



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:50 PM GMT

PDB ID : 4AOU
Title : CtIDH bound to NADP. The complex structures of Isocitrate dehydrogenase from *Clostridium thermocellum* and *Desulfotalea psychrophila*, support a new active site locking mechanism
Authors : Leiros, H.-K.S.; Fedoy, A.-E.; Leiros, I.; Steen, I.H.
Deposited on : 2012-03-30
Resolution : 2.50 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

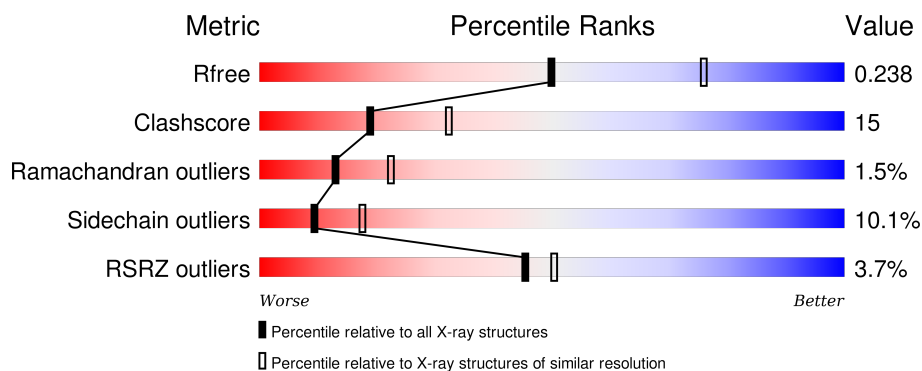
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 ≥ 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	402	

2 Entry composition [i](#)

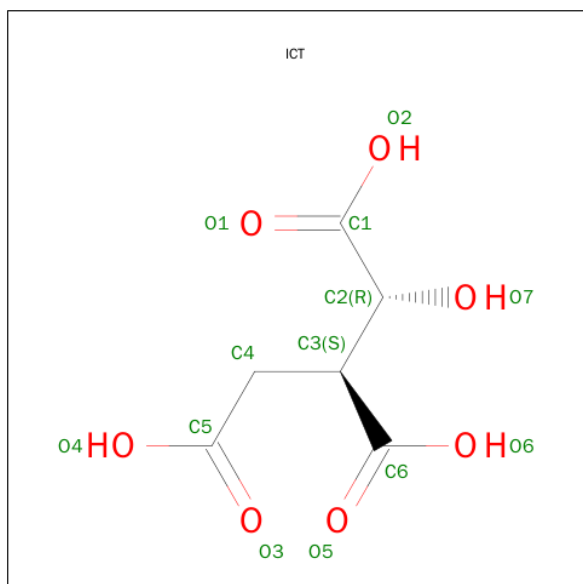
There are 5 unique types of molecules in this entry. The entry contains 3313 atoms, of which 0 are hydrogens and 0 are deuteriums.

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].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	401	Total	C	N	O	S	29	0	0
			3210	2042	535	615	18			

- Molecule 2 is ISOCITRIC ACID (three-letter code: ICT) (formula: C₆H₈O₇).



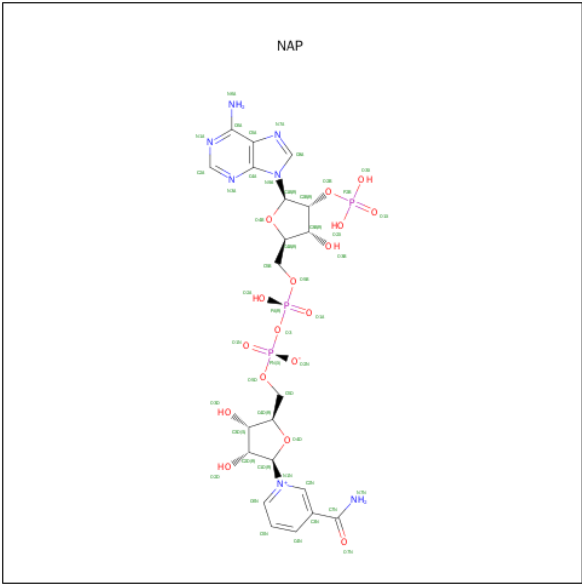
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE

