



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:41 am GMT

PDB ID : 4KP7  
Title : Structure of Plasmodium IspC in complex with a beta-thia-isostere derivative of Fosmidomycin  
Authors : Kunfermann, A.; Bacher, A.; Groll, M.  
Deposited on : 2013-05-13  
Resolution : 2.00 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

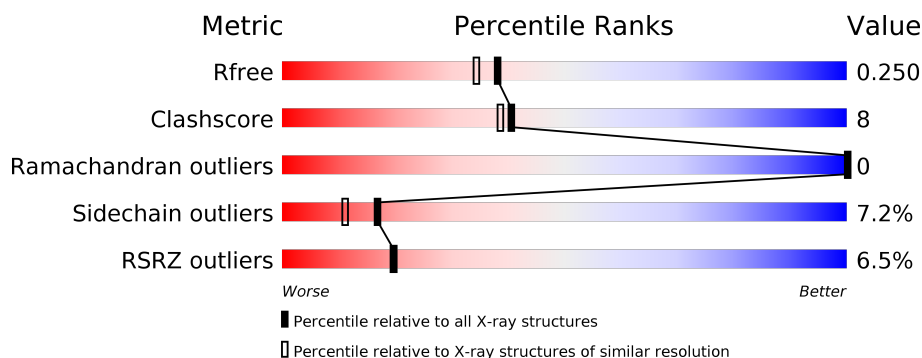
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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	427	<div> <div>4%</div> <div> <div></div> <div>80%</div> <div>14%</div> <div>• •</div> </div> </div>
1	B	427	<div> <div>8%</div> <div> <div></div> <div>78%</div> <div>14%</div> <div>• 6%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6790 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 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplast.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	0	0
			3268	2099	535	614	20			
1	B	402	Total	C	N	O	S	0	0	0
			3200	2053	520	607	20			

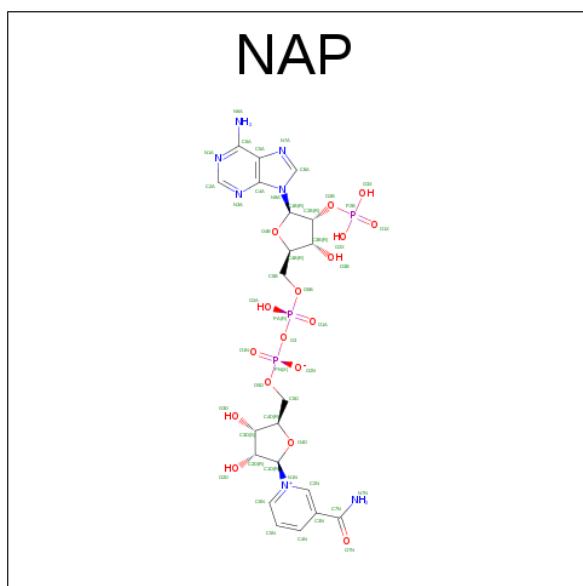
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	62	MET	-	EXPRESSION TAG	UNP O96693
A	63	ARG	-	EXPRESSION TAG	UNP O96693
A	64	GLY	-	EXPRESSION TAG	UNP O96693
A	65	SER	-	EXPRESSION TAG	UNP O96693
A	66	HIS	-	EXPRESSION TAG	UNP O96693
A	67	HIS	-	EXPRESSION TAG	UNP O96693
A	68	HIS	-	EXPRESSION TAG	UNP O96693
A	69	HIS	-	EXPRESSION TAG	UNP O96693
A	70	HIS	-	EXPRESSION TAG	UNP O96693
A	71	HIS	-	EXPRESSION TAG	UNP O96693
A	72	GLY	-	EXPRESSION TAG	UNP O96693
A	73	SER	-	EXPRESSION TAG	UNP O96693
B	62	MET	-	EXPRESSION TAG	UNP O96693
B	63	ARG	-	EXPRESSION TAG	UNP O96693
B	64	GLY	-	EXPRESSION TAG	UNP O96693
B	65	SER	-	EXPRESSION TAG	UNP O96693
B	66	HIS	-	EXPRESSION TAG	UNP O96693
B	67	HIS	-	EXPRESSION TAG	UNP O96693
B	68	HIS	-	EXPRESSION TAG	UNP O96693
B	69	HIS	-	EXPRESSION TAG	UNP O96693
B	70	HIS	-	EXPRESSION TAG	UNP O96693
B	71	HIS	-	EXPRESSION TAG	UNP O96693
B	72	GLY	-	EXPRESSION TAG	UNP O96693
B	73	SER	-	EXPRESSION TAG	UNP O96693

