



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2021 – 06:22 AM EDT

PDB ID : 3I2X  
Title : Crystal structure of a chimeric trypsin inhibitor having reactive site loop of ETI on the scaffold of WCI  
Authors : Sen, U.; Khamrui, S.; Dasgupta, J.; Dattagupta, J.K.; Majumder, S.  
Deposited on : 2009-06-30  
Resolution : 2.85 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

<https://www.wwpdb.org/validation/2017/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)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

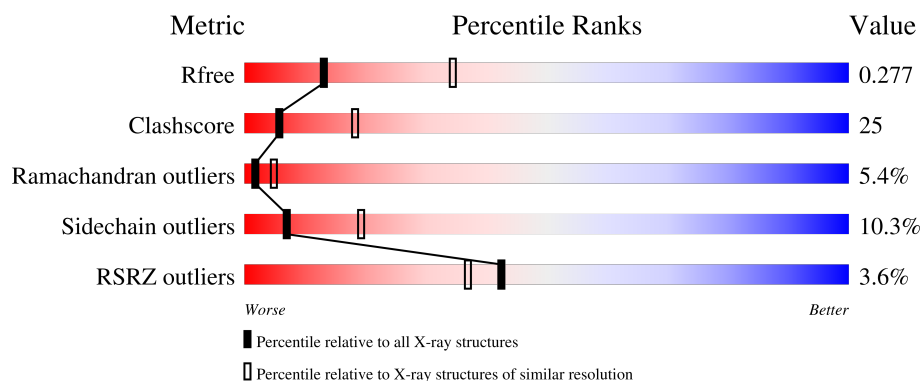
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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))
$R_{free}$	130704	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	187	<div> <div>6%</div> <div>55% 32% 6% 5%</div> </div>
1	B	187	<div> <div>6%</div> <div>49% 40% 6% . .</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2931 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 Chymotrypsin inhibitor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	178	Total	C	N	O	S	0	0	0
			1391	879	245	262	5			
1	B	181	Total	C	N	O	S	0	0	0
			1406	888	250	263	5			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P10822
A	1	SER	-	expression tag	UNP P10822
A	2	HIS	-	expression tag	UNP P10822
A	3	MET	-	expression tag	UNP P10822
A	66	ARG	GLN	engineered mutation	UNP P10822
A	67	LEU	PHE	engineered mutation	UNP P10822
A	68	ARG	LEU	engineered mutation	UNP P10822
A	70	ALA	LEU	engineered mutation	UNP P10822
B	0	GLY	-	expression tag	UNP P10822
B	1	SER	-	expression tag	UNP P10822
B	2	HIS	-	expression tag	UNP P10822
B	3	MET	-	expression tag	UNP P10822
B	66	ARG	GLN	engineered mutation	UNP P10822
B	67	LEU	PHE	engineered mutation	UNP P10822
B	68	ARG	LEU	engineered mutation	UNP P10822
B	70	ALA	LEU	engineered mutation	UNP P10822

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	76	Total	O	0	0
			76	76		
2	B	58	Total	O	0	0
			58	58		



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.80Å 40.16Å 121.55Å 90.00° 101.33° 90.00°	Depositor
Resolution (Å)	19.87 – 2.85 29.80 – 2.84	Depositor EDS
% Data completeness (in resolution range)	92.1 (19.87-2.85) 91.5 (29.80-2.84)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.02 (at 2.85Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.225 , 0.285 0.220 , 0.277	Depositor DCC
$R_{free}$ test set	393 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.9	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 53.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for $1/2^*h-3/2^*k,-1/2^*h-1/2^*k,-1/2^*h+1/2^*k-l$ 0.016 for $1/2^*h+3/2^*k,1/2^*h-1/2^*k,-1/2^*h-1/2^*k-l$	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	2931	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.02% 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](#)

