



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:09 PM GMT

PDB ID : 4XRX  
Title : Crystal structure of a metabolic reductase with (E)-5-((1-methyl-5-oxo-2-thioxoimidazolidin-4-ylidene)methyl)pyridin-2(1H)-one  
Authors : Zheng, B.; Wu, F.; Jiang, H.; Kogiso, M.; Yao, Y.; Zhou, C.; Li, X.; Song, Y.  
Deposited on : 2015-01-21  
Resolution : 3.20 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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
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) : rb-20026982

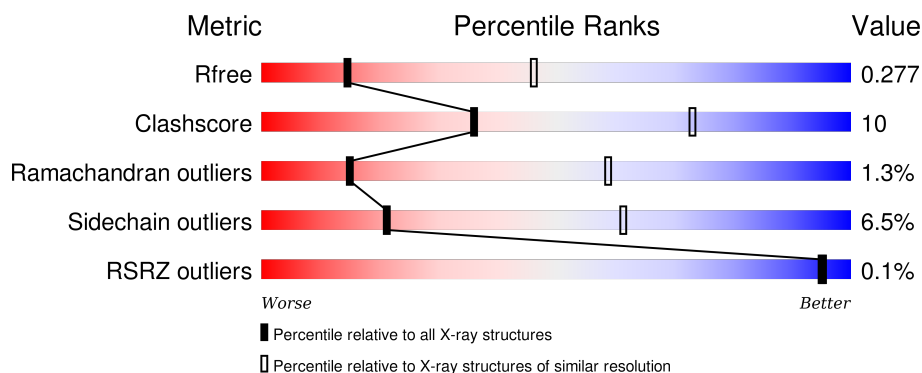
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	414	 73% 20% • 6%
1	B	414	 63% 27% • 7%

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	42V	A	502	-	-	-	X

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6275 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.

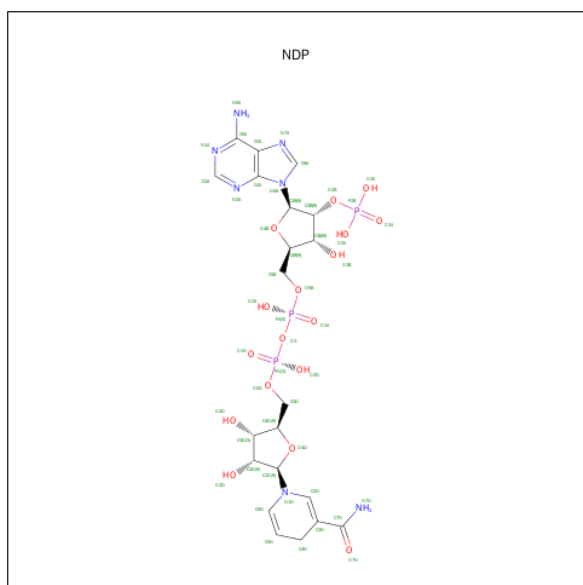
- Molecule 1 is a protein called Isocitrate dehydrogenase [NADP] cytoplasmic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	0	0
			3102	1979	527	578	18			
1	B	386	Total	C	N	O	S	0	0	0
			3061	1952	518	573	18			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	132	HIS	ARG	engineered mutation	UNP O75874
B	132	HIS	ARG	engineered mutation	UNP O75874

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula:  $C_{21}H_{30}N_7O_{17}P_3$ ).



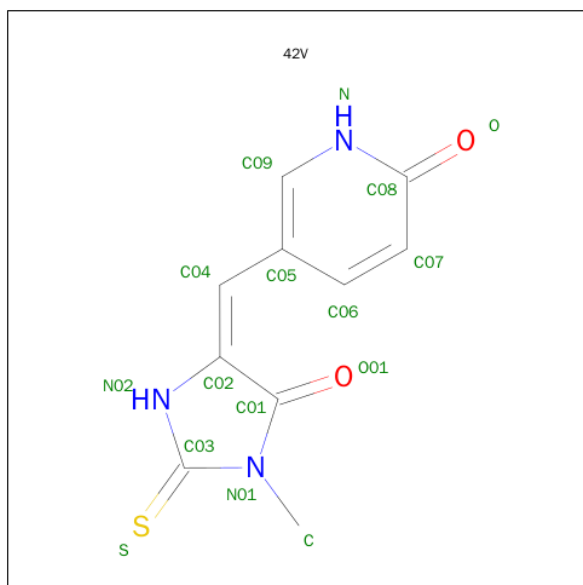
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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

- Molecule 3 is 5-[(E)-(1-methyl-5-oxo-2-thioxoimidazolidin-4-ylidene)methyl]pyridin-2(1H)-one (three-letter code: 42V) (formula: C<sub>10</sub>H<sub>9</sub>N<sub>3</sub>O<sub>2</sub>S).

