



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 06:06 am GMT

PDB ID : 3EIA  
Title : Crystal structure of K270Q variant of LL-diaminopimelate aminotransferase from Arabidopsis thaliana complexed with L-Glu: External aldimine form  
Authors : Watanabe, N.; Clay, M.D.; van Belkum, M.J.; Cherney, M.M.; Vederas, J.C.; James, M.N.G.  
Deposited on : 2008-09-15  
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](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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

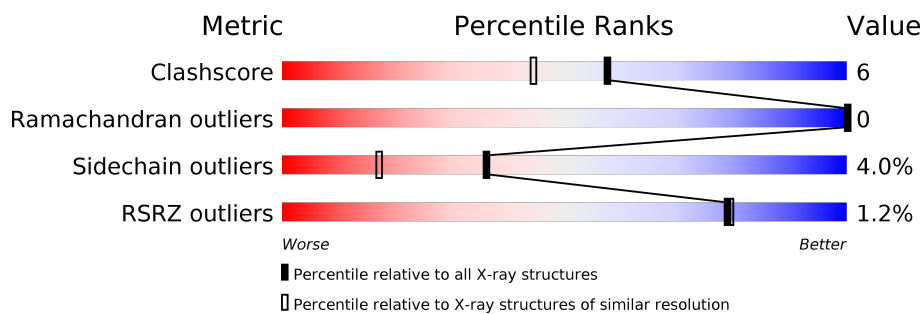
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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))
Clashscore	112137	2083 (1.86-1.86)
Ramachandran outliers	110173	2060 (1.86-1.86)
Sidechain outliers	110143	2060 (1.86-1.86)
RSRZ outliers	101464	1932 (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 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	432	<div> <div>%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>• 5%</div> </div> </div>
1	B	432	<div> <div>%</div> <div> <div></div> <div>84%</div> <div>9%</div> <div>• 5%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7152 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 LL-diaminopimelate aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	412	Total	C	N	O	S	0	0	0
			3184	2026	536	606	16			
1	B	409	Total	C	N	O	S	0	0	0
			3154	2008	527	603	16			

There are 14 discrepancies between the modelled and reference sequences:

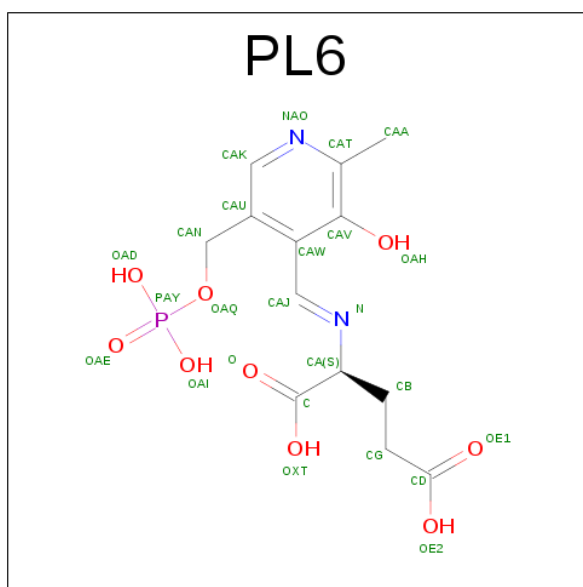
Chain	Residue	Modelled	Actual	Comment	Reference
A	270	GLN	LYS	ENGINEERED	UNP Q93ZN9
A	427	HIS	-	EXPRESSION TAG	UNP Q93ZN9
A	428	HIS	-	EXPRESSION TAG	UNP Q93ZN9
A	429	HIS	-	EXPRESSION TAG	UNP Q93ZN9
A	430	HIS	-	EXPRESSION TAG	UNP Q93ZN9
A	431	HIS	-	EXPRESSION TAG	UNP Q93ZN9
A	432	HIS	-	EXPRESSION TAG	UNP Q93ZN9
B	270	GLN	LYS	ENGINEERED	UNP Q93ZN9
B	427	HIS	-	EXPRESSION TAG	UNP Q93ZN9
B	428	HIS	-	EXPRESSION TAG	UNP Q93ZN9
B	429	HIS	-	EXPRESSION TAG	UNP Q93ZN9
B	430	HIS	-	EXPRESSION TAG	UNP Q93ZN9
B	431	HIS	-	EXPRESSION TAG	UNP Q93ZN9
B	432	HIS	-	EXPRESSION TAG	UNP Q93ZN9