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	0.46	0/1424	0.89	4/1936 (0.2%)
1	B	0.41	0/1440	0.83	2/1958 (0.1%)
All	All	0.44	0/2864	0.86	6/3894 (0.2%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142	GLU	N-CA-C	9.93	137.82	111.00
1	A	141	ASP	N-CA-C	6.49	128.51	111.00
1	B	126	SER	N-CA-C	5.92	126.98	111.00
1	A	118	LEU	CA-CB-CG	5.08	126.97	115.30
1	B	142	GLU	N-CA-CB	-5.07	101.48	110.60
1	A	141	ASP	C-N-CA	5.01	134.23	121.70

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	1391	0	1377	57	0
1	B	1406	0	1388	84	0
2	A	76	0	0	14	0
2	B	58	0	0	3	0
All	All	2931	0	2765	141	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 25.

All (141) 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:2:HIS:HB2	1:B:5:ASP:OD1	1.66	0.94
1:B:66:ARG:HH21	1:B:117:ILE:CD1	1.84	0.91
1:B:153:ILE:HG22	1:B:154:HIS:H	1.43	0.83
1:B:35:GLU:HB3	1:B:59:GLU:HG2	1.61	0.82
1:B:2:HIS:HB2	1:B:5:ASP:CG	1.99	0.82
1:B:123:GLU:OE1	1:B:136:LEU:HD11	1.81	0.81
1:B:125:VAL:HG22	1:B:132:VAL:HB	1.65	0.78
1:B:74:ARG:HG2	1:B:74:ARG:HH11	1.49	0.77
1:B:153:ILE:HG21	1:B:161:ARG:HB3	1.67	0.76
1:A:152:GLY:HA3	1:A:166:THR:OG1	1.87	0.74
1:B:125:VAL:CG2	1:B:132:VAL:HB	2.18	0.74
1:B:141:ASP:HB3	1:B:144:ASP:HB3	1.70	0.73
1:B:153:ILE:HG22	1:B:154:HIS:N	2.03	0.73
1:A:128:SER:O	1:A:129:ASN:HB2	1.89	0.72
1:A:170:PRO:HB3	2:A:428:HOH:O	1.89	0.71
1:A:179:LYS:N	1:A:179:LYS:HD3	2.05	0.70
1:B:157:ARG:O	1:B:157:ARG:HD3	1.92	0.70
1:A:99:SER:HB3	1:A:102:GLY:O	1.92	0.70
1:B:39:THR:O	1:B:42:GLU:HB2	1.92	0.69
1:B:26:HIS:CE1	1:B:127:HIS:HE2	2.11	0.68
1:A:170:PRO:HG2	2:A:499:HOH:O	1.93	0.68
1:A:141:ASP:OD2	2:A:406:HOH:O	2.13	0.67
1:B:156:ASP:OD2	1:B:160:ASN:HB2	1.95	0.67
1:A:41:ASN:HB2	2:A:444:HOH:O	1.95	0.67
1:B:2:HIS:HB2	1:B:5:ASP:OD2	1.96	0.66
1:B:41:ASN:ND2	1:B:42:GLU:H	1.94	0.66
1:B:138:CYS:O	1:B:139:GLN:O	2.13	0.66
1:A:21:TYR:CE2	1:A:177:LYS:HB2	2.31	0.64
1:B:164:VAL:O	1:B:166:THR:HG23	1.96	0.64
1:B:66:ARG:HH21	1:B:117:ILE:HD12	1.60	0.64
1:B:155:ARG:HA	1:B:160:ASN:O	1.97	0.63
1:A:35:GLU:HB2	2:A:430:HOH:O	1.99	0.62
1:A:104:ALA:HA	1:A:164:VAL:HG12	1.82	0.62
1:B:66:ARG:NH2	1:B:117:ILE:CD1	2.61	0.61
1:B:134:LYS:HA	1:B:171:LEU:O	2.00	0.61
1:A:91:SER:HB2	1:A:92:PRO:HD2	1.82	0.61