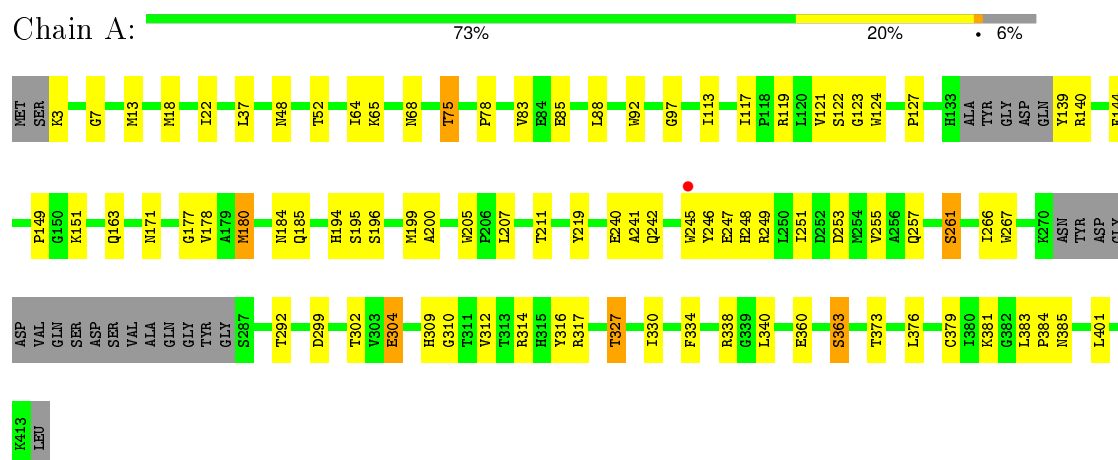


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			16	10	3	2	1		

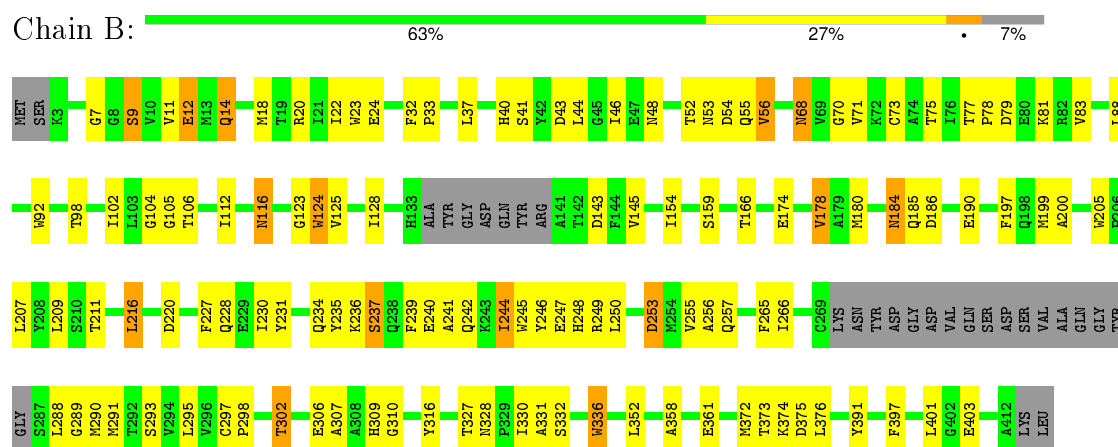
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Isocitrate dehydrogenase [NADP] cytoplasmic



- Molecule 1: Isocitrate dehydrogenase [NADP] cytoplasmic



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.41Å 82.41Å 304.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.26 – 3.20 46.26 – 3.20	Depositor EDS
% Data completeness (in resolution range)	96.0 (46.26-3.20) 96.1 (46.26-3.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.99 (at 3.19Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.191 , 0.277 0.191 , 0.277	Depositor DCC
$R_{free}$ test set	896 reflections (5.38%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.2	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 33.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 17566 reflections	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	6275	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, 42V