- Molecule 2 is MANGANESE (III) ION (three-letter code: MN3) (formula: Mn).

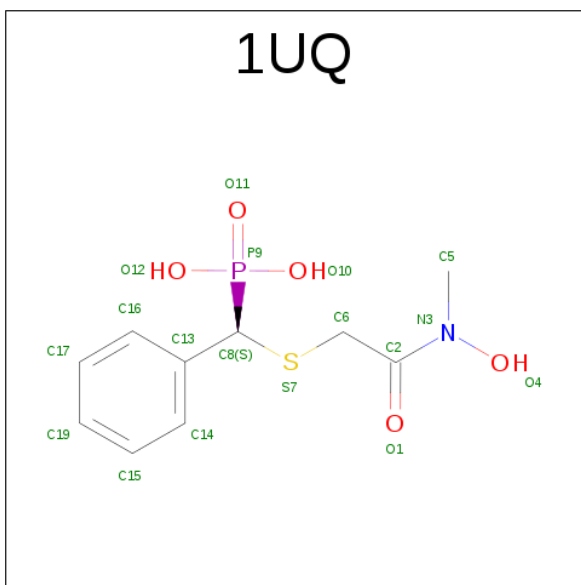
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mn	0	0
			1	1		
2	A	1	Total	Mn	0	0
			1	1		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is [(S)-({2-[HYDROXY(METHYL)AMINO]-2-OXOETHYL}SULFANYL)(PHENYL)METHYL]PHOSPHONIC ACID (three-letter code: 1UQ) (formula: C<sub>10</sub>H<sub>14</sub>NO<sub>5</sub>PS).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			18	10	1	5	1	1		
4	B	1	Total	C	N	O	P	S	0	0
			18	10	1	5	1	1		

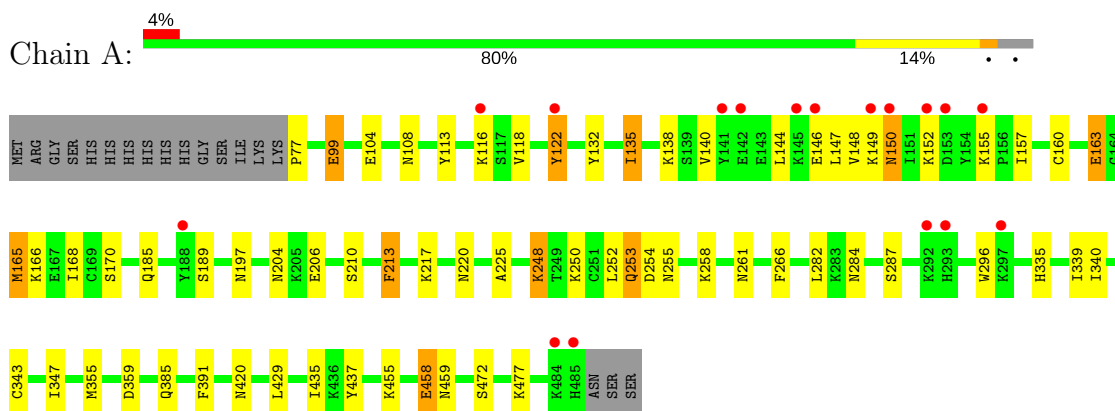
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	129	Total	O	0	0
			129	129		
5	B	107	Total	O	0	0
			107	107		

