



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 03:05 am GMT

PDB ID : 3E4Z
Title : Crystal structure of human insulin degrading enzyme in complex with insulin-like growth factor II
Authors : Guo, Q.; Manolopoulou, M.; Tang, W.-J.
Deposited on : 2008-08-12
Resolution : 2.28 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
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

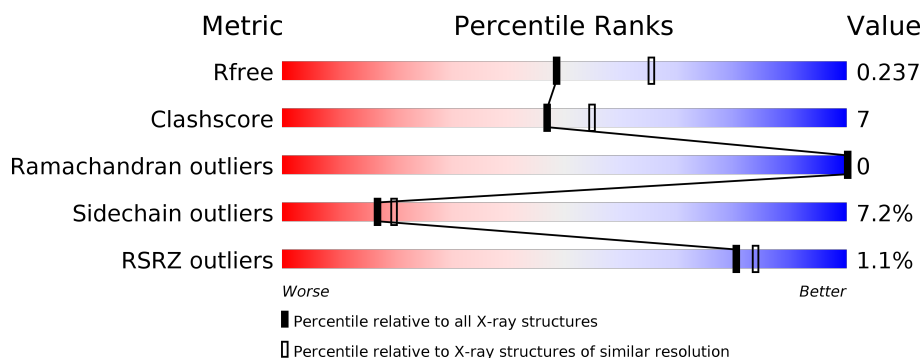
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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	5609 (2.30-2.26)
Clashscore	112137	6364 (2.30-2.26)
Ramachandran outliers	110173	6281 (2.30-2.26)
Sidechain outliers	110143	6281 (2.30-2.26)
RSRZ outliers	101464	5639 (2.30-2.26)

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	990	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 15%, green 79%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 79% 15% • • </div> </div>
1	B	990	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 16%, green 78%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 78% 16% • • </div> </div>
2	C	67	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 4%, orange 10%, yellow 1%, green 87%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 4% 10% • • 87% </div> </div>
2	D	67	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 4%, orange 9%, yellow 1%, green 87%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 4% 9% • 87% </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ZN	B	2	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16411 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 Insulin-degrading enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	953	Total	C	N	O	S	0	0	0
			7783	5014	1306	1441	22			
1	B	952	Total	C	N	O	S	0	0	0
			7778	5011	1305	1440	22			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	MET	-	EXPRESSION TAG	UNP Q5T5N2
A	31	HIS	-	EXPRESSION TAG	UNP Q5T5N2
A	32	HIS	-	EXPRESSION TAG	UNP Q5T5N2
A	33	HIS	-	EXPRESSION TAG	UNP Q5T5N2
A	34	HIS	-	EXPRESSION TAG	UNP Q5T5N2
A	35	HIS	-	EXPRESSION TAG	UNP Q5T5N2
A	36	HIS	-	EXPRESSION TAG	UNP Q5T5N2
A	37	ALA	-	EXPRESSION TAG	UNP Q5T5N2
A	38	ALA	-	EXPRESSION TAG	UNP Q5T5N2
A	39	GLY	-	EXPRESSION TAG	UNP Q5T5N2
A	40	ILE	-	EXPRESSION TAG	UNP Q5T5N2
A	41	PRO	-	EXPRESSION TAG	UNP Q5T5N2
A	110	LEU	CYS	ENGINEERED	UNP Q5T5N2
A	111	GLN	GLU	ENGINEERED	UNP Q5T5N2
A	171	SER	CYS	ENGINEERED	UNP Q5T5N2
A	178	ALA	CYS	ENGINEERED	UNP Q5T5N2
A	257	VAL	CYS	ENGINEERED	UNP Q5T5N2
A	414	LEU	CYS	ENGINEERED	UNP Q5T5N2
A	573	ASN	CYS	ENGINEERED	UNP Q5T5N2
A	590	SER	CYS	ENGINEERED	UNP Q5T5N2
A	789	SER	CYS	ENGINEERED	UNP Q5T5N2
A	812	ALA	CYS	ENGINEERED	UNP Q5T5N2
A	819	ALA	CYS	ENGINEERED	UNP Q5T5N2
A	904	SER	CYS	ENGINEERED	UNP Q5T5N2
A	908	TYR	TRP	ENGINEERED	UNP Q5T5N2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	30	MET	-	EXPRESSION TAG	UNP Q5T5N2
B	31	HIS	-	EXPRESSION TAG	UNP Q5T5N2
B	32	HIS	-	EXPRESSION TAG	UNP Q5T5N2
B	33	HIS	-	EXPRESSION TAG	UNP Q5T5N2
B	34	HIS	-	EXPRESSION TAG	UNP Q5T5N2
B	35	HIS	-	EXPRESSION TAG	UNP Q5T5N2
B	36	HIS	-	EXPRESSION TAG	UNP Q5T5N2
B	37	ALA	-	EXPRESSION TAG	UNP Q5T5N2
B	38	ALA	-	EXPRESSION TAG	UNP Q5T5N2
B	39	GLY	-	EXPRESSION TAG	UNP Q5T5N2
B	40	ILE	-	EXPRESSION TAG	UNP Q5T5N2
B	41	PRO	-	EXPRESSION TAG	UNP Q5T5N2
B	110	LEU	CYS	ENGINEERED	UNP Q5T5N2
B	111	GLN	GLU	ENGINEERED	UNP Q5T5N2
B	171	SER	CYS	ENGINEERED	UNP Q5T5N2
B	178	ALA	CYS	ENGINEERED	UNP Q5T5N2
B	257	VAL	CYS	ENGINEERED	UNP Q5T5N2
B	414	LEU	CYS	ENGINEERED	UNP Q5T5N2
B	573	ASN	CYS	ENGINEERED	UNP Q5T5N2
B	590	SER	CYS	ENGINEERED	UNP Q5T5N2
B	789	SER	CYS	ENGINEERED	UNP Q5T5N2
B	812	ALA	CYS	ENGINEERED	UNP Q5T5N2
B	819	ALA	CYS	ENGINEERED	UNP Q5T5N2
B	904	SER	CYS	ENGINEERED	UNP Q5T5N2
B	908	TYR	TRP	ENGINEERED	UNP Q5T5N2