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 3 is (E)-N-({3-HYDROXY-2-METHYL-5-[(PHOSPHONOOXY)METHYL]PYRIDIN-4-YL}METHYLIDENE)-L-GLUTAMIC ACID (three-letter code: PL6) (formula: C<sub>13</sub>H<sub>17</sub>N<sub>2</sub>O<sub>9</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0
			25	13	2	9	1	

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			25	13	2	9	1		

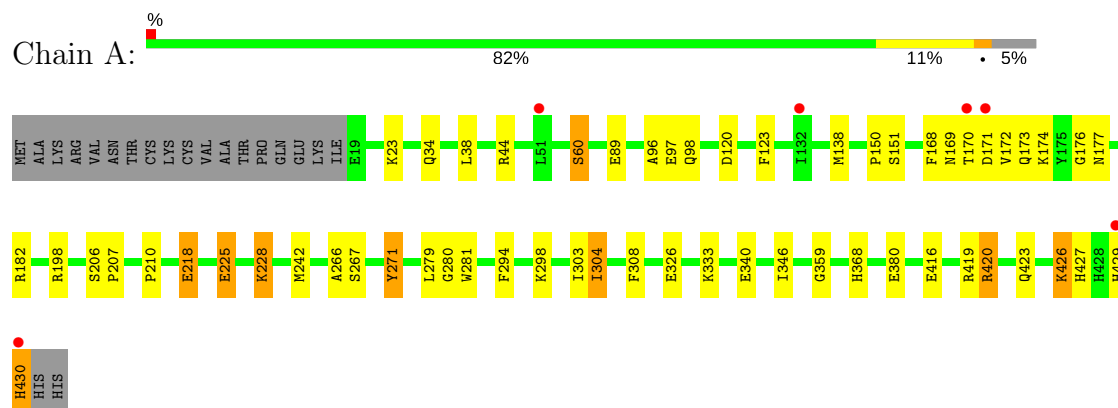
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	375	Total	O	0	0
			375	375		
4	B	379	Total	O	0	0
			379	379		

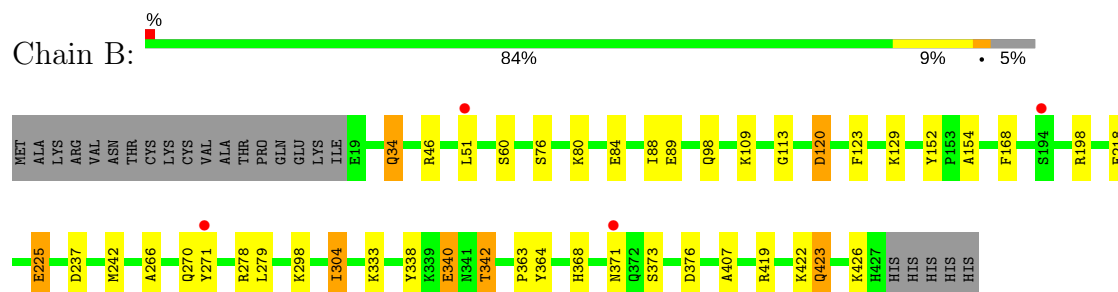
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: LL-diaminopimelate aminotransferase



