



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 03:26 pm GMT

PDB ID : 2OMT  
Title : Crystal structure of InlA G194S+S/hEC1 complex  
Authors : Wollert, T.; Heinz, D.W.; Schubert, W.D.  
Deposited on : 2007-01-23  
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
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

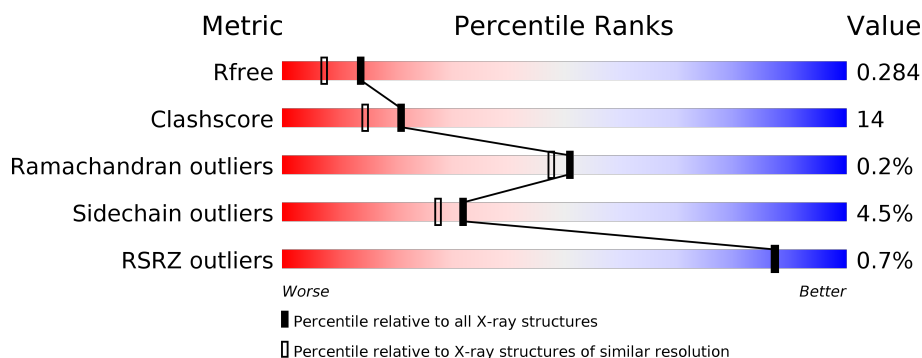
# 1 Overall quality at a glance

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	462	<div> <div>72%</div> <div>26%</div> <div>•</div> </div>
2	B	105	<div> <div>2%</div> <div>65%</div> <div>33%</div> <div>•</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5119 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 Internalin-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	462	Total	C	N	O	S	0	16	1
			3624	2267	602	753	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	194	SER	GLY	ENGINEERED	UNP P25146
A	195	SER	ASN	ENGINEERED	UNP P25146

- Molecule 2 is a protein called Epithelial-cadherin; E-Cad/CTF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	105	Total	C	N	O	S	0	10	1
			891	566	152	171	2			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	EXPRESSION TAG	UNP P12830
B	-2	PRO	-	EXPRESSION TAG	UNP P12830
B	-1	LEU	-	EXPRESSION TAG	UNP P12830
B	0	GLY	-	EXPRESSION TAG	UNP P12830
B	1	SER	-	EXPRESSION TAG	UNP P12830

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

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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Cl 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	491	Total 495	O 495	0	4
5	B	107	Total 107	O 107	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.24Å 88.47Å 110.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00 19.99 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.5 (40.00-2.00) 96.6 (19.99-2.00)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.75 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.194 , 0.283 0.197 , 0.284	Depositor DCC
$R_{free}$ test set	1800 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	16.6	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 43.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5119	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.91% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, CL

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	1.05	3/3677 (0.1%)	1.08	13/5031 (0.3%)
2	B	1.09	2/911 (0.2%)	0.94	1/1237 (0.1%)
All	All	1.06	5/4588 (0.1%)	1.06	14/6268 (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
2	B	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	39	THR	C-N	-8.99	1.13	1.34
2	B	69	GLU	CG-CD	6.67	1.61	1.51
2	B	22	VAL	CB-CG1	6.39	1.66	1.52
1	A	491	VAL	CB-CG2	6.02	1.65	1.52
1	A	461	TRP	CE3-CZ3	5.22	1.47	1.38

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	40	GLN	N-CA-CB	9.16	127.08	110.60
1	A	39	THR	O-C-N	-8.74	108.72	122.70
1	A	39	THR	N-CA-C	6.51	128.58	111.00
1	A	156	ASP	CB-CG-OD2	-6.49	112.46	118.30
1	A	171	LEU	CA-CB-CG	6.35	129.90	115.30
1	A	39	THR	CA-C-N	6.20	130.84	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	257	LEU	CB-CG-CD2	-5.86	101.04	111.00
1	A	40	GLN	N-CA-C	-5.76	95.44	111.00
1	A	116	LEU	CA-CB-CG	5.41	127.75	115.30
1	A	301	LEU	CB-CG-CD2	-5.33	101.94	111.00
2	B	44	ASP	CB-CG-OD1	5.18	122.97	118.30
1	A	144	LEU	CB-CG-CD1	-5.15	102.24	111.00
1	A	276	LEU	CB-CG-CD2	5.15	119.75	111.00
1	A	303	LEU	CB-CG-CD2	-5.04	102.43	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	54	GLU	Mainchain

## 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	3624	0	3690	93	0
2	B	891	0	894	35	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	495	0	0	27	2
5	B	107	0	0	11	1
All	All	5119	0	4584	125	2

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 14.