(three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	8	0
			48	21	7	17	3		

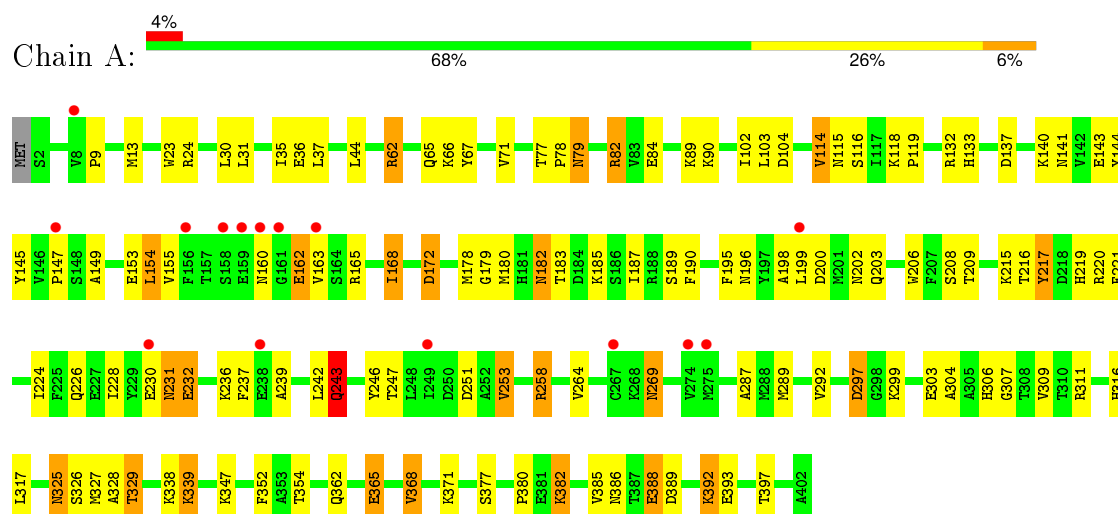
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	41	Total	O	0	0
			41	41		

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: ISOCITRATE DEHYDROGENASE [NADP]



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	129.20 Å 129.20 Å 60.59 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.00 – 2.50 42.29 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.00-2.50) 99.9 (42.29-2.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 2.51 Å)	Xtriage
Refinement program	REFMAC 5.4.0069	Depositor
R, R_{free}	0.189 , 0.244 0.189 , 0.238	Depositor DCC
R_{free} test set	1043 reflections (5.39%)	DCC
Wilson B-factor (Å ²)	48.2	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 35.0	EDS
Estimated twinning fraction	0.044 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 20389 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3313	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: NAP, MG, ICT

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	1.14	7/3275 (0.2%)	1.00	10/4416 (0.2%)

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 (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	371	LYS	CE-NZ	-26.08	0.83	1.49
1	A	162	GLU	CG-CD	-25.29	1.14	1.51
1	A	392	LYS	CE-NZ	-19.98	0.99	1.49
1	A	392	LYS	CG-CD	-12.81	1.08	1.52
1	A	243	GLN	CD-NE2	8.70	1.54	1.32
1	A	185	LYS	CD-CE	-8.21	1.30	1.51
1	A	84	GLU	CG-CD	-6.01	1.43	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	371	LYS	CB-CG-CD	18.05	158.53	111.60
1	A	392	LYS	CB-CG-CD	11.76	142.18	111.60
1	A	243	GLN	OE1-CD-NE2	-10.21	98.41	121.90
1	A	347	LYS	CA-CB-CG	6.30	127.26	113.40
1	A	253	VAL	CB-CA-C	-6.29	99.44	111.40
1	A	339	LYS	CD-CE-NZ	5.98	125.45	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	339	LYS	CG-CD-CE	5.72	129.07	111.90
1	A	258	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	A	371	LYS	CG-CD-CE	5.13	127.30	111.90
1	A	82	ARG	NE-CZ-NH2	-5.07	117.77	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	243	GLN	Sidechain

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	3210	0	3180	98	0
2	A	13	0	4	0	0
3	A	1	0	0	0	0
4	A	48	0	25	0	0
5	A	41	0	0	5	0
All	All	3313	0	3209	98	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 15.