#### • Molecule 1: LL-diaminopimelate aminotransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.68Å 102.68Å 172.01Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.50 – 1.85 39.50 – 1.85	Depositor EDS
% Data completeness (in resolution range)	95.6 (39.50-1.85) 95.6 (39.50-1.85)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.51 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.186 , 0.230 0.188 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	28.0	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 44.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7152	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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, 0.333 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: PL6, 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	1.07	7/3263 (0.2%)	0.91	3/4423 (0.1%)
1	B	1.05	6/3230 (0.2%)	0.92	4/4378 (0.1%)
All	All	1.06	13/6493 (0.2%)	0.91	7/8801 (0.1%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	218	GLU	CG-CD	7.32	1.62	1.51
1	A	225	GLU	CG-CD	7.13	1.62	1.51
1	A	89	GLU	CG-CD	6.73	1.62	1.51
1	A	340	GLU	CG-CD	5.96	1.60	1.51
1	B	89	GLU	CG-CD	5.83	1.60	1.51
1	B	113	GLY	N-CA	5.57	1.54	1.46
1	A	271	TYR	CD1-CE1	5.38	1.47	1.39
1	B	340	GLU	CG-CD	5.31	1.59	1.51
1	A	225	GLU	CD-OE1	5.18	1.31	1.25
1	B	89	GLU	CB-CG	5.17	1.61	1.52
1	A	218	GLU	CD-OE1	5.08	1.31	1.25
1	B	364	TYR	CE2-CZ	5.05	1.45	1.38
1	B	225	GLU	CG-CD	5.01	1.59	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	120	ASP	CB-CG-OD1	7.42	124.98	118.30
1	A	120	ASP	CB-CG-OD1	6.32	123.99	118.30
1	A	420	ARG	NE-CZ-NH1	6.25	123.43	120.30
1	B	237	ASP	CB-CG-OD1	5.86	123.57	118.30
1	A	420	ARG	NE-CZ-NH2	-5.61	117.50	120.30
1	B	376	ASP	CB-CG-OD1	5.23	123.01	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	278	ARG	NE-CZ-NH2	-5.10	117.75	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	3184	0	3087	39	0
1	B	3154	0	3066	32	0
2	A	5	0	0	0	0
2	B	5	0	0	1	0
3	A	25	0	12	0	0
3	B	25	0	12	0	0
4	A	375	0	0	15	0
4	B	379	0	0	16	0
All	All	7152	0	6177	70	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 (70) 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:60:SER:HB3	4:A:500:HOH:O	1.68	0.94
1:B:225:GLU:HG3	4:B:608:HOH:O	1.71	0.91
1:A:242:MET:HE1	4:A:602:HOH:O	1.78	0.83
1:A:225:GLU:HG3	4:A:556:HOH:O	1.81	0.80
1:A:34:GLN:HG3	1:A:168:PHE:CD2	2.18	0.79
1:A:346:ILE:HD11	1:A:359:GLY:HA3	1.65	0.76
1:A:172:VAL:HG23	1:A:174:LYS:HB2	1.69	0.75
1:A:34:GLN:HG3	1:A:168:PHE:CG	2.26	0.71
1:B:34:GLN:HG2	1:B:168:PHE:CG	2.27	0.69
1:A:242:MET:HG2	1:A:271:TYR:CZ	2.28	0.68
1:B:34:GLN:CG	1:B:168:PHE:CD2	2.77	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:ARG:HD2	4:A:789:HOH:O	1.94	0.68
1:B:242:MET:HE1	4:B:627:HOH:O	1.96	0.65
1:A:242:MET:HB2	1:A:271:TYR:CE1	2.31	0.65
1:B:342:THR:HG21	1:B:363:PRO:HA	1.77	0.65
1:A:23:LYS:NZ	4:A:799:HOH:O	2.33	0.61
1:B:34:GLN:HG2	1:B:168:PHE:CD2	2.37	0.60
1:B:368:HIS:HE1	4:B:691:HOH:O	1.86	0.58
1:A:60:SER:CB	4:A:500:HOH:O	2.39	0.57
1:A:368:HIS:HD2	4:A:499:HOH:O	1.88	0.57
1:A:416:GLU:OE2	1:A:420:ARG:HD2	2.06	0.56
1:A:138:MET:HB2	1:A:303:ILE:HG13	1.89	0.54
1:A:151:SER:HA	1:A:210:PRO:HD3	1.89	0.54
1:A:308:PHE:O	1:B:129:LYS:HE2	2.07	0.54
1:A:429:HIS:HB3	1:A:430:HIS:C	2.27	0.54
1:A:98:GLN:HG2	1:A:123:PHE:CD2	2.43	0.53
1:B:88:ILE:CD1	4:B:766:HOH:O	2.57	0.52
1:A:170:THR:O	1:A:173:GLN:NE2	2.41	0.51
1:B:80:LYS:HE3	1:B:84:GLU:OE2	2.10	0.51
1:A:206:SER:HA	1:A:207:PRO:C	2.30	0.51
1:A:426:LYS:HD2	1:A:427:HIS:CE1	2.46	0.51
1:B:120:ASP:HB3	2:B:434:SO4:O3	2.11	0.51
1:B:34:GLN:HG3	1:B:168:PHE:CE2	2.47	0.49
1:A:266:ALA:HB3	1:A:281:TRP:CE2	2.48	0.48
1:B:88:ILE:HD11	4:B:766:HOH:O	2.14	0.48
1:B:270:GLN:HG2	4:B:591:HOH:O	2.14	0.48
1:B:304:ILE:HG12	4:B:585:HOH:O	2.14	0.47
1:A:326:GLU:HB3	4:A:657:HOH:O	2.15	0.47
1:B:423:GLN:OE1	4:B:713:HOH:O	2.20	0.47
1:B:98:GLN:HB2	4:B:492:HOH:O	2.14	0.47
1:A:97:GLU:OE2	4:A:807:HOH:O	2.20	0.47
1:B:34:GLN:HG3	1:B:168:PHE:CD2	2.49	0.47
1:A:294:PHE:CZ	1:A:298:LYS:HE2	2.51	0.46
1:B:152:TYR:CE2	1:B:154:ALA:HB3	2.51	0.46
1:A:169:ASN:OD1	1:A:171:ASP:HB2	2.16	0.46
1:A:304:ILE:HG12	4:A:588:HOH:O	2.16	0.45
1:B:422:LYS:O	1:B:426:LYS:HB3	2.16	0.45
1:B:266:ALA:HB1	4:B:469:HOH:O	2.16	0.45
1:B:60:SER:HB3	4:B:459:HOH:O	2.16	0.45
1:A:267:SER:HA	1:A:280:GLY:HA2	2.00	0.44
1:B:340:GLU:HB2	4:B:721:HOH:O	2.17	0.44
1:A:150:PRO:O	1:A:151:SER:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:423:GLN:HG2	4:B:759:HOH:O	2.17	0.44
1:B:218:GLU:HG2	4:B:777:HOH:O	2.18	0.43
1:A:96:ALA:N	4:A:790:HOH:O	2.47	0.43
1:B:342:THR:HG22	1:B:407:ALA:CB	2.48	0.43
1:A:228:LYS:HB2	1:A:228:LYS:HE2	1.25	0.43
1:A:368:HIS:CD2	4:A:499:HOH:O	2.69	0.42
1:A:430:HIS:HA	4:A:728:HOH:O	2.19	0.42
1:B:242:MET:HG2	1:B:271:TYR:CZ	2.55	0.42
1:A:176:GLY:O	1:A:177:ASN:CB	2.67	0.41
1:B:338:TYR:O	1:B:342:THR:HG22	2.20	0.41
1:A:380:GLU:HB2	4:A:761:HOH:O	2.19	0.41
1:A:423:GLN:HA	1:A:423:GLN:NE2	2.35	0.41
1:B:338:TYR:O	1:B:342:THR:CG2	2.69	0.41
1:B:98:GLN:CB	4:B:492:HOH:O	2.69	0.41
1:B:98:GLN:HG3	1:B:123:PHE:CD2	2.56	0.41
1:A:430:HIS:N	4:A:728:HOH:O	2.52	0.41
1:A:346:ILE:HD11	1:A:359:GLY:CA	2.43	0.40
1:B:422:LYS:HD2	4:B:539:HOH:O	2.21	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	410/432 (95%)	400 (98%)	10 (2%)	0	100	100
1	B	407/432 (94%)	398 (98%)	9 (2%)	0	100	100
All	All	817/864 (95%)	798 (98%)	19 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	338/356 (95%)	326 (96%)	12 (4%)	40	20
1	B	335/356 (94%)	320 (96%)	15 (4%)	32	13
All	All	673/712 (94%)	646 (96%)	27 (4%)	36	17