All (125) 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)
2:B:70[A]:ARG:NH1	5:B:178:HOH:O	1.78	1.14
2:B:25[B]:LYS:HE3	2:B:29:ASP:OD2	1.55	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:7:ILE:HD12	2:B:94[A]:ILE:CG2	1.94	0.97
1:A:242:ILE:HG23	5:A:1090:HOH:O	1.68	0.92
1:A:329:GLN:NE2	5:A:1020:HOH:O	2.04	0.90
1:A:129:ASN:HB2	5:A:1051:HOH:O	1.71	0.89
1:A:112:ASP:OD1	1:A:114:THR:HG23	1.71	0.88
1:A:45:ASN:HD21	1:A:67:THR:HG22	1.39	0.88
1:A:366:ARG:HG2	1:A:388:TRP:HB2	1.57	0.85
2:B:25[B]:LYS:CE	2:B:29:ASP:OD2	2.29	0.79
1:A:89:LYS:HE2	5:A:1091:HOH:O	1.82	0.78
1:A:197:GLN:HG3	5:A:839:HOH:O	1.84	0.77
2:B:25[A]:LYS:NZ	5:B:176:HOH:O	1.60	0.77
2:B:25[B]:LYS:CE	5:B:140:HOH:O	2.33	0.74
2:B:7:ILE:HD12	2:B:94[A]:ILE:HG21	1.68	0.73
1:A:98:ASN:HB2	5:A:995:HOH:O	1.87	0.73
1:A:45:ASN:HB3	1:A:66[B]:VAL:HG12	1.72	0.71
2:B:70[B]:ARG:NH1	5:B:106:HOH:O	2.09	0.69
1:A:43:PRO:HG2	1:A:46:GLN:NE2	2.08	0.68
2:B:7:ILE:CD1	2:B:94[A]:ILE:HG21	2.23	0.68
1:A:320:LEU:HD12	1:A:339:LEU:HD13	1.75	0.67
1:A:36:ALA:N	5:A:1022:HOH:O	2.30	0.65
1:A:165:ASN:OD1	5:A:865:HOH:O	2.13	0.65
1:A:318:THR:O	5:A:612:HOH:O	2.14	0.65
1:A:377[B]:VAL:HG22	1:A:380:LEU:HD12	1.78	0.65
1:A:227:ALA:HB3	5:A:1031:HOH:O	1.97	0.64
2:B:70[B]:ARG:NE	5:B:193:HOH:O	2.20	0.63
1:A:178:ASP:OD1	1:A:180:SER:OG	2.17	0.63
1:A:356:SER:HA	5:A:1010:HOH:O	1.98	0.63
2:B:41[B]:GLN:HE22	2:B:75:THR:H	1.44	0.62
2:B:41[A]:GLN:HG3	5:B:191:HOH:O	1.99	0.62
1:A:377[B]:VAL:HG13	1:A:402:LEU:HD21	1.82	0.61
1:A:45:ASN:ND2	1:A:67:THR:HG22	2.12	0.61
1:A:117:LYS:HD2	5:A:1083:HOH:O	2.02	0.60
1:A:359:SER:O	1:A:382[B]:ASN:ND2	2.35	0.59
1:A:75:LEU:HB2	5:A:1075:HOH:O	2.03	0.58
1:A:211:GLU:OE1	5:A:1001:HOH:O	2.17	0.57
2:B:7:ILE:CD1	2:B:94[A]:ILE:CG2	2.76	0.57
1:A:373:LYS:HE3	5:A:876:HOH:O	2.03	0.57
1:A:285:GLN:OE1	5:A:638:HOH:O	2.18	0.57
2:B:1:SER:HB3	2:B:27:ASN:HB2	1.87	0.56
1:A:179:ILE:HB	1:A:182:LEU:HD12	1.86	0.56
1:A:143:ASN:O	5:A:1048:HOH:O	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:ILE:HB	1:A:182:LEU:CD1	2.36	0.55
1:A:414[B]:ASN:ND2	1:A:414[B]:ASN:H	2.04	0.55
2:B:25[B]:LYS:HE2	5:B:140:HOH:O	2.02	0.55
1:A:342:LEU:HD12	1:A:361:LEU:HD13	1.89	0.55
1:A:332[B]:ASP:OD1	1:A:332[B]:ASP:C	2.42	0.54
1:A:213[B]:LEU:HD21	1:A:215:ILE:HG23	1.89	0.54
1:A:380:LEU:HB3	5:A:1064:HOH:O	2.07	0.54
1:A:393:HIS:ND1	1:A:393:HIS:O	2.40	0.54
1:A:157:ILE:HD11	1:A:179:ILE:HA	1.89	0.53
1:A:199[A]:THR:HG22	1:A:219[A]:LYS:HB2	1.91	0.53
1:A:126:LEU:HA	1:A:148:THR:HB	1.90	0.53
1:A:408:ILE:HG22	1:A:483:GLY:HA3	1.91	0.53
1:A:67:THR:OG1	5:A:1077:HOH:O	2.19	0.52
2:B:76:LEU:HB2	2:B:94[B]:ILE:HG13	1.90	0.52
1:A:425:TYR:H	1:A:497:ALA:N	2.07	0.52
2:B:41[A]:GLN:HG2	2:B:46:PRO:O	2.08	0.52
1:A:91:ILE:O	1:A:94:VAL:HG12	2.10	0.52
1:A:170:GLU:HG2	2:B:17:PHE:O	2.10	0.52
2:B:95:LEU:HD12	5:B:139:HOH:O	2.09	0.51
