



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:31 AM GMT

PDB ID : 2DEX  
Title : Crystal structure of human peptidylarginine deiminase 4 in complex with histone H3 N-terminal peptide including Arg17  
Authors : Arita, K.; Shimizu, T.; Hashimoto, H.; Hidaka, Y.; Yamada, M.; Sato, M.  
Deposited on : 2006-02-18  
Resolution : 2.10 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

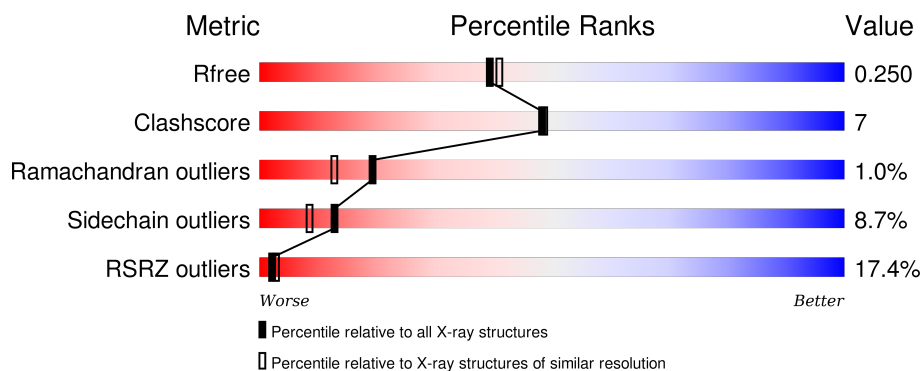
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	X	671	<div> <div>16%</div> <div> <div></div> <div>75%</div> <div>16%</div> <div>•</div> <div>7%</div> </div> </div>
2	A	10	<div> <div>30%</div> <div> <div>30%</div> <div>20%</div> <div>50%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5190 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
1	X	627	Total	C	N	O	S	0	0	0
			4937	3153	828	922	34			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	-7	GLY	-	CLONING ARTIFACT	UNP Q9UM07
X	-6	PRO	-	CLONING ARTIFACT	UNP Q9UM07
X	-5	LEU	-	CLONING ARTIFACT	UNP Q9UM07
X	-4	GLY	-	CLONING ARTIFACT	UNP Q9UM07
X	-3	SER	-	CLONING ARTIFACT	UNP Q9UM07
X	-2	PRO	-	CLONING ARTIFACT	UNP Q9UM07
X	-1	GLU	-	CLONING ARTIFACT	UNP Q9UM07
X	0	PHE	-	CLONING ARTIFACT	UNP Q9UM07
X	645	ALA	CYS	ENGINEERED	UNP Q9UM07

- Molecule 2 is a protein called 10-mer peptide from histone H3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	A	5	Total	C	N	O	0	0	0
			41	25	10	6			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	X	5	Total	Ca	0	0
			5	5		