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	0.59	4/3166 (0.1%)	0.68	0/4264
1	B	0.61	5/3124 (0.2%)	0.70	0/4210
All	All	0.60	9/6290 (0.1%)	0.69	0/8474

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	92	TRP	CD2-CE2	5.35	1.47	1.41
1	A	245	TRP	CD2-CE2	5.21	1.47	1.41
1	A	267	TRP	CD2-CE2	5.19	1.47	1.41
1	A	124	TRP	CD2-CE2	5.14	1.47	1.41
1	B	205	TRP	CD2-CE2	5.09	1.47	1.41
1	B	245	TRP	CD2-CE2	5.09	1.47	1.41
1	A	205	TRP	CD2-CE2	5.07	1.47	1.41
1	B	124	TRP	CD2-CE2	5.06	1.47	1.41
1	B	336	TRP	CD2-CE2	5.01	1.47	1.41

There are no bond angle outliers.

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	3102	0	3097	55	0
1	B	3061	0	3049	73	0
2	A	48	0	26	3	0
2	B	48	0	26	1	0
3	A	16	0	9	3	0
All	All	6275	0	6207	120	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 (120) 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)
3:A:502:42V:O01	3:A:502:42V:H7	1.52	1.08
1:A:180:MET:CE	1:B:216:LEU:HD21	1.90	1.01
1:A:151:LYS:HE3	1:A:171:ASN:ND2	1.89	0.87
1:A:151:LYS:HE3	1:A:171:ASN:HD22	1.39	0.86
1:A:180:MET:HE2	1:B:216:LEU:HD21	1.55	0.86
1:A:180:MET:HE3	1:B:216:LEU:HD21	1.62	0.81
1:A:200:ALA:HA	1:A:266:ILE:HD12	1.66	0.77
1:B:7:GLY:HA3	1:B:37:LEU:HD23	1.72	0.71
1:B:68:ASN:HA	1:B:302:THR:HG23	1.73	0.70
1:A:7:GLY:HA3	1:A:37:LEU:HD23	1.75	0.68
1:A:22:ILE:HD11	1:A:327:THR:HB	1.77	0.65
1:A:68:ASN:HA	1:A:302:THR:HG23	1.77	0.65
3:A:502:42V:H7	3:A:502:42V:C01	2.26	0.63
1:B:211:THR:HB	1:B:220:ASP:HB3	1.82	0.62
1:A:330:ILE:CD1	1:A:363:SER:HB3	2.30	0.62
1:A:309:HIS:HD2	1:A:310:GLY:O	1.84	0.61
1:A:314:ARG:NE	2:A:501:NDP:O3X	2.23	0.60
1:B:43:ASP:HB3	1:B:48:ASN:ND2	2.17	0.60
1:A:177:GLY:HA2	1:B:186:ASP:OD1	2.02	0.60
1:A:219:TYR:CD1	1:B:178:VAL:HG13	2.38	0.59
1:A:200:ALA:HA	1:A:266:ILE:CD1	2.32	0.59
1:B:123:GLY:HA2	1:B:124:TRP:HB2	1.83	0.58
1:B:18:MET:HB2	1:B:316:TYR:HB2	1.86	0.57
1:A:330:ILE:HD12	1:A:363:SER:HB3	1.84	0.57
1:B:116:ASN:H	1:B:116:ASN:HD22	1.52	0.57
1:A:48:ASN:O	1:A:52:THR:HG23	2.05	0.56
1:A:257:GLN:O	1:A:261:SER:HB3	2.05	0.56
1:B:248:HIS:CD2	1:B:249:ARG:N	2.73	0.56
1:B:32:PHE:N	1:B:33:PRO:CD	2.68	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:374:LYS:HD2	1:B:391:TYR:CZ	2.41	0.55
1:A:75:THR:O	2:A:501:NDP:H2N	2.07	0.54
1:B:197:PHE:CD2	1:B:207:LEU:HD23	2.43	0.54
1:B:231:TYR:HD1	1:B:235:TYR:HB2	1.73	0.54
1:B:9:SER:OG	1:B:40:HIS:HE1	1.92	0.53
1:A:83:VAL:HA	1:A:88:LEU:HD12	1.89	0.53
1:B:190:GLU:HG2	1:B:230:ILE:HD11	1.91	0.53
1:A:7:GLY:HA3	1:A:37:LEU:CD2	2.39	0.53
1:B:248:HIS:CG	1:B:249:ARG:N	2.77	0.53
1:A:381:LYS:O	1:A:385:ASN:HB2	2.09	0.53
1:A:85:GLU:OE2	1:A:317:ARG:NH2	2.41	0.52
1:A:13:MET:CE	1:A:64:ILE:HD11	2.40	0.52
1:B:235:TYR:C	1:B:237:SER:N	2.64	0.51
1:B:52:THR:OG1	1:B:56:VAL:HG22	2.11	0.51
1:B:309:HIS:CE1	1:B:331:ALA:HB3	2.46	0.51
1:A:97:GLY:HA2	3:A:502:42V:C07	2.41	0.50
1:B:306:GLU:HG3	1:B:307:ALA:O	2.11	0.50
1:A:211:THR:OG1	1:A:248:HIS:CE1	2.65	0.50
1:A:3:LYS:HD3	1:A:3:LYS:C	2.32	0.50
1:B:199:MET:HG3	1:B:266:ILE:HD12	1.94	0.50
1:B:22:ILE:HD11	1:B:327:THR:HB	1.94	0.49
1:B:235:TYR:C	1:B:237:SER:H	2.15	0.49
1:A:249:ARG:NH1	1:A:253:ASP:HB3	2.27	0.49