1:A:54:ALA:HB1	1:A:66[B]:VAL:HG13	1.91	0.50
1:A:113:ILE:HB	1:A:116:LEU:HD22	1.93	0.50
1:A:360:SER:O	5:A:634:HOH:O	2.18	0.50
1:A:423:VAL:O	1:A:495:LEU:HA	2.11	0.49
1:A:43:PRO:HG3	5:A:803:HOH:O	2.12	0.49
1:A:97:LEU:HD12	1:A:100:LEU:HD11	1.93	0.49
1:A:366:ARG:HG2	1:A:388:TRP:CB	2.34	0.49
1:A:358:VAL:HG22	5:A:1010:HOH:O	2.13	0.48
2:B:67:ASP:HB3	2:B:70[B]:ARG:HB2	1.96	0.48
2:B:71:ILE:HG22	2:B:73[A]:THR:O	2.14	0.48
1:A:158:ASP:O	1:A:161:LYS:HG2	2.14	0.48
1:A:359:SER:HB3	1:A:379[B]:SER:HB2	1.96	0.48
1:A:44:ILE:HB	1:A:66[B]:VAL:O	2.14	0.47
1:A:377[B]:VAL:CG1	1:A:402:LEU:HD21	2.43	0.47
1:A:399:LEU:HD11	1:A:487:PHE:CD2	2.49	0.47
1:A:54:ALA:HB1	1:A:66[B]:VAL:CG1	2.45	0.47
1:A:111:THR:HG22	1:A:131:GLN:HB2	1.96	0.47
1:A:395:GLN:HG2	1:A:417:ALA:O	2.16	0.46
1:A:56:LYS:HE2	1:A:82:GLN:O	2.15	0.46
1:A:45:ASN:HB3	1:A:66[B]:VAL:CG1	2.44	0.46
1:A:455:THR:O	1:A:456:GLU:C	2.53	0.46
1:A:75:LEU:CB	5:A:1075:HOH:O	2.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:7:ILE:HD12	2:B:94[A]:ILE:HG23	1.87	0.46
1:A:136:THR:N	1:A:137:PRO:CD	2.79	0.45
1:A:44:ILE:HD13	1:A:58:LYS:HA	1.98	0.45
2:B:43:ALA:HB2	2:B:76:LEU:HD22	1.98	0.45
1:A:259:LEU:HD13	1:A:264:LEU:HD11	1.98	0.45
1:A:111:THR:HG22	1:A:131:GLN:O	2.16	0.45
1:A:459:ILE:HD13	1:A:472:TYR:CD1	2.51	0.45
1:A:229:LEU:HB3	1:A:232:LEU:HG	1.98	0.45
2:B:41[A]:GLN:CG	2:B:46:PRO:O	2.65	0.45
2:B:57:THR:HG1	2:B:59:TRP:HD1	1.62	0.45
1:A:366:ARG:HD2	2:B:6:PRO:HD3	1.98	0.45
1:A:266:ASP:OD1	1:A:266:ASP:C	2.55	0.44
2:B:32:GLY:HA2	2:B:33[B]:LYS:HE2	1.98	0.44
2:B:4:ILE:HA	2:B:5:PRO:HD3	1.72	0.44
1:A:113:ILE:O	1:A:116:LEU:HB2	2.17	0.44
1:A:414[B]:ASN:HD22	1:A:414[B]:ASN:H	1.64	0.44
1:A:153:GLN:HE21	1:A:153:GLN:HB2	1.66	0.44
1:A:114:THR:HA	1:A:137:PRO:HB3	1.99	0.44
1:A:418:TRP:CE2	1:A:491:VAL:HG22	2.53	0.44
1:A:73:THR:O	1:A:77:GLN:HG2	2.16	0.44
2:B:25[B]:LYS:NZ	5:B:140:HOH:O	1.96	0.44
1:A:366:ARG:HG2	1:A:388:TRP:CG	2.52	0.43
1:A:207:LEU:HA	5:A:1087:HOH:O	2.18	0.43
1:A:82:GLN:HE22	1:A:102:GLN:HE22	1.66	0.43
1:A:66[B]:VAL:HG23	5:A:791:HOH:O	2.17	0.43
1:A:331[B]:GLU:CD	1:A:351:ASN:ND2	2.72	0.43
1:A:331[B]:GLU:CG	1:A:351:ASN:ND2	2.82	0.43
2:B:78:SER:O	2:B:91:PRO:HA	2.19	0.43
1:A:194:SER:HA	1:A:216:SER:O	2.19	0.42
1:A:138:LEU:CD2	1:A:141:LEU:HD12	2.49	0.42
2:B:25[B]:LYS:HG2	2:B:26:SER:N	2.34	0.42
1:A:123:VAL:CG1	5:A:1082:HOH:O	2.67	0.42
1:A:424:ASN:HB3	5:A:874:HOH:O	2.17	0.42
1:A:274:THR:O	1:A:297:LYS:HD2	2.19	0.42
1:A:390:SER:HB2	2:B:-1:LEU:HD21	2.02	0.42
1:A:138:LEU:HD23	1:A:141:LEU:HD12	2.01	0.42
1:A:41:ASP:HB3	1:A:69:THR:HB	2.01	0.42
2:B:33[A]:LYS:HD2	5:B:159:HOH:O	2.19	0.41
2:B:77:PHE:HA	2:B:92:MET:O	2.20	0.41
1:A:142:THR:O	1:A:165:ASN:ND2	2.52	0.40
2:B:101:GLN:N	5:B:171:HOH:O	2.55	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:844:HOH:O	5:A:1018:HOH:O[2_565]	2.18	0.02
5:A:1073:HOH:O	5:B:182:HOH:O[4_556]	2.18	0.02