All (98) 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:368:VAL:HG21	1:A:393:GLU:HG2	1.44	1.00
1:A:303:GLU:HG3	1:A:304:ALA:O	1.72	0.89
1:A:226:GLN:O	1:A:230:GLU:HG2	1.73	0.88
1:A:297:ASP:O	1:A:297:ASP:OD1	1.92	0.87
1:A:325:ASN:ND2	1:A:327:MET:H	1.76	0.83
1:A:242:LEU:HD12	1:A:242:LEU:O	1.81	0.80
1:A:237:PHE:CD2	1:A:242:LEU:CD1	2.67	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:LYS:HE2	1:A:67:TYR:CZ	2.21	0.76
1:A:180:MET:HE2	1:A:217:TYR:CZ	2.20	0.75
1:A:231:ASN:C	1:A:231:ASN:HD22	1.90	0.75
1:A:203:GLN:HE21	1:A:264:VAL:HG23	1.53	0.73
1:A:237:PHE:CD2	1:A:242:LEU:HD12	2.25	0.72
1:A:306:HIS:HD2	1:A:307:GLY:O	1.73	0.71
1:A:325:ASN:HD21	1:A:327:MET:HG2	1.58	0.69
1:A:297:ASP:C	1:A:297:ASP:OD1	2.31	0.68
1:A:237:PHE:HD2	1:A:242:LEU:O	1.76	0.68
1:A:325:ASN:HD22	1:A:325:ASN:C	1.98	0.66
1:A:154:LEU:HD22	1:A:155:VAL:N	2.14	0.63
1:A:325:ASN:HD22	1:A:327:MET:H	1.45	0.62
1:A:23:TRP:HH2	1:A:71:VAL:HG13	1.63	0.62
1:A:103:LEU:HD23	1:A:103:LEU:N	2.15	0.61
1:A:180:MET:CE	1:A:217:TYR:CZ	2.83	0.61
1:A:23:TRP:CH2	1:A:71:VAL:HG13	2.38	0.59
1:A:325:ASN:HD22	1:A:326:SER:N	2.00	0.59
1:A:65:GLN:O	1:A:299:LYS:HE3	2.01	0.59
1:A:102:ILE:HG22	1:A:103:LEU:HD23	1.84	0.58
1:A:236:LYS:O	1:A:239:ALA:HB3	2.03	0.58
1:A:377:SER:HB3	1:A:382:LYS:HD2	1.86	0.58
1:A:79:ASN:ND2	1:A:82:ARG:H	2.02	0.58
1:A:153:GLU:C	1:A:168:ILE:HD12	2.24	0.57
1:A:311:ARG:HG3	5:A:2032:HOH:O	2.04	0.57
1:A:116:SER:OG	1:A:365:GLU:OE1	2.14	0.57
1:A:306:HIS:HE1	5:A:2031:HOH:O	1.88	0.57
1:A:89:LYS:O	1:A:90:LYS:HG2	2.04	0.57
1:A:71:VAL:O	1:A:71:VAL:CG1	2.54	0.56
1:A:182:ASN:HD22	1:A:183:THR:H	1.54	0.55
1:A:287:ALA:O	1:A:328:ALA:HB2	2.07	0.55
1:A:154:LEU:N	1:A:168:ILE:HD12	2.22	0.54
1:A:368:VAL:HG21	1:A:393:GLU:CG	2.30	0.53
1:A:153:GLU:OE1	1:A:165:ARG:NH2	2.42	0.53
1:A:237:PHE:CE2	1:A:242:LEU:HD13	2.44	0.52
1:A:237:PHE:CD2	1:A:242:LEU:O	2.60	0.52
1:A:228:ILE:O	1:A:232:GLU:HB2	2.09	0.52
1:A:149:ALA:HB2	1:A:172:ASP:HA	1.92	0.51
1:A:137:ASP:HB3	5:A:2018:HOH:O	2.11	0.51
1:A:71:VAL:O	1:A:71:VAL:HG13	2.11	0.51
1:A:386:ASN:HD21	1:A:388:GLU:HB2	1.76	0.51
1:A:325:ASN:HD21	1:A:327:MET:CG	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:VAL:HG23	1:A:365:GLU:HG2	1.93	0.50