1:B:128:ILE:HG23	1:B:265:PHE:CE1	2.47	0.49
1:A:246:TYR:CG	1:A:247:GLU:N	2.81	0.48
1:A:251:ILE:O	1:A:255:VAL:HG23	2.13	0.48
1:A:180:MET:HE3	1:B:216:LEU:CD2	2.39	0.48
1:A:18:MET:HB2	1:A:316:TYR:HB2	1.94	0.48
1:B:11:VAL:O	1:B:70:GLY:HA2	2.13	0.48
1:A:240:GLU:C	1:A:242:GLN:H	2.17	0.48
1:A:249:ARG:HH11	1:A:253:ASP:HB3	1.79	0.47
1:B:43:ASP:O	1:B:48:ASN:ND2	2.41	0.47
1:B:209:LEU:HD13	1:B:227:PHE:CE2	2.50	0.47
1:B:12:GLU:HG3	1:B:41:SER:HA	1.96	0.47
1:B:53:ASN:O	1:B:55:GLN:N	2.48	0.47
1:B:200:ALA:HA	1:B:266:ILE:HG13	1.97	0.46
1:B:309:HIS:HD2	1:B:310:GLY:O	1.98	0.46
1:B:240:GLU:C	1:B:242:GLN:H	2.19	0.46
1:B:79:ASP:O	1:B:83:VAL:HG23	2.15	0.46
1:A:113:ILE:HD11	1:A:127:PRO:HA	1.97	0.46
1:B:77:THR:HA	1:B:78:PRO:HD3	1.73	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:MET:HG3	1:A:266:ILE:HD13	1.98	0.46
1:A:121:VAL:HG12	1:A:123:GLY:H	1.81	0.45
1:B:239:PHE:O	1:B:244:ILE:CG2	2.65	0.45
1:A:360:GLU:O	1:A:363:SER:HB2	2.15	0.45
1:A:334:PHE:O	1:A:338:ARG:HG2	2.17	0.45
1:B:373:THR:OG1	1:B:375:ASP:OD1	2.26	0.45
1:B:397:PHE:CZ	1:B:401:LEU:HD21	2.52	0.44
1:B:227:PHE:O	1:B:228:GLN:C	2.56	0.44
1:B:7:GLY:HA2	1:B:352:LEU:HD22	1.99	0.44
1:B:200:ALA:CA	1:B:266:ILE:HG13	2.48	0.44
1:B:246:TYR:CG	1:B:247:GLU:N	2.86	0.44
1:A:211:THR:OG1	1:A:248:HIS:HE1	2.00	0.43
1:B:288:LEU:C	1:B:290:MET:H	2.21	0.43
1:B:309:HIS:HE1	1:B:331:ALA:HB3	1.83	0.43
1:B:105:GLY:HA3	1:B:297:CYS:HA	2.01	0.43
1:B:23:TRP:CD2	1:B:73:CYS:HB2	2.54	0.43
1:B:98:THR:O	1:B:102:ILE:HG12	2.18	0.43
1:A:149:PRO:HB2	1:B:159:SER:OG	2.19	0.43
1:B:14:GLN:O	1:B:44:LEU:HB2	2.19	0.43
1:B:75:THR:O	2:B:501:NDP:H2N	2.18	0.43
1:B:297:CYS:HB3	1:B:298:PRO:HD2	2.01	0.42
1:B:235:TYR:O	1:B:237:SER:N	2.52	0.42
1:B:328:ASN:OD1	1:B:330:ILE:HG12	2.19	0.42
1:B:71:VAL:HG11	1:B:336:TRP:HA	2.02	0.42
1:A:383:LEU:HB3	1:A:384:PRO:HD3	2.01	0.42
1:B:230:ILE:HG22	1:B:235:TYR:HE1	1.84	0.42
1:A:246:TYR:CD2	1:A:247:GLU:N	2.85	0.42
1:B:104:GLY:O	1:B:295:LEU:HD11	2.20	0.42
1:A:144:PHE:HE1	1:B:154:ILE:HD13	1.84	0.42
1:A:376:LEU:O	1:A:379:CYS:HB2	2.20	0.42
1:A:340:LEU:HD23	1:A:340:LEU:HA	1.86	0.42
1:A:401:LEU:HA	1:A:401:LEU:HD23	1.62	0.42
1:B:207:LEU:HD13	1:B:266:ILE:HB	2.02	0.41
1:A:219:TYR:HB2	1:B:143:ASP:HB2	2.02	0.41
1:B:358:ALA:O	1:B:361:GLU:HB2	2.21	0.41
1:A:64:ILE:HD13	1:A:304:GLU:HG3	2.01	0.41
1:A:219:TYR:CE1	1:B:178:VAL:HG13	2.55	0.41
1:A:64:ILE:O	1:A:65:LYS:C	2.59	0.41
1:B:289:GLY:HA3	1:B:328:ASN:HB3	2.01	0.41
1:B:20:ARG:O	1:B:24:GLU:HG2	2.21	0.41
1:B:46:ILE:HG13	1:B:88:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:HIS:O	1:A:195:SER:C	2.59	0.41
1:B:53:ASN:C	1:B:55:GLN:H	2.25	0.40
1:A:78:PRO:HG2	1:A:92:TRP:O	2.20	0.40
1:A:310:GLY:HA3	2:A:501:NDP:C6N	2.51	0.40
1:B:372:MET:HB2	1:B:376:LEU:HD12	2.02	0.40
1:A:196:SER:HB3	1:A:207:LEU:HD21	2.03	0.40
1:B:249:ARG:HG3	1:B:250:LEU:H	1.86	0.40
1:B:403:GLU:OE1	1:B:403:GLU:HA	2.21	0.40
1:B:253:ASP:OD1	1:B:253:ASP:N	2.55	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	384/414 (93%)	340 (88%)	41 (11%)	3 (1%)	24	69
1	B	380/414 (92%)	328 (86%)	45 (12%)	7 (2%)	11	51
All	All	764/828 (92%)	668 (87%)	86 (11%)	10 (1%)	15	59