1:B:74:ARG:HH11	1:B:74:ARG:CG	2.13	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2:HIS:CB	1:B:5:ASP:OD1	2.47	0.59
1:B:33:GLY:HA3	1:B:57:LYS:O	2.02	0.59
1:B:41:ASN:HD22	1:B:41:ASN:N	2.01	0.59
1:B:77:LEU:HD21	1:B:138:CYS:SG	2.43	0.58
1:A:155:ARG:HA	1:A:160:ASN:O	2.04	0.57
1:B:91:SER:HG	1:B:93:TRP:HD1	1.51	0.57
1:B:153:ILE:CG2	1:B:154:HIS:H	2.16	0.57
1:B:158:ASN:HD22	1:B:158:ASN:N	2.03	0.56
1:B:77:LEU:HD23	1:B:120:PHE:O	2.05	0.56
1:B:104:ALA:HA	1:B:164:VAL:HG12	1.86	0.56
1:A:82:PHE:O	1:A:85:PRO:HD3	2.05	0.56
1:B:35:GLU:HB3	1:B:59:GLU:CG	2.32	0.56
1:A:4:ASP:CG	2:A:404:HOH:O	2.44	0.55
1:B:180:SER:HB3	2:B:526:HOH:O	2.06	0.55
1:B:1:SER:O	1:B:2:HIS:ND1	2.40	0.54
1:A:4:ASP:HB3	2:A:404:HOH:O	2.06	0.54
1:B:62:ARG:HD3	2:B:437:HOH:O	2.08	0.54
1:A:22:TYR:N	1:A:176:LEU:O	2.36	0.54
1:B:41:ASN:HD22	1:B:41:ASN:H	1.56	0.54
1:B:177:LYS:HG3	1:B:178:ALA:O	2.07	0.54
1:B:153:ILE:CG2	1:B:161:ARG:HB3	2.37	0.53
1:B:117:ILE:HG13	1:B:118:LEU:N	2.23	0.53
1:B:157:ARG:HD3	1:B:157:ARG:C	2.28	0.53
1:A:43:PRO:HG2	1:A:44:CYS:SG	2.48	0.53
1:A:27:ILE:HD12	1:A:30:HIS:HB2	1.90	0.53
1:B:91:SER:OG	1:B:93:TRP:HD1	1.92	0.53
1:A:29:ALA:HA	1:A:54:GLU:HG2	1.91	0.53
1:B:26:HIS:CE1	1:B:127:HIS:NE2	2.78	0.52
1:B:6:ASP:HB2	1:B:14:LEU:CD2	2.40	0.52
1:B:5:ASP:O	1:B:73:PRO:HA	2.09	0.52
1:B:31:GLY:HA3	1:B:161:ARG:HH12	1.73	0.51
1:B:141:ASP:HB3	1:B:144:ASP:CB	2.39	0.51
1:A:49:VAL:HG12	1:A:162:ARG:HA	1.92	0.51
1:A:20:THR:HA	1:A:61:ILE:O	2.11	0.51
1:A:179:LYS:HD3	1:A:179:LYS:H	1.76	0.51
1:B:31:GLY:CA	1:B:161:ARG:HH22	2.24	0.51
1:A:85:PRO:HG3	1:A:92:PRO:HB3	1.93	0.51
1:A:86:PRO:HD2	1:A:107:LEU:CD1	2.41	0.51
1:B:151:ILE:O	1:B:171:LEU:HG	2.10	0.51
1:B:41:ASN:ND2	1:B:42:GLU:N	2.59	0.50
1:B:6:ASP:HA	1:B:73:PRO:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:153:ILE:CG2	1:B:154:HIS:N	2.73	0.50
1:A:9:ASP:HB2	1:A:175:LEU:O	2.12	0.49
1:B:74:ARG:CG	1:B:74:ARG:NH1	2.72	0.49
1:A:91:SER:HB2	1:A:92:PRO:CD	2.43	0.49
1:A:140:HIS:HA	2:A:456:HOH:O	2.13	0.49
1:B:3:MET:O	1:B:4:ASP:HB2	2.11	0.49
1:A:37:ALA:N	1:A:45:PRO:HB3	2.28	0.49
1:B:91:SER:OG	1:B:92:PRO:HD2	2.13	0.49
1:B:17:ASN:ND2	1:B:67:LEU:O	2.47	0.48
1:B:141:ASP:CB	1:B:144:ASP:HB3	2.43	0.48
1:A:53:ASN:OD1	1:A:55:VAL:HG22	2.14	0.48
1:A:20:THR:OG1	1:A:178:ALA:HB3	2.14	0.47
1:A:113:PRO:HD3	2:A:521:HOH:O	2.14	0.47