## 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	476/462 (103%)	423 (89%)	52 (11%)	1 (0%)	51	48
2	B	113/105 (108%)	106 (94%)	7 (6%)	0	100	100
All	All	589/567 (104%)	529 (90%)	59 (10%)	1 (0%)	51	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	481	GLY

### 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	433/417 (104%)	414 (96%)	19 (4%)	33	28
2	B	101/92 (110%)	97 (96%)	4 (4%)	36	32
All	All	534/509 (105%)	511 (96%)	23 (4%)	32	29

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	SER
1	A	91	ILE
1	A	116	LEU
1	A	129	ASN
1	A	140	ASN
1	A	142	THR
1	A	153	GLN
1	A	167	ASN
1	A	170	GLU
1	A	180	SER
1	A	197	GLN
1	A	221	SER
1	A	229	LEU
1	A	272	SER
1	A	297	LYS
1	A	336	ILE
1	A	386	ILE
1	A	468	ASN
1	A	469	GLU
2	B	31	GLU
2	B	54	GLU
2	B	95	LEU
2	B	100	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	GLN
1	A	46	GLN
1	A	65	ASN
1	A	72	GLN
1	A	77	GLN
1	A	82	GLN
1	A	107	ASN
1	A	131	GLN
1	A	153	GLN
1	A	285	GLN
1	A	365	GLN
1	A	395	GLN
1	A	424	ASN
2	B	86	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 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 [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	462/462 (100%)	-0.34	2 (0%) 92 92	9, 16, 30, 48	0
2	B	105/105 (100%)	-0.12	2 (1%) 67 66	9, 19, 30, 38	0
All	All	567/567 (100%)	-0.30	4 (0%) 87 87	9, 16, 31, 48	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	39	THR	3.6
2	B	100	ASP	2.3
2	B	8[A]	SER	2.3
1	A	38	ILE	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( $\text{\AA}^2$ )	Q<0.9
3	CA	A	601	1/1	0.97	0.06	-1.21	24,24,24,24	1
4	CL	A	602	1/1	0.98	0.04	-1.76	17,17,17,17	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.