD22	1:A:649:VAL:H	1.54	0.55
1:A:272:LEU:CD2	1:A:283:VAL:HG22	2.37	0.55
1:A:497:CYS:HB3	1:A:570:LEU:HD13	1.87	0.55
1:A:80:MET:CE	1:A:112:ALA:HB2	2.37	0.54
1:A:488:ARG:HG2	1:A:565:ILE:HG13	1.90	0.54
1:A:80:MET:HE2	1:A:112:ALA:HB2	1.89	0.53
1:A:585:ASN:HD21	1:A:587:VAL:HG12	1.72	0.53
1:A:276:ASN:HB2	1:A:279:LEU:HD12	1.91	0.53
1:A:619:LEU:HA	4:A:935:HOH:O	2.09	0.52
1:A:149:ILE:HD13	1:A:659:TRP:CE3	2.46	0.51
1:A:505:GLN:HE21	1:A:527:LYS:HA	1.75	0.51
1:A:495:ARG:NH1	3:A:906:SO4:O2	2.43	0.51
1:A:495:ARG:HB2	1:A:543:GLU:OE2	2.10	0.51
1:A:9:VAL:HG21	1:A:94:ILE:HD13	1.93	0.50
1:A:362:LYS:CE	1:A:364:LEU:HD22	2.42	0.50
1:A:358:GLN:HB2	1:A:363:THR:HB	1.93	0.50
1:A:639:ARG:O	1:A:640:HIS:HB2	2.12	0.50
1:A:307:GLU:OE2	1:A:650:ARG:NH1	2.44	0.49
1:A:171:VAL:CG2	1:A:171:VAL:O	2.61	0.49
1:A:171:VAL:HG23	1:A:171:VAL:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:610:CYS:SG	1:A:612:LEU:HB2	2.53	0.49
1:A:362:LYS:HB3	1:A:362:LYS:NZ	2.25	0.49
1:A:473:ASP:OD2	1:A:644:HIS:CE1	2.66	0.48
1:A:189:THR:HB	1:A:190:PRO:HD2	1.96	0.47
1:A:484:ARG:O	1:A:485:LYS:HB2	2.14	0.47
1:A:114:GLU:O	1:A:187:THR:HA	2.14	0.47
1:A:329:LYS:HB3	1:A:595:HIS:CE1	2.50	0.47
1:A:617:CYS:O	1:A:621:GLU:HB2	2.13	0.47
1:A:351:GLU:HG2	1:A:372:ARG:NE	2.30	0.47
1:A:583:PHE:HB2	1:A:584:PRO:HD2	1.97	0.47
1:A:296:TRP:CZ3	1:A:298:MET:HG3	2.50	0.46
1:A:320:LEU:O	1:A:324:THR:OG1	2.27	0.46
1:A:29:ILE:HD12	1:A:76:VAL:HG21	1.96	0.46
1:A:308:VAL:HB	1:A:334:LEU:HD23	1.97	0.46
1:A:299:THR:HG22	1:A:299:THR:O	2.13	0.45
1:A:321:LYS:HA	1:A:324:THR:OG1	2.16	0.45
1:A:122:THR:O	1:A:124:THR:HG22	2.16	0.45
1:A:632:ASP:OD1	1:A:632:ASP:C	2.54	0.45
1:A:491:LEU:CD1	1:A:550:ARG:HG3	2.46	0.45
1:A:632:ASP:HB2	1:A:636:TYR:HB2	1.99	0.45
1:A:337:CYS:HA	1:A:338:PRO:HD3	1.87	0.44
1:A:615:LYS:O	1:A:619:LEU:HG	2.17	0.44
1:A:473:ASP:OD2	1:A:644:HIS:ND1	2.50	0.44
1:A:203:VAL:CG2	1:A:229:LEU:HD13	2.46	0.44
1:A:299:THR:HG21	4:A:924:HOH:O	2.18	0.44
1:A:358:GLN:HG2	1:A:658:TRP:HD1	1.83	0.44
1:A:484:ARG:O	4:A:955:HOH:O	2.21	0.44
1:A:358:GLN:CB	1:A:363:THR:HB	2.47	0.43
1:A:358:GLN:HG2	1:A:658:TRP:CD1	2.53	0.43
1:A:74:VAL:HG13	1:A:74:VAL:O	2.19	0.43
1:A:139:TRP:CD1	1:A:147:GLY:HA3	2.54	0.42
1:A:351:GLU:OE2	1:A:372:ARG:O	2.37	0.42
1:A:52:ILE:O	1:A:52:ILE:HG23	2.19	0.42
1:A:179:ASP:OD1	1:A:362:LYS:CE	2.67	0.42
1:A:24:LEU:CD2	1:A:77:THR:HG21	2.47	0.42
1:A:261:PHE:CZ	1:A:263:GLY:HA2	2.54	0.42
1:A:158:ASN:O	1:A:159:LEU:C	2.58	0.41
1:A:209:ASP:OD1	1:A:210:LYS:NZ	2.53	0.41
1:A:552:LEU:HD12	1:A:552:LEU:HA	1.90	0.41
1:A:488:ARG:HG2	1:A:565:ILE:CG1	2.50	0.41
1:A:505:GLN:NE2	1:A:527:LYS:HA	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:GLY:O	1:A:473:ASP:HB2	2.21	0.41
1:A:13:GLN:HE21	1:A:13:GLN:HB3	1.71	0.41
1:A:457:GLN:O	1:A:458:ALA:C	2.59	0.41
1:A:212:ARG:HD3	1:A:227:VAL:CG1	2.50	0.41
1:A:441:ARG:NH1	1:A:441:ARG:HG3	2.34	0.41
1:A:591:VAL:O	1:A:651:ARG:NH2	2.52	0.41
1:A:586:MET:HA	1:A:599:PRO:HD2	2.03	0.41
1:A:308:VAL:HG12	1:A:309:TYR:N	2.36	0.40
1:A:468:SER:HA	1:A:578:LYS:HB3	2.03	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	585/670 (87%)	553 (94%)	28 (5%)	4 (1%)	26 51