1:A:169:ASN:N	1:A:170:PRO:CD	2.77	0.47
1:B:168:GLU:H	1:B:168:GLU:CD	2.18	0.47
1:A:164:VAL:HG23	1:A:166:THR:HG23	1.97	0.46
1:A:31:GLY:HA3	1:A:50:ARG:HD3	1.97	0.46
1:B:14:LEU:HD13	1:B:71:PHE:CE2	2.51	0.46
1:B:2:HIS:C	1:B:3:MET:HG3	2.35	0.46
1:A:4:ASP:CB	2:A:404:HOH:O	2.62	0.45
1:B:104:ALA:CA	1:B:164:VAL:HG12	2.47	0.45
1:A:95:THR:HG23	1:A:116:ASP:O	2.16	0.45
1:B:131:HIS:ND1	1:B:131:HIS:N	2.65	0.45
1:B:65:SER:O	1:B:66:ARG:HB2	2.16	0.45
1:B:41:ASN:O	1:B:42:GLU:C	2.55	0.44
1:A:23:LEU:HD13	1:A:61:ILE:HG13	1.99	0.44
1:A:95:THR:CG2	1:A:96:VAL:N	2.80	0.44
1:B:15:VAL:HG13	1:B:21:TYR:CE1	2.53	0.44
1:A:117:ILE:HG13	1:A:118:LEU:N	2.33	0.44
1:B:31:GLY:HA3	1:B:161:ARG:HH22	1.83	0.44
1:B:95:THR:HG21	1:B:112:LEU:HD21	2.00	0.43
1:B:132:VAL:HG12	1:B:133:TYR:N	2.32	0.43
1:A:113:PRO:O	1:A:114:GLU:C	2.57	0.43
1:B:145:VAL:O	1:B:146:LYS:HG3	2.18	0.43
1:A:95:THR:HG22	1:A:96:VAL:N	2.33	0.43
1:B:103:PRO:HB2	1:B:165:VAL:CG2	2.47	0.43
1:B:104:ALA:CB	1:B:164:VAL:HG12	2.48	0.43
1:B:97:VAL:HG12	1:B:98:ASP:N	2.34	0.43
1:A:90:ALA:CB	1:A:110:GLN:C	2.87	0.43
1:A:20:THR:O	1:A:177:LYS:HD2	2.20	0.42
1:B:140:HIS:O	1:B:141:ASP:O	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:LYS:O	1:B:179:LYS:HG3	2.18	0.42
1:A:127:HIS:CD2	1:A:127:HIS:C	2.91	0.42
1:A:85:PRO:HA	1:A:86:PRO:HD3	1.93	0.42
1:A:168:GLU:HB2	2:A:484:HOH:O	2.18	0.42
1:B:15:VAL:HG13	1:B:21:TYR:CZ	2.54	0.41
1:A:49:VAL:HG23	2:A:430:HOH:O	2.20	0.41
1:B:86:PRO:C	1:B:88:CYS:H	2.24	0.41
1:A:179:LYS:H	1:A:179:LYS:CD	2.33	0.41
1:B:90:ALA:HB1	1:B:111:LYS:HG3	2.02	0.41
1:B:125:VAL:CG1	1:B:134:LYS:HG3	2.51	0.41
1:B:30:HIS:O	1:B:50:ARG:HD3	2.20	0.41
1:A:28:TRP:CE3	1:A:28:TRP:HA	2.56	0.41
1:A:153:ILE:HG13	1:A:171:LEU:HD21	2.03	0.41
1:B:136:LEU:HD21	1:B:150:TYR:CZ	2.55	0.41
1:A:142:GLU:HB3	1:A:143:GLU:HG2	2.03	0.41
1:A:62:ARG:NH2	2:A:455:HOH:O	2.51	0.40
1:A:95:THR:OG1	1:A:117:ILE:HA	2.21	0.40
1:A:90:ALA:HB3	1:A:110:GLN:O	2.21	0.40
1:A:141:ASP:CG	1:A:142:GLU:H	2.25	0.40
1:A:115:LYS:HG3	2:A:410:HOH:O	2.21	0.40
1:B:134:LYS:HE2	2:B:509:HOH:O	2.21	0.40
1:B:137:TYR:CE2	1:B:139:GLN:HG2	2.57	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	176/187 (94%)	153 (87%)	13 (7%)	10 (6%)	1	4
1	B	179/187 (96%)	149 (83%)	21 (12%)	9 (5%)	2	6
All	All	355/374 (95%)	302 (85%)	34 (10%)	19 (5%)	2	5