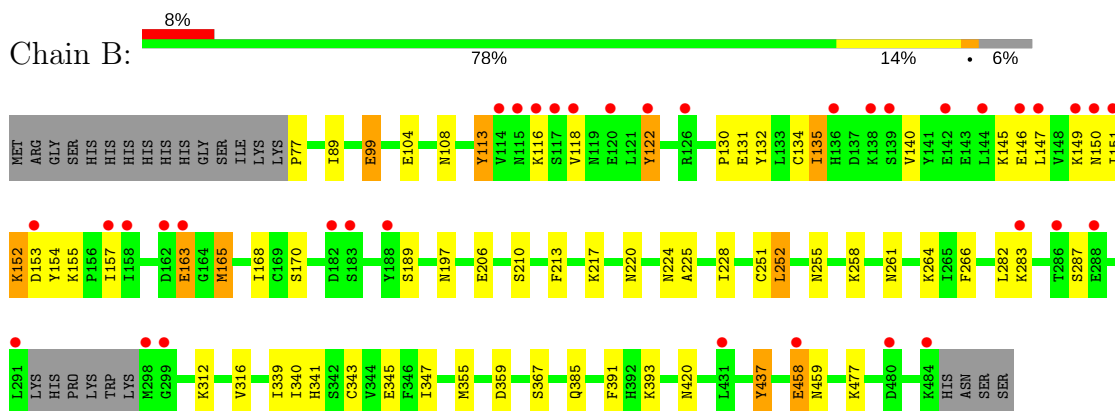
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplast



- Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplast



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.46Å 78.12Å 99.99Å 90.00° 91.53° 90.00°	Depositor
Resolution (Å)	15.00 – 2.00 14.95 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.1 (15.00-2.00) 97.1 (14.95-2.00)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.03 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.185 , 0.249 0.183 , 0.250	Depositor DCC
$R_{free}$ test set	2594 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.1	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 47.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.039 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6790	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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: 1UQ, NAP, MN3

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	0.53	1/3331 (0.0%)	0.62	1/4498 (0.0%)
1	B	0.50	0/3257	0.61	0/4397
All	All	0.52	1/6588 (0.0%)	0.61	1/8895 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	296	TRP	CD2-CE2	5.34	1.47	1.41

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	248	LYS	CD-CE-NZ	5.67	124.75	111.70

There are no chirality outliers.

There are no planarity outliers.

### 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	3268	0	3316	51	0
1	B	3200	0	3245	57	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	48	0	25	8	0
4	A	18	0	11	0	0
4	B	18	0	11	0	0
5	A	129	0	0	6	0
5	B	107	0	0	6	0
All	All	6790	0	6608	108	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 8.