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



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

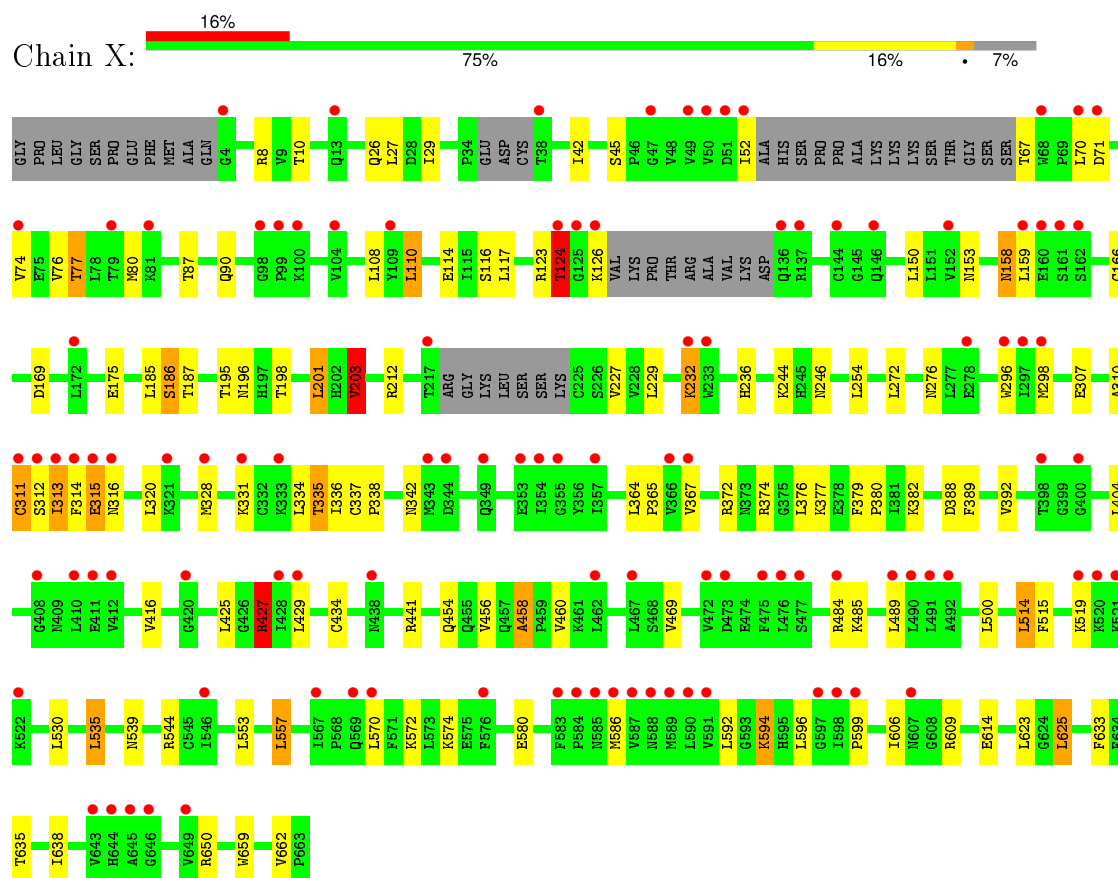
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	O	0	0
			2	2		
5	X	190	Total	O	0	0
			190	190		

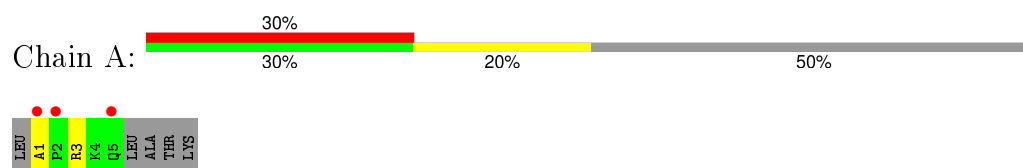
### 3 Residue-property plots

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 ( $\text{RSRZ} > 2$ ). 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: Protein-arginine deiminase type IV



#### • Molecule 2: 10-mer peptide from histone H3



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	146.07Å 60.10Å 115.70Å 90.00° 124.32° 90.00°	Depositor
Resolution (Å)	33.13 – 2.10 33.13 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.6 (33.13-2.10) 94.6 (33.13-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.46 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.203 , 0.247 0.210 , 0.250	Depositor DCC
$R_{free}$ test set	4628 reflections (11.17%)	DCC
Wilson B-factor (Å <sup>2</sup> )	54.4	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 67.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 46064 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5190	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% 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	X	0.57	1/5056 (0.0%)	0.74	7/6861 (0.1%)
2	A	0.58	0/41	0.77	0/53
All	All	0.57	1/5097 (0.0%)	0.74	7/6914 (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	X	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	311	CYS	CB-SG	-5.93	1.72	1.81

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	650	ARG	NE-CZ-NH1	6.23	123.42	120.30
1	X	650	ARG	NE-CZ-NH2	-6.13	117.23	120.30
1	X	203	VAL	CB-CA-C	-5.94	100.11	111.40
1	X	372	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	X	427	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	X	367	VAL	CB-CA-C	-5.14	101.64	111.40
1	X	201	LEU	CA-CB-CG	5.13	127.10	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	X	313	ILE	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	X	4937	0	4900	72	0
2	A	41	0	48	2	0
3	X	5	0	0	0	0
4	X	15	0	0	0	0
5	A	2	0	0	1	0
5	X	190	0	0	7	0
All	All	5190	0	4948	73	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 7.