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	LEU
1	A	44	ARG
1	A	60	SER
1	A	198	ARG
1	A	218	GLU
1	A	228	LYS
1	A	279	LEU
1	A	304	ILE
1	A	333	LYS
1	A	419	ARG
1	A	426	LYS
1	A	430	HIS
1	B	34	GLN
1	B	46	ARG
1	B	51	LEU
1	B	76	SER
1	B	109	LYS
1	B	198	ARG
1	B	279	LEU
1	B	298	LYS
1	B	304	ILE
1	B	333	LYS
1	B	342	THR
1	B	371	ASN
1	B	373	SER
1	B	419	ARG
1	B	423	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	248	ASN
1	A	368	HIS
1	A	423	GLN
1	A	427	HIS
1	B	248	ASN
1	B	372	GLN
1	B	423	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 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	433	-	4,4,4	0.39	0	6,6,6	0.22	0
3	PL6	A	434	-	19,25,25	2.37	5 (26%)	24,35,35	3.33	6 (25%)
3	PL6	B	433	-	19,25,25	1.75	5 (26%)	24,35,35	2.64	13 (54%)
2	SO4	B	434	-	4,4,4	0.42	0	6,6,6	0.17	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
2	SO4	A	433	-	-	0/0/0/0	0/0/0/0
3	PL6	A	434	-	-	0/14/20/20	0/1/1/1
3	PL6	B	433	-	-	0/14/20/20	0/1/1/1
2	SO4	B	434	-	-	0/0/0/0	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	434	PL6	OAQ-CAN	-2.88	1.33	1.44
3	B	433	PL6	CAV-CAT	-2.38	1.39	1.40
3	B	433	PL6	CAW-CAJ	-2.14	1.42	1.46
3	B	433	PL6	CB-CA	2.28	1.56	1.53
3	A	434	PL6	CAK-CAU	2.50	1.43	1.37
3	A	434	PL6	CB-CA	2.67	1.57	1.53
3	B	433	PL6	CA-N	3.11	1.50	1.47
3	B	433	PL6	CAJ-N	4.34	1.35	1.27
3	A	434	PL6	CA-N	5.72	1.53	1.47
3	A	434	PL6	CAJ-N	5.91	1.38	1.27