All (108) 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:145:LYS:O	1:B:149:LYS:HE2	1.34	1.23
1:B:152:LYS:H	1:B:152:LYS:HE3	0.92	1.05
1:B:145:LYS:O	1:B:149:LYS:CE	2.10	1.00
1:B:152:LYS:HE3	1:B:152:LYS:N	1.76	0.99
1:B:282:LEU:HD22	1:B:437:TYR:CE2	2.01	0.96
1:B:146:GLU:HA	1:B:149:LYS:NZ	1.82	0.94
1:B:282:LEU:HD22	1:B:437:TYR:HE2	1.31	0.92
1:B:122:TYR:C	1:B:122:TYR:HD1	1.75	0.88
1:B:122:TYR:O	1:B:122:TYR:HD1	1.60	0.85
1:B:197:ASN:HD22	1:B:224:ASN:HB2	1.40	0.84
1:A:122:TYR:CD2	1:A:147:LEU:HB3	2.14	0.83
1:B:146:GLU:HA	1:B:149:LYS:HZ2	1.41	0.83
1:A:185:GLN:HE21	3:A:502:NAP:H62A	1.24	0.82
1:B:437:TYR:O	1:B:437:TYR:HD1	1.64	0.81
1:B:122:TYR:CD1	1:B:122:TYR:C	2.50	0.80
1:A:255:ASN:ND2	1:A:258:LYS:HE2	1.97	0.80
1:A:122:TYR:HD2	1:A:147:LEU:HB3	1.46	0.77
1:A:122:TYR:C	1:A:122:TYR:HD1	1.87	0.77
1:A:122:TYR:CD1	1:A:122:TYR:C	2.60	0.75
1:A:284:ASN:HB2	5:A:628:HOH:O	1.88	0.72
1:B:437:TYR:C	1:B:437:TYR:HD1	1.95	0.70
1:A:359:ASP:HB3	5:A:615:HOH:O	1.91	0.70
1:B:132:TYR:HD2	1:B:168:ILE:HG12	1.56	0.69
1:B:122:TYR:CD2	1:B:147:LEU:HB3	2.28	0.69
1:B:341:HIS:CE1	5:B:634:HOH:O	2.45	0.69
1:A:99:GLU:OE1	1:A:99:GLU:HA	1.92	0.69
1:B:437:TYR:C	1:B:437:TYR:CD1	2.67	0.68
1:A:340:ILE:HD12	1:A:391:PHE:HZ	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:340:ILE:HD12	1:B:391:PHE:HZ	1.62	0.64
1:B:130:PRO:O	1:B:154:TYR:OH	2.08	0.64
1:B:122:TYR:CD1	1:B:122:TYR:O	2.48	0.64
1:A:185:GLN:NE2	3:A:502:NAP:N6A	2.41	0.63
1:B:146:GLU:HA	1:B:149:LYS:CE	2.29	0.62
1:B:113:TYR:HE2	1:B:165:MET:HG3	1.65	0.61
1:A:150:ASN:HD22	1:A:150:ASN:N	1.98	0.61
1:A:217:LYS:HE3	1:A:458:GLU:O	2.01	0.61
1:B:99:GLU:OE1	1:B:99:GLU:HA	2.02	0.59
1:B:217:LYS:HE3	1:B:458:GLU:O	2.03	0.58
1:A:135:ILE:CD1	1:A:140:VAL:HG23	2.35	0.57
1:B:197:ASN:HA	1:B:225:ALA:HB2	1.86	0.57
1:A:282:LEU:HD22	1:A:437:TYR:CE2	2.41	0.56
1:A:185:GLN:HG2	3:A:502:NAP:N6A	2.20	0.56
1:B:217:LYS:CE	1:B:458:GLU:O	2.53	0.56
1:A:250:LYS:HE3	5:A:642:HOH:O	2.04	0.56
1:B:255:ASN:ND2	1:B:258:LYS:HE3	2.21	0.56
1:A:132:TYR:HD2	1:A:168:ILE:HG12	1.70	0.56
1:A:185:GLN:NE2	3:A:502:NAP:H62A	1.98	0.56
1:B:122:TYR:CD2	1:B:147:LEU:HD22	2.41	0.55
1:B:152:LYS:O	1:B:152:LYS:HG2	2.05	0.55
1:B:165:MET:SD	1:B:189:SER:HA	2.48	0.54
1:B:135:ILE:CD1	1:B:140:VAL:HG23	2.37	0.54
1:A:253:GLN:HG3	5:A:642:HOH:O	2.06	0.54
1:A:113:TYR:CE1	3:A:502:NAP:H2A	2.44	0.53
1:B:77:PRO:N	5:B:640:HOH:O	2.43	0.52
1:A:122:TYR:CD2	1:A:147:LEU:HD22	2.45	0.52
1:A:213:PHE:HB2	5:A:625:HOH:O	2.10	0.51
1:A:122:TYR:O	1:A:122:TYR:HD1	1.92	0.51
1:A:113:TYR:CZ	3:A:502:NAP:H2A	2.45	0.51