All (73) 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:X:454:GLN:O	5:X:909:HOH:O	1.79	1.00
1:X:425:LEU:HD12	1:X:456:VAL:HG13	1.58	0.86
1:X:315:GLU:HG3	1:X:316:ASN:HD22	1.43	0.82
1:X:574:LYS:NZ	1:X:580:GLU:OE1	2.11	0.81
1:X:313:ILE:HB	1:X:338:PRO:HA	1.62	0.79
1:X:572:LYS:HE3	1:X:574:LYS:HZ2	1.47	0.78
1:X:26:GLN:OE1	1:X:77:THR:HB	1.84	0.76
1:X:316:ASN:O	5:X:1097:HOH:O	2.07	0.73
2:A:1:ALA:N	5:A:188:HOH:O	2.23	0.72
1:X:195:THR:HG22	1:X:196:ASN:ND2	2.05	0.72
1:X:572:LYS:HE3	1:X:574:LYS:NZ	2.07	0.70
1:X:236:HIS:ND1	5:X:968:HOH:O	2.26	0.69
1:X:310:ALA:O	1:X:336:ILE:HA	1.95	0.66
1:X:203:VAL:CG2	1:X:229:LEU:HD13	2.27	0.64
1:X:312:SER:HB2	1:X:320:LEU:HD12	1.82	0.62
1:X:662:VAL:HG23	1:X:662:VAL:O	2.00	0.61
1:X:52:ILE:HD12	1:X:76:VAL:HG22	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:315:GLU:HG3	1:X:316:ASN:ND2	2.16	0.57
1:X:586:MET:HA	1:X:599:PRO:HG2	1.85	0.57
1:X:203:VAL:HG22	1:X:229:LEU:HD13	1.86	0.57
1:X:312:SER:CB	1:X:320:LEU:HD12	2.35	0.57
1:X:594:LYS:NZ	5:X:1009:HOH:O	2.20	0.56
1:X:311:CYS:CB	1:X:337:CYS:HB3	2.36	0.56
1:X:45:SER:OG	1:X:90:GLN:NE2	2.38	0.56
1:X:334:LEU:C	1:X:334:LEU:HD13	2.27	0.55
1:X:27:LEU:HB3	1:X:29:ILE:CD1	2.36	0.55
1:X:123:ARG:O	1:X:124:THR:OG1	2.24	0.54
1:X:307:GLU:OE2	1:X:335:THR:CG2	2.57	0.53
1:X:311:CYS:HB3	1:X:337:CYS:HB3	1.91	0.53
1:X:307:GLU:OE2	1:X:335:THR:HG21	2.09	0.51
1:X:514:LEU:HD13	1:X:515:PHE:CE2	2.45	0.51
1:X:153:ASN:HB3	1:X:166:CYS:HB3	1.93	0.51
1:X:441:ARG:HG3	1:X:441:ARG:HH11	1.76	0.51
1:X:441:ARG:NH1	5:X:921:HOH:O	2.44	0.51
1:X:425:LEU:HD12	1:X:456:VAL:CG1	2.35	0.51
1:X:108:LEU:HG	1:X:110:LEU:HD13	1.93	0.51
1:X:158:ASN:HD22	1:X:159:LEU:N	2.10	0.50
1:X:158:ASN:C	1:X:158:ASN:HD22	2.15	0.50
1:X:123:ARG:HD3	1:X:659:TRP:CD1	2.47	0.49
1:X:166:CYS:HB2	1:X:254:LEU:HD22	1.94	0.49
1:X:186:SER:OG	1:X:246:ASN:ND2	2.46	0.49
1:X:434:CYS:HB2	5:X:961:HOH:O	2.14	0.47
1:X:633:PHE:CE1	1:X:638:ILE:HD11	2.50	0.46
1:X:596:LEU:HD11	1:X:625:LEU:HG	1.98	0.46
1:X:311:CYS:HB2	1:X:342:ASN:OD1	2.15	0.46
1:X:126:LYS:N	5:X:1036:HOH:O	2.47	0.46
1:X:633:PHE:O	1:X:638:ILE:HG12	2.15	0.45
1:X:379:PHE:HB3	1:X:380:PRO:HD3	1.98	0.45
1:X:623:LEU:HB2	1:X:625:LEU:HD22	1.98	0.45
1:X:74:VAL:HG13	1:X:74:VAL:O	2.17	0.44
1:X:313:ILE:CB	1:X:338:PRO:HA	2.40	0.44
1:X:320:LEU:HD23	1:X:320:LEU:O	2.17	0.44
1:X:553:LEU:O	1:X:557:LEU:HB2	2.18	0.44
1:X:427:ARG:HG2	1:X:460:VAL:HG23	2.00	0.44
1:X:80:MET:CE	1:X:90:GLN:HG3	2.48	0.43
1:X:71:ASP:O	1:X:74:VAL:HG12	2.18	0.43
1:X:42:ILE:CD1	1:X:76:VAL:HG11	2.48	0.43
1:X:535:LEU:HD22	1:X:539:ASN:ND2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:311:CYS:O	1:X:311:CYS:SG	2.77	0.43
1:X:594:LYS:HA	1:X:625:LEU:HD12	2.00	0.43
1:X:296:TRP:CZ3	1:X:298:MET:HG3	2.53	0.43
1:X:198:THR:HG23	1:X:272:LEU:HD12	2.00	0.42
1:X:374:ARG:O	1:X:377:LYS:HB2	2.19	0.42
1:X:427:ARG:HG3	1:X:458:ALA:O	2.19	0.42
1:X:313:ILE:O	1:X:342:ASN:ND2	2.53	0.42
1:X:203:VAL:HG23	1:X:229:LEU:HD13	1.99	0.42
1:X:334:LEU:HD11	1:X:336:ILE:CD1	2.50	0.41
1:X:114:GLU:O	1:X:187:THR:HA	2.20	0.41
1:X:80:MET:HE3	1:X:90:GLN:HG3	2.02	0.41
1:X:232:LYS:O	1:X:232:LYS:HD2	2.20	0.41
1:X:365:PRO:HD2	1:X:388:ASP:O	2.21	0.41
1:X:212:ARG:HD3	1:X:227:VAL:CG1	2.51	0.41
1:X:469:VAL:HG11	2:A:3:ARG:HD3	2.03	0.41