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	140	HIS
1	A	141	ASP
1	A	142	GLU
1	A	143	GLU
1	B	128	SER
1	B	139	GLN
1	B	140	HIS
1	B	141	ASP
1	A	29	ALA
1	A	129	ASN
1	B	2	HIS
1	A	115	LYS
1	A	88	CYS
1	A	144	ASP
1	B	1	SER
1	B	45	PRO
1	B	158	ASN
1	B	170	PRO
1	A	45	PRO

### 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	155/162 (96%)	140 (90%)	15 (10%)	8	22
1	B	155/162 (96%)	138 (89%)	17 (11%)	6	17
All	All	310/324 (96%)	278 (90%)	32 (10%)	7	19

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ASP
1	A	27	ILE
1	A	44	CYS
1	A	63	ILE

*Continued on next page...*

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Mol	Chain	Res	Type
1	A	65	SER
1	A	69	SER
1	A	85	PRO
1	A	87	SER
1	A	92	PRO
1	A	126	SER
1	A	130	ILE
1	A	140	HIS
1	A	141	ASP
1	A	144	ASP
1	A	179	LYS
1	B	2	HIS
1	B	3	MET
1	B	4	ASP
1	B	35	GLU
1	B	41	ASN
1	B	47	THR
1	B	99	SER
1	B	110	GLN
1	B	112	LEU
1	B	114	GLU
1	B	131	HIS
1	B	139	GLN
1	B	141	ASP
1	B	157	ARG
1	B	158	ASN
1	B	168	GLU
1	B	179	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	HIS
1	A	158	ASN
1	B	26	HIS
1	B	41	ASN
1	B	139	GLN
1	B	158	ASN
1	B	160	ASN
1	B	169	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 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	178/187 (95%)	-0.41	1 (0%) 89 89	7, 22, 55, 94	0
1	B	181/187 (96%)	0.05	12 (6%) 18 14	9, 33, 90, 131	0
All	All	359/374 (95%)	-0.18	13 (3%) 42 37	7, 28, 79, 131	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	0	GLY	9.0
1	B	2	HIS	5.3
1	A	180	SER	5.0
1	B	1	SER	4.9
1	B	180	SER	3.6
1	B	144	ASP	3.4
1	B	127	HIS	3.3
1	B	129	ASN	2.9
1	B	128	SER	2.8
1	B	157	ARG	2.5
1	B	141	ASP	2.4
1	B	3	MET	2.3
1	B	130	ILE	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.