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	363	SER
1	B	54	ASP
1	B	236	LYS
1	B	174	GLU
1	A	241	ALA
1	A	299	ASP
1	B	241	ALA
1	B	256	ALA
1	B	184	ASN

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Mol	Chain	Res	Type
1	B	255	VAL

### 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	332/350 (95%)	315 (95%)	17 (5%)	29	70
1	B	328/350 (94%)	302 (92%)	26 (8%)	15	53
All	All	660/700 (94%)	617 (94%)	43 (6%)	21	61

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	THR
1	A	117	ILE
1	A	119	ARG
1	A	122	SER
1	A	139	TYR
1	A	140	ARG
1	A	163	GLN
1	A	178	VAL
1	A	180	MET
1	A	184	ASN
1	A	185	GLN
1	A	261	SER
1	A	292	THR
1	A	304	GLU
1	A	312	VAL
1	A	327	THR
1	A	373	THR
1	B	9	SER
1	B	12	GLU
1	B	14	GLN
1	B	56	VAL
1	B	68	ASN

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Mol	Chain	Res	Type
1	B	81	LYS
1	B	106	THR
1	B	112	ILE
1	B	116	ASN
1	B	125	VAL
1	B	145	VAL
1	B	166	THR
1	B	178	VAL
1	B	180	MET
1	B	184	ASN
1	B	185	GLN
1	B	216	LEU
1	B	234	GLN
1	B	237	SER
1	B	244	ILE
1	B	253	ASP
1	B	257	GLN
1	B	291	MET
1	B	293	SER
1	B	302	THR
1	B	332	SER