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	X	617/671 (92%)	591 (96%)	20 (3%)	6 (1%)	19	13
2	A	3/10 (30%)	3 (100%)	0	0	100	100
All	All	620/681 (91%)	594 (96%)	20 (3%)	6 (1%)	19	13

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	484	ARG
1	X	124	THR
1	X	315	GLU

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Mol	Chain	Res	Type
1	X	458	ALA
1	X	485	LYS
1	X	519	LYS

### 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	X	557/593 (94%)	508 (91%)	49 (9%)	12	8
2	A	4/8 (50%)	4 (100%)	0	100	100
All	All	561/601 (93%)	512 (91%)	49 (9%)	13	8

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	8	ARG
1	X	10	THR
1	X	67	THR
1	X	70	LEU
1	X	77	THR
1	X	87	THR
1	X	110	LEU
1	X	116	SER
1	X	117	LEU
1	X	124	THR
1	X	150	LEU
1	X	158	ASN
1	X	169	ASP
1	X	175	GLU
1	X	185	LEU
1	X	186	SER
1	X	201	LEU
1	X	203	VAL
1	X	232	LYS
1	X	244	LYS

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Mol	Chain	Res	Type
1	X	276	ASN
1	X	314	PHE
1	X	328	MET
1	X	331	LYS
1	X	335	THR
1	X	364	LEU
1	X	376	LEU
1	X	382	LYS
1	X	389	PHE
1	X	392	VAL
1	X	404	LEU
1	X	416	VAL
1	X	427	ARG
1	X	429	LEU
1	X	489	LEU
1	X	500	LEU
1	X	514	LEU
1	X	530	LEU
1	X	535	LEU
1	X	544	ARG
1	X	557	LEU
1	X	570	LEU
1	X	592	LEU
1	X	594	LYS
1	X	606	ILE
1	X	609	ARG
1	X	614	GLU
1	X	625	LEU
1	X	635	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	90	GLN
1	X	158	ASN
1	X	178	GLN
1	X	196	ASN
1	X	246	ASN
1	X	303	GLN
1	X	316	ASN
1	X	346	GLN
1	X	448	GLN

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Mol	Chain	Res	Type
1	X	505	GLN
1	X	538	HIS

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	$\# Z  > 2$
4	SO4	X	905	-	4,4,4	0.24	0	6,6,6	0.39	0
4	SO4	X	906	-	4,4,4	0.18	0	6,6,6	0.29	0
4	SO4	X	907	-	4,4,4	0.25	0	6,6,6	0.21	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
4	SO4	X	905	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	X	906	-	-	0/0/0/0	0/0/0/0
4	SO4	X	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.

No monomer is involved in short contacts.