- Molecule 2 is a protein called Insulin-like growth factor II.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	9	Total	C	N	O	0	0	0
			62	39	10	13			
2	D	9	Total	C	N	O	0	0	0
			62	39	10	13			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		
3	C	1	Total	Zn	0	0
			1	1		

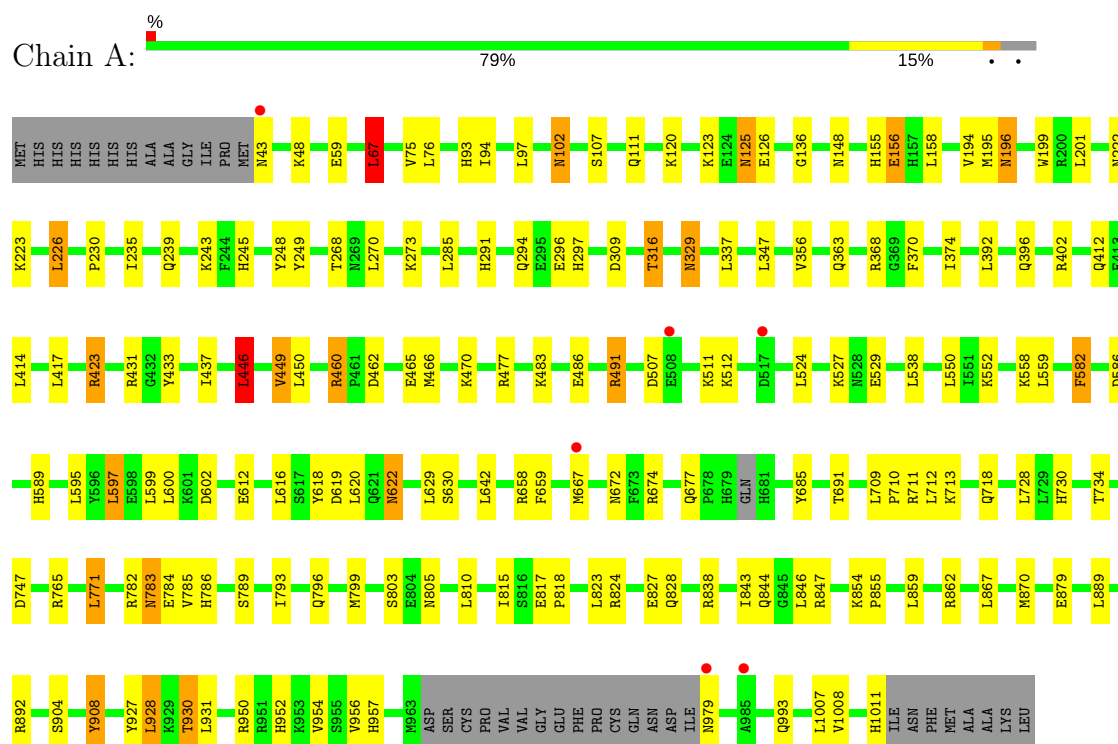
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	384	Total 384	O 384	0	0
4	B	338	Total 338	O 338	0	0
4	C	2	Total 2	O 2	0	0

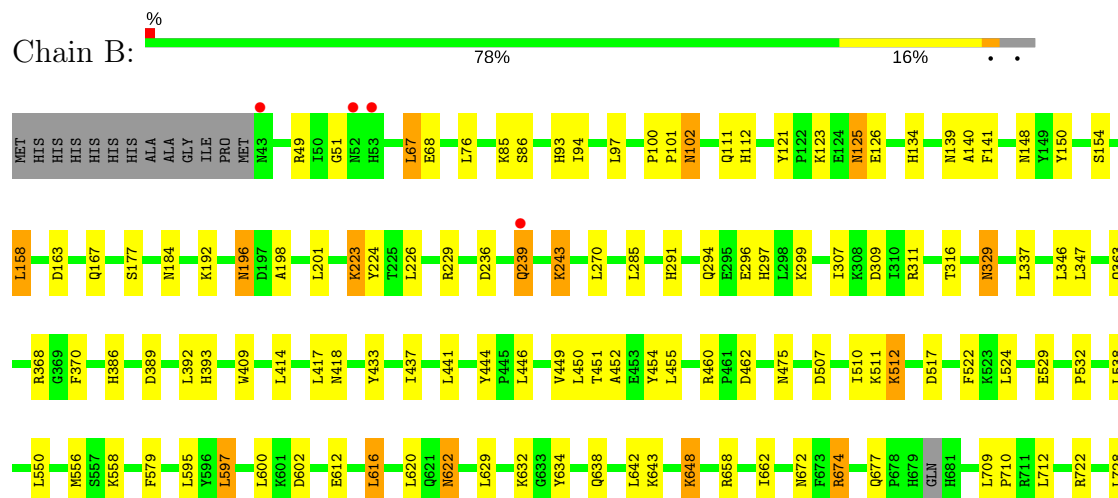
3 Residue-property plots