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

Mol	Chain	Res	Type
1	A	67	HIS
1	A	170	HIS
1	A	198	GLN
1	A	248	HIS
1	A	309	HIS
1	B	40	HIS
1	B	116	ASN
1	B	228	GLN
1	B	234	GLN
1	B	248	HIS
1	B	309	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 ⓘ

3 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	NDP	A	501	-	44,52,52	1.12	5 (11%)	55,80,80	1.55	7 (12%)
3	42V	A	502	-	15,17,17	4.06	9 (60%)	19,24,24	2.60	6 (31%)
2	NDP	B	501	-	44,52,52	1.15	4 (9%)	55,80,80	1.49	5 (9%)

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	NDP	A	501	-	-	0/30/77/77	0/5/5/5
3	42V	A	502	-	-	0/2/20/20	0/2/2/2
2	NDP	B	501	-	-	0/30/77/77	0/5/5/5

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	42V	C02-C01	2.04	1.51	1.49
2	B	501	NDP	C2N-C3N	2.05	1.40	1.34
2	A	501	NDP	C2A-N3A	2.06	1.35	1.32
2	A	501	NDP	C2N-C3N	2.32	1.41	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NDP	O4B-C1B	2.33	1.44	1.41
2	B	501	NDP	O4B-C1B	2.72	1.45	1.41
3	A	502	42V	C05-C04	2.79	1.52	1.46
2	A	501	NDP	C5A-C4A	3.11	1.47	1.40
2	B	501	NDP	C5A-C4A	3.30	1.47	1.40
2	A	501	NDP	C6N-C5N	3.80	1.40	1.33
2	B	501	NDP	C6N-C5N	3.84	1.40	1.33
3	A	502	42V	C06-C05	3.84	1.46	1.39
3	A	502	42V	C08-N	3.99	1.40	1.33
3	A	502	42V	C09-N	4.54	1.44	1.34
3	A	502	42V	O-C08	5.13	1.37	1.24
3	A	502	42V	C03-N02	5.50	1.47	1.36
3	A	502	42V	C02-N02	7.60	1.51	1.37
3	A	502	42V	C04-C02	7.68	1.49	1.34

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	NDP	N3A-C2A-N1A	-7.77	122.77	128.87
2	A	501	NDP	N3A-C2A-N1A	-7.22	123.20	128.87
3	A	502	42V	C05-C04-C02	-6.77	118.69	130.62
2	A	501	NDP	C2B-C1B-N9A	-2.57	106.14	113.48
3	A	502	42V	C07-C08-N	-2.56	120.03	124.64
2	A	501	NDP	O2B-P2B-O1X	-2.27	102.05	107.48
2	B	501	NDP	O2B-P2B-O1X	-2.10	102.47	107.48
2	B	501	NDP	O4D-C1D-C2D	-2.04	101.99	106.61
3	A	502	42V	C04-C02-N02	-2.03	123.43	130.81
3	A	502	42V	C09-N-C08	2.03	120.32	117.06
2	A	501	NDP	O2N-PN-O1N	2.04	123.19	112.56
3	A	502	42V	C02-C01-N01	2.06	106.74	105.48
2	B	501	NDP	O3X-P2B-O2X	2.14	115.28	107.44
2	B	501	NDP	N6A-C6A-N1A	2.15	122.12	118.52
2	A	501	NDP	O4D-C1D-N1N	2.18	112.26	108.09
2	A	501	NDP	O3X-P2B-O2X	2.38	116.20	107.44
2	A	501	NDP	N6A-C6A-N1A	3.56	124.49	118.52
3	A	502	42V	C04-C02-C01	6.79	132.94	121.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	NDP	3	0
3	A	502	42V	3	0
2	B	501	NDP	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	390/414 (94%)	-0.33	1 (0%) 94 93	24, 40, 79, 105	0
1	B	386/414 (93%)	-0.30	0 100 100	22, 41, 88, 104	0
All	All	776/828 (93%)	-0.31	1 (0%) 95 95	22, 40, 84, 105	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	245	TRP	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	42V	A	502	16/16	0.85	0.22	2.08	78,85,91,92	0
2	NDP	B	501	48/48	0.98	0.14	-1.03	23,28,33,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NDP	A	501	48/48	0.97	0.15	-1.03	26,34,41,44	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.