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	LEU
1	A	484	ARG
1	A	52	ILE
1	A	458	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	535/592 (90%)	463 (86%)	72 (14%)	<b>5</b> <b>8</b>

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	26	GLN
1	A	27	LEU
1	A	32	SER
1	A	42	ILE
1	A	52	ILE
1	A	70	LEU
1	A	75	GLU
1	A	80	MET
1	A	81	LYS
1	A	89	ASP
1	A	90	GLN
1	A	100	LYS
1	A	104	VAL
1	A	110	LEU
1	A	124	THR
1	A	138	THR
1	A	160	GLU
1	A	167	GLU
1	A	169	ASP
1	A	170	GLU
1	A	184	THR
1	A	185	LEU
1	A	190	PRO
1	A	201	LEU
1	A	258	ASP
1	A	259	THR
1	A	269	ILE
1	A	279	LEU
1	A	299	THR
1	A	318	ASP
1	A	320	LEU
1	A	321	LYS
1	A	322	SER
1	A	324	THR
1	A	332	CYS

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Mol	Chain	Res	Type
1	A	335	THR
1	A	351	GLU
1	A	352	MET
1	A	362	LYS
1	A	363	THR
1	A	372	ARG
1	A	376	LEU
1	A	381	ILE
1	A	389	PHE
1	A	392	VAL
1	A	401	ILE
1	A	412	VAL
1	A	429	LEU
1	A	432	ASP
1	A	439	ASP
1	A	456	VAL
1	A	476	LEU
1	A	489	LEU
1	A	500	LEU
1	A	504	GLN
1	A	514	LEU
1	A	538	HIS
1	A	544	ARG
1	A	552	LEU
1	A	570	LEU
1	A	585	ASN
1	A	592	LEU
1	A	600	LYS
1	A	605	VAL
1	A	609	ARG
1	A	618	SER
1	A	621	GLU
1	A	639	ARG
1	A	648	ASN
1	A	650	ARG
1	A	662	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	26	GLN

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Mol	Chain	Res	Type
1	A	197	HIS
1	A	202	HIS
1	A	236	HIS
1	A	276	ASN
1	A	445	GLN
1	A	448	GLN
1	A	505	GLN
1	A	506	ASN
1	A	509	HIS
1	A	523	GLN
1	A	538	HIS
1	A	585	ASN
1	A	648	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 5 are monoatomic - leaving 3 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	$\# Z  > 2$
3	SO4	A	905	-	4,4,4	0.43	0	6,6,6	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SO4	A	906	-	4,4,4	0.30	0	6,6,6	0.56	0
3	SO4	A	907	-	4,4,4	0.23	0	6,6,6	0.43	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	SO4	A	905	-	-	0/0/0/0	0/0/0/0
3	SO4	A	906	-	-	0/0/0/0	0/0/0/0
3	SO4	A	907	-	-	0/0/0/0	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	906	SO4	1	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	603/670 (90%)	0.19	39 (6%)	22 16	41, 58, 79, 90	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	137	ARG	5.3
1	A	328	MET	4.7
1	A	375	GLY	4.7
1	A	156	ARG	4.5
1	A	333	LYS	4.0
1	A	398	THR	3.8
1	A	217	THR	3.7
1	A	13	GLN	3.6
1	A	53	ALA	3.2
1	A	419	ARG	2.9
1	A	70	LEU	2.9
1	A	71	ASP	2.8
1	A	259	THR	2.8
1	A	74	VAL	2.7
1	A	484	ARG	2.7
1	A	213	VAL	2.7
1	A	146	GLN	2.6
1	A	387	PRO	2.6
1	A	150	LEU	2.5
1	A	170	GLU	2.5
1	A	102	PRO	2.5
1	A	169	ASP	2.4
1	A	634	PHE	2.4
1	A	483	ASP	2.4
1	A	377	LYS	2.3
1	A	338	PRO	2.3
1	A	576	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	12	GLU	2.3
1	A	140	THR	2.2
1	A	635	THR	2.2
1	A	27	LEU	2.2
1	A	109	TYR	2.1
1	A	527	LYS	2.1
1	A	69	PRO	2.1
1	A	138	THR	2.1
1	A	4	GLY	2.1
1	A	151	LEU	2.1
1	A	317	GLU	2.0
1	A	216	ALA	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	SO4	A	906	5/5	0.87	0.26	3.32	75,75,77,77	0
2	CA	A	904	1/1	0.72	0.12	-0.90	71,71,71,71	0
2	CA	A	903	1/1	0.92	0.06	-1.65	67,67,67,67	0
2	CA	A	900	1/1	0.95	0.04	-2.46	57,57,57,57	0
2	CA	A	902	1/1	0.98	0.07	-2.46	75,75,75,75	0
2	CA	A	901	1/1	0.99	0.03	-3.57	65,65,65,65	0
3	SO4	A	907	5/5	0.94	0.23	-	77,77,79,80	0
3	SO4	A	905	5/5	0.96	0.20	-	76,76,79,80	0

## 6.5 Other polymers

There are no such residues in this entry.