1:B:113:TYR:CE2	1:B:165:MET:HG3	2.44	0.51
1:A:132:TYR:CE1	1:A:157:ILE:HD12	2.47	0.50
1:A:144:LEU:O	1:A:148:VAL:HG23	2.12	0.50
1:A:135:ILE:HD11	1:A:140:VAL:HG23	1.93	0.49
1:B:339:ILE:O	1:B:341:HIS:HD2	1.95	0.49
1:A:335:HIS:HE1	1:A:339:ILE:H	1.61	0.48
1:A:217:LYS:CE	1:A:458:GLU:O	2.61	0.48
1:B:132:TYR:CE1	1:B:157:ILE:HD12	2.48	0.48
1:A:150:ASN:ND2	1:A:150:ASN:N	2.60	0.48
1:A:255:ASN:HD22	1:A:258:LYS:HE2	1.74	0.48
1:A:122:TYR:CD1	1:A:122:TYR:O	2.66	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:TYR:HD2	1:B:147:LEU:HB3	1.78	0.47
1:B:312:LYS:O	1:B:316:VAL:HG23	2.14	0.47
1:A:185:GLN:HG2	3:A:502:NAP:H61A	1.78	0.47
1:B:135:ILE:HD11	1:B:140:VAL:HG23	1.95	0.47
1:B:339:ILE:O	1:B:341:HIS:CD2	2.67	0.47
1:B:163:GLU:N	1:B:163:GLU:OE1	2.45	0.47
1:A:165:MET:SD	1:A:189:SER:HA	2.55	0.47
1:A:206:GLU:HG3	1:A:420:ASN:HD21	1.80	0.47
1:A:335:HIS:CE1	1:A:339:ILE:H	2.33	0.47
1:B:228:ILE:HG21	1:B:367:SER:HA	1.95	0.47
1:B:131:GLU:C	1:B:132:TYR:HD1	2.18	0.46
1:A:135:ILE:HD12	1:A:140:VAL:HG23	1.98	0.45
1:A:261:ASN:HB3	1:A:347:ILE:HG12	1.98	0.45
1:B:206:GLU:HG3	1:B:420:ASN:HD21	1.81	0.45
1:B:359:ASP:HB3	5:B:704:HOH:O	2.17	0.45
1:B:393:LYS:HG2	5:B:690:HOH:O	2.16	0.45
1:B:89:ILE:HD13	5:B:653:HOH:O	2.16	0.45
1:A:77:PRO:HB2	5:A:720:HOH:O	2.17	0.45
1:B:341:HIS:HE1	5:B:634:HOH:O	1.94	0.44
1:A:429:LEU:HB3	1:A:435:ILE:HG12	1.99	0.44
1:B:135:ILE:HD12	1:B:140:VAL:HG23	2.01	0.43
1:B:266:PHE:HB2	1:B:343:CYS:HB2	2.00	0.43
1:A:163:GLU:N	1:A:163:GLU:OE1	2.43	0.43
1:A:165:MET:HE3	1:A:166:LYS:HG3	2.02	0.42
1:A:197:ASN:HA	1:A:225:ALA:HB2	2.01	0.42
1:B:113:TYR:HA	1:B:134:CYS:O	2.20	0.42
1:B:264:LYS:HB3	1:B:345:GLU:HB3	2.01	0.42
1:A:138:LYS:HE2	1:A:160:CYS:SG	2.60	0.42
1:A:204:ASN:HA	3:A:502:NAP:O3D	2.19	0.42
1:B:152:LYS:O	1:B:153:ASP:HB3	2.19	0.41
1:A:266:PHE:HB2	1:A:343:CYS:HB2	2.01	0.41
1:B:122:TYR:CE2	1:B:147:LEU:HD22	2.56	0.41
1:A:132:TYR:HE1	1:A:157:ILE:HD12	1.84	0.41
1:A:254:ASP:O	1:A:255:ASN:HB2	2.21	0.41
1:B:255:ASN:ND2	1:B:258:LYS:CE	2.83	0.41
1:A:146:GLU:O	1:A:149:LYS:HG3	2.21	0.40
1:A:340:ILE:HD12	1:A:391:PHE:CZ	2.47	0.40
1:B:261:ASN:HB3	1:B:347:ILE:HG12	2.03	0.40
1:B:251:CYS:O	1:B:252:LEU:HB2	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	407/427 (95%)	395 (97%)	12 (3%)	0	100	100
1	B	398/427 (93%)	387 (97%)	11 (3%)	0	100	100
All	All	805/854 (94%)	782 (97%)	23 (3%)	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	376/392 (96%)	349 (93%)	27 (7%)	17	11
1	B	369/392 (94%)	342 (93%)	27 (7%)	16	11
All	All	745/784 (95%)	691 (93%)	54 (7%)	17	11