1:A:13:MET:HB3	1:A:44:LEU:HD22	1.94	0.50
1:A:187:ILE:HG12	1:A:221:PHE:CE2	2.47	0.49
1:A:220:ARG:HG3	1:A:224:ILE:HD12	1.95	0.49
1:A:178:MET:HE3	1:A:180:MET:HG2	1.93	0.49
1:A:231:ASN:C	1:A:231:ASN:ND2	2.62	0.49
1:A:231:ASN:O	1:A:232:GLU:HG3	2.12	0.48
1:A:35:ILE:HD11	1:A:352:PHE:CD2	2.48	0.48
1:A:62:ARG:NH2	5:A:2012:HOH:O	2.47	0.48
1:A:237:PHE:CD2	1:A:242:LEU:HD13	2.47	0.47
1:A:199:LEU:O	1:A:200:ASP:C	2.51	0.47
1:A:137:ASP:OD1	1:A:217:TYR:OH	2.29	0.47
1:A:132:ARG:HE	1:A:269:ASN:HD22	1.62	0.47
1:A:118:LYS:HA	1:A:118:LYS:HD3	1.31	0.47
1:A:385:VAL:HB	1:A:389:ASP:HB2	1.97	0.47
1:A:141:ASN:OD1	1:A:143:GLU:HG3	2.15	0.47
1:A:114:VAL:O	1:A:115:ASN:C	2.54	0.46
1:A:79:ASN:HD22	1:A:82:ARG:H	1.64	0.46
1:A:133:HIS:CD2	1:A:190:PHE:HB2	2.51	0.46
1:A:79:ASN:C	1:A:79:ASN:HD22	2.19	0.46
1:A:144:TYR:CE2	1:A:145:TYR:O	2.69	0.46
1:A:231:ASN:O	1:A:232:GLU:CG	2.65	0.45
1:A:329:THR:HG23	5:A:2031:HOH:O	2.16	0.45
1:A:37:LEU:HD12	1:A:37:LEU:HA	1.68	0.45
1:A:203:GLN:HE21	1:A:264:VAL:CG2	2.27	0.45
1:A:178:MET:HG2	1:A:179:GLY:N	2.32	0.45
1:A:154:LEU:C	1:A:154:LEU:HD22	2.37	0.44
1:A:230:GLU:HA	1:A:230:GLU:OE1	2.17	0.44
1:A:178:MET:CE	1:A:180:MET:HG2	2.48	0.44
1:A:208:SER:O	1:A:209:THR:HG22	2.16	0.44
1:A:247:THR:OG1	1:A:251:ASP:OD2	2.21	0.43
1:A:246:TYR:CD1	1:A:246:TYR:C	2.92	0.43
1:A:118:LYS:HA	1:A:119:PRO:HD3	1.87	0.42
1:A:195:PHE:O	1:A:196:ASN:C	2.56	0.42
1:A:386:ASN:ND2	1:A:388:GLU:N	2.68	0.42
1:A:154:LEU:CD2	1:A:155:VAL:N	2.80	0.42
1:A:339:LYS:HA	1:A:339:LYS:HD3	1.92	0.42
1:A:215:LYS:O	1:A:219:HIS:HB2	2.20	0.42
1:A:198:ALA:O	1:A:202:ASN:N	2.53	0.42
1:A:206:TRP:CD1	1:A:206:TRP:N	2.88	0.42
1:A:215:LYS:O	1:A:219:HIS:CB	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:GLU:H	1:A:162:GLU:HG3	1.59	0.41
1:A:326:SER:O	1:A:327:MET:C	2.57	0.41
1:A:386:ASN:ND2	1:A:388:GLU:H	2.19	0.41
1:A:231:ASN:ND2	1:A:231:ASN:H	2.19	0.41
1:A:66:LYS:HE2	1:A:67:TYR:CE1	2.55	0.41
1:A:30:LEU:C	1:A:31:LEU:HD23	2.41	0.41
1:A:208:SER:C	1:A:209:THR:CG2	2.89	0.40
1:A:9:PRO:HG2	1:A:67:TYR:CD1	2.57	0.40
1:A:77:THR:HA	1:A:78:PRO:HD3	1.85	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	399/402 (99%)	361 (90%)	32 (8%)	6 (2%)	13	22