## 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<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	X	627/671 (93%)	0.80	107 (17%) <b>2</b> <b>3</b>	51, 63, 80, 95	0
2	A	5/10 (50%)	2.64	3 (60%) <b>0</b> <b>0</b>	67, 71, 75, 77	0
All	All	632/681 (92%)	0.81	110 (17%) <b>2</b> <b>3</b>	51, 63, 80, 95	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	312	SER	8.4
1	X	314	PHE	6.8
1	X	587	VAL	5.7
2	A	1	ALA	5.2
1	X	476	LEU	5.1
1	X	74	VAL	5.0
1	X	124	THR	4.8
1	X	520	LYS	4.6
1	X	410	LEU	4.6
1	X	38	THR	4.5
1	X	98	GLY	4.3
1	X	546	ILE	4.3
1	X	217	THR	4.1
1	X	484	ARG	3.9
1	X	328	MET	3.9
1	X	137	ARG	3.8
1	X	47	GLY	3.8
1	X	462	LEU	3.8
1	X	159	LEU	3.8
1	X	491	LEU	3.8
1	X	367	VAL	3.7
1	X	354	ILE	3.7
2	A	2	PRO	3.7
1	X	475	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
1	X	136	GLN	3.6
1	X	649	VAL	3.6
1	X	522	LYS	3.4
1	X	4	GLY	3.4
1	X	313	ILE	3.4
1	X	366	VAL	3.3
1	X	567	ILE	3.3
1	X	586	MET	3.2
1	X	311	CYS	3.2
1	X	233	TRP	3.2
1	X	588	ASN	3.2
1	X	126	LYS	3.1
1	X	477	SER	3.1
1	X	519	LYS	3.1
1	X	125	GLY	3.1
1	X	99	PRO	3.1
1	X	591	VAL	3.0
1	X	585	ASN	3.0
1	X	52	ILE	2.9
1	X	321	LYS	2.9
1	X	315	GLU	2.9
1	X	161	SER	2.9
1	X	343	MET	2.9
1	X	589	MET	2.9
1	X	49	VAL	2.9
1	X	104	VAL	2.8
1	X	68	TRP	2.8
1	X	490	LEU	2.8
1	X	398	THR	2.8
1	X	644	HIS	2.8
1	X	412	VAL	2.8
1	X	472	VAL	2.8
1	X	400	GLY	2.8
1	X	70	LEU	2.7
1	X	81	LYS	2.7
1	X	232	LYS	2.6
1	X	357	ILE	2.6
1	X	13	GLN	2.6
2	A	5	GLN	2.6
1	X	583	PHE	2.6
1	X	645	ALA	2.6
1	X	51	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	X	71	ASP	2.6
1	X	467	LEU	2.6
1	X	296	TRP	2.5
1	X	473	ASP	2.5
1	X	598	ILE	2.5
1	X	331	LYS	2.5
1	X	50	VAL	2.5
1	X	100	LYS	2.5
1	X	152	VAL	2.5
1	X	489	LEU	2.5
1	X	79	THR	2.4
1	X	298	MET	2.4
1	X	162	SER	2.4
1	X	297	ILE	2.4
1	X	344	ASP	2.4
1	X	278	GLU	2.3
1	X	408	GLY	2.3
1	X	492	ALA	2.3
1	X	643	VAL	2.3
1	X	576	PHE	2.3
1	X	420	GLY	2.3
1	X	146	GLN	2.3
1	X	355	GLY	2.2
1	X	599	PRO	2.2
1	X	428	ILE	2.2
1	X	316	ASN	2.2
1	X	411	GLU	2.2
1	X	569	GLN	2.2
1	X	144	CYS	2.2
1	X	172	LEU	2.2
1	X	438	ASN	2.2
1	X	590	LEU	2.2
1	X	353	GLU	2.2
1	X	333	LYS	2.2
1	X	429	LEU	2.1
1	X	160	GLU	2.1
1	X	349	GLN	2.1
1	X	597	GLY	2.1
1	X	646	GLY	2.1
1	X	521	LYS	2.0
1	X	570	LEU	2.0
1	X	584	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	X	607	ASN	2.0
1	X	109	TYR	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
4	SO4	X	906	5/5	0.97	0.16	0.12	86,86,87,87	0
4	SO4	X	905	5/5	0.96	0.12	-0.64	73,73,74,75	0
3	CA	X	902	1/1	0.97	0.07	-1.05	65,65,65,65	0
3	CA	X	904	1/1	0.94	0.08	-1.33	62,62,62,62	0
3	CA	X	903	1/1	0.98	0.06	-2.28	62,62,62,62	0
3	CA	X	901	1/1	0.98	0.04	-2.83	61,61,61,61	0
3	CA	X	900	1/1	1.00	0.10	-4.29	53,53,53,53	0
4	SO4	X	907	5/5	0.95	0.24	-	87,88,88,89	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.