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	GLU
1	A	104	GLU
1	A	108	ASN
1	A	116	LYS
1	A	118	VAL
1	A	122	TYR
1	A	135	ILE
1	A	150	ASN

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Mol	Chain	Res	Type
1	A	152	LYS
1	A	155	LYS
1	A	163	GLU
1	A	165	MET
1	A	170	SER
1	A	210	SER
1	A	213	PHE
1	A	220	ASN
1	A	248	LYS
1	A	252	LEU
1	A	253	GLN
1	A	287	SER
1	A	355	MET
1	A	385	GLN
1	A	455	LYS
1	A	458	GLU
1	A	459	ASN
1	A	472	SER
1	A	477	LYS
1	B	99	GLU
1	B	104	GLU
1	B	108	ASN
1	B	113	TYR
1	B	116	LYS
1	B	118	VAL
1	B	122	TYR
1	B	135	ILE
1	B	150	ASN
1	B	151	ILE
1	B	152	LYS
1	B	155	LYS
1	B	163	GLU
1	B	165	MET
1	B	170	SER
1	B	210	SER
1	B	213	PHE
1	B	220	ASN
1	B	252	LEU
1	B	283	LYS
1	B	287	SER
1	B	355	MET
1	B	385	GLN

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Mol	Chain	Res	Type
1	B	437	TYR
1	B	458	GLU
1	B	459	ASN
1	B	477	LYS

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	108	ASN
1	A	150	ASN
1	A	185	GLN
1	A	255	ASN
1	A	335	HIS
1	A	420	ASN
1	A	433	ASN
1	B	108	ASN
1	B	136	HIS
1	B	150	ASN
1	B	197	ASN
1	B	253	GLN
1	B	255	ASN
1	B	328	ASN
1	B	420	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 5 ligands modelled in this entry, 2 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	NAP	A	502	-	44,52,52	2.52	16 (36%)	51,80,80	2.00	8 (15%)
4	1UQ	A	503	2	14,18,18	3.26	5 (35%)	13,25,25	0.94	0
4	1UQ	B	502	2	14,18,18	2.43	4 (28%)	13,25,25	0.85	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	NAP	A	502	-	-	0/27/67/67	0/5/5/5
4	1UQ	A	503	2	-	0/13/19/19	0/1/1/1
4	1UQ	B	502	2	-	0/13/19/19	0/1/1/1

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	NAP	C2N-C3N	-6.46	1.29	1.39
3	A	502	NAP	C6N-C5N	-3.09	1.31	1.38
4	B	502	1UQ	P9-O10	-2.79	1.50	1.54
3	A	502	NAP	C2D-C3D	-2.22	1.47	1.53
4	A	503	1UQ	P9-C8	-2.11	1.80	1.83
3	A	502	NAP	C6N-N1N	-2.06	1.30	1.35
3	A	502	NAP	PA-O5B	2.00	1.67	1.59
3	A	502	NAP	P2B-O2B	2.06	1.63	1.59
3	A	502	NAP	C3B-C4B	2.17	1.58	1.53
3	A	502	NAP	C2A-N1A	2.25	1.38	1.33
4	A	503	1UQ	C14-C13	2.32	1.42	1.39
4	B	502	1UQ	C6-C2	2.39	1.55	1.51
3	A	502	NAP	PA-O1A	2.41	1.60	1.50
3	A	502	NAP	P2B-O1X	2.42	1.59	1.50
3	A	502	NAP	C3B-C2B	2.85	1.59	1.53
4	A	503	1UQ	P9-O12	2.90	1.59	1.54
3	A	502	NAP	C5B-C4B	3.14	1.61	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	NAP	C2A-N3A	3.16	1.37	1.32
4	B	502	1UQ	P9-O12	3.40	1.60	1.54
4	A	503	1UQ	C6-C2	4.54	1.59	1.51
3	A	502	NAP	O4D-C1D	5.83	1.49	1.41
3	A	502	NAP	C5N-C4N	6.03	1.50	1.38
4	B	502	1UQ	C6-S7	6.79	1.87	1.81
3	A	502	NAP	C4N-C3N	7.77	1.52	1.39
4	A	503	1UQ	C6-S7	10.20	1.91	1.81