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	434	PL6	CAV-CAW-CAU	-5.48	114.07	118.24
3	B	433	PL6	CAA-CAT-CAV	-2.53	117.94	120.96
3	B	433	PL6	CAN-CAU-CAK	-2.33	115.31	119.33
3	A	434	PL6	OAI-PAY-OAE	-2.28	101.57	110.50
3	B	433	PL6	OAI-PAY-OAE	-2.13	102.18	110.50
3	B	433	PL6	CAV-CAW-CAJ	-2.00	116.69	120.52
3	B	433	PL6	OAD-PAY-OAE	2.00	118.33	110.50
3	B	433	PL6	CAK-NAO-CAT	2.02	123.15	119.26
3	A	434	PL6	OAD-PAY-OAE	2.08	118.66	110.50
3	B	433	PL6	CG-CB-CA	2.23	117.99	113.47
3	B	433	PL6	CAA-CAT-NAO	2.59	123.08	117.89
3	B	433	PL6	CAN-CAU-CAW	2.62	126.24	121.66
3	B	433	PL6	CB-CA-N	2.72	115.49	109.91
3	A	434	PL6	CAU-CAW-CAJ	2.99	125.83	121.36
3	B	433	PL6	CAU-CAW-CAJ	3.05	125.92	121.36
3	B	433	PL6	OAD-PAY-OAQ	4.11	117.68	106.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	434	PL6	CAW-CAV-CAT	4.53	122.94	120.15
3	B	433	PL6	CA-N-CAJ	8.42	127.41	117.29
3	A	434	PL6	CA-N-CAJ	13.32	133.30	117.29

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
2	B	434	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	412/432 (95%)	-0.17	6 (1%) 74 74	21, 28, 47, 70	0
1	B	409/432 (94%)	-0.24	4 (0%) 82 82	22, 29, 40, 54	0
All	All	821/864 (95%)	-0.21	10 (1%) 79 79	21, 29, 43, 70	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	171	ASP	3.2
1	A	429	HIS	2.9
1	B	51	LEU	2.7
1	A	170	THR	2.7
1	A	430	HIS	2.4
1	B	371	ASN	2.4
1	B	194	SER	2.3
1	A	132	ILE	2.2
1	B	271	TYR	2.1
1	A	51	LEU	2.1

### 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	PL6	A	434	25/25	0.95	0.17	1.11	26,38,49,50	0
3	PL6	B	433	25/25	0.98	0.12	-0.14	25,39,44,46	0
2	SO4	B	434	5/5	0.86	0.28	-	124,124,125,126	0
2	SO4	A	433	5/5	0.76	0.28	-	142,143,143,143	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.