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	160	ASN
1	A	104	ASP
1	A	232	GLU
1	A	217	TYR
1	A	147	PRO
1	A	380	PRO

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	346/347 (100%)	311 (90%)	35 (10%)	9 17

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ARG
1	A	36	GLU
1	A	62	ARG
1	A	79	ASN
1	A	114	VAL
1	A	140	LYS
1	A	154	LEU
1	A	163	VAL
1	A	168	ILE
1	A	172	ASP
1	A	182	ASN
1	A	189	SER
1	A	216	THR
1	A	231	ASN
1	A	243	GLN
1	A	253	VAL
1	A	258	ARG
1	A	269	ASN
1	A	289	MET
1	A	292	VAL
1	A	297	ASP
1	A	309	VAL
1	A	316	HIS
1	A	317	LEU
1	A	325	ASN
1	A	329	THR
1	A	338	LYS
1	A	354	THR
1	A	362	GLN
1	A	365	GLU
1	A	368	VAL
1	A	382	LYS
1	A	388	GLU
1	A	392	LYS

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Mol	Chain	Res	Type
1	A	397	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	A	79	ASN
1	A	87	ASN
1	A	115	ASN
1	A	160	ASN
1	A	182	ASN
1	A	203	GLN
1	A	231	ASN
1	A	269	ASN
1	A	306	HIS
1	A	325	ASN
1	A	386	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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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
2	ICT	A	1403	3	2,12,12	0.52	0	2,16,16	1.95	1 (50%)
4	NAP	A	1520	-	42,52,52	1.72	4 (9%)	54,80,80	2.15	8 (14%)

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	ICT	A	1403	3	-	0/6/16/16	0/0/0/0
4	NAP	A	1520	-	-	0/27/67/67	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1520	NAP	C2A-N1A	2.03	1.37	1.33
4	A	1520	NAP	C2A-N3A	3.06	1.37	1.32
4	A	1520	NAP	C6N-N1N	4.56	1.47	1.35
4	A	1520	NAP	O7N-C7N	8.37	1.42	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1520	NAP	N3A-C2A-N1A	-11.79	119.87	128.89
4	A	1520	NAP	O2B-P2B-O1X	-4.08	96.92	107.11
4	A	1520	NAP	O7N-C7N-C3N	-3.70	115.55	119.59
4	A	1520	NAP	C5N-C6N-N1N	-2.70	115.79	120.47
2	A	1403	ICT	O7-C2-C3	-2.62	100.83	108.40
4	A	1520	NAP	O7N-C7N-N7N	2.09	125.53	122.59
4	A	1520	NAP	O2A-PA-O3	2.17	114.93	105.09
4	A	1520	NAP	P2B-O2B-C2B	2.46	127.47	121.56
4	A	1520	NAP	O4D-C1D-N1N	4.65	113.24	108.13

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 [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, 95th 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 ²)	Q<0.9
1	A	401/402 (99%)	0.07	15 (3%)	45 50	30, 42, 65, 85	13 (3%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	160	ASN	4.7
1	A	159	GLU	4.4
1	A	274	VAL	2.9
1	A	275	MET	2.8
1	A	158	SER	2.8
1	A	156	PHE	2.6
1	A	147	PRO	2.4
1	A	230	GLU	2.3
1	A	249	ILE	2.2
1	A	161	GLY	2.1
1	A	267	CYS	2.1
1	A	238	GLU	2.1
1	A	199	LEU	2.1
1	A	163	VAL	2.1
1	A	8	VAL	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, 95th 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(\AA^2)	Q<0.9
2	ICT	A	1403	13/13	0.98	0.23	0.85	34,37,40,41	0
4	NAP	A	1520	48/48	0.96	0.12	-1.28	38,46,79,80	8
3	MG	A	1404	1/1	0.92	0.14	-3.67	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.