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	NAP	C5N-C4N-C3N	-8.06	110.87	120.35
3	A	502	NAP	N3A-C2A-N1A	-7.32	122.48	128.86
3	A	502	NAP	C4A-C5A-N7A	-4.13	105.42	109.41
3	A	502	NAP	O7N-C7N-C3N	-2.24	117.00	119.62
3	A	502	NAP	C2A-N1A-C6A	2.13	122.49	118.77
3	A	502	NAP	N6A-C6A-N1A	2.41	123.55	118.77
3	A	502	NAP	C3N-C2N-N1N	3.88	124.34	120.43
3	A	502	NAP	C3N-C7N-N7N	3.95	122.28	117.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	NAP	8	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	409/427 (95%)	0.00	17 (4%) 37 37	16, 29, 62, 96	0
1	B	402/427 (94%)	0.29	36 (8%) 10 10	15, 33, 79, 114	0
All	All	811/854 (94%)	0.14	53 (6%) 20 20	15, 30, 75, 114	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	291	LEU	6.3
1	B	116	LYS	5.5
1	A	141	TYR	5.5
1	B	122	TYR	4.6
1	B	142	GLU	4.6
1	B	298	MET	4.3
1	B	288	GLU	4.2
1	A	293	HIS	4.1
1	B	147	LEU	3.8
1	A	485	HIS	3.7
1	B	153	ASP	3.7
1	A	145	LYS	3.6
1	A	292	LYS	3.5
1	A	146	GLU	3.5
1	B	114	VAL	3.4
1	B	484	LYS	3.3
1	B	146	GLU	3.3
1	B	151	ILE	3.2
1	B	138	LYS	3.2
1	B	126	ARG	3.2
1	B	299	GLY	3.1
1	B	120	GLU	3.1
1	B	163	GLU	3.1
1	B	158	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	150	ASN	3.0
1	B	162	ASP	3.0
1	B	115	ASN	3.0
1	A	188	TYR	2.8
1	B	149	LYS	2.8
1	B	182	ASP	2.7
1	A	297	LYS	2.7
1	B	118	VAL	2.7
1	B	136	HIS	2.7
1	B	150	ASN	2.7
1	A	142	GLU	2.5
1	B	139	SER	2.5
1	B	286	THR	2.4
1	A	116	LYS	2.4
1	B	157	ILE	2.4
1	A	122	TYR	2.4
1	B	117	SER	2.3
1	A	149	LYS	2.3
1	B	183	SER	2.2
1	B	188	TYR	2.2
1	B	431	LEU	2.1
1	B	458	GLU	2.1
1	B	480	ASP	2.1
1	A	152	LYS	2.1
1	A	153	ASP	2.1
1	A	155	LYS	2.0
1	B	144	LEU	2.0
1	A	484	LYS	2.0
1	B	283	LYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

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	NAP	A	502	48/48	0.94	0.13	0.03	23,33,45,58	0
4	1UQ	B	502	18/18	0.98	0.11	-0.09	30,37,44,45	0
4	1UQ	A	503	18/18	0.98	0.08	-0.38	21,29,32,33	0
2	MN3	B	501	1/1	0.99	0.04	-4.14	33,33,33,33	0
2	MN3	A	501	1/1	0.99	0.03	-6.22	26,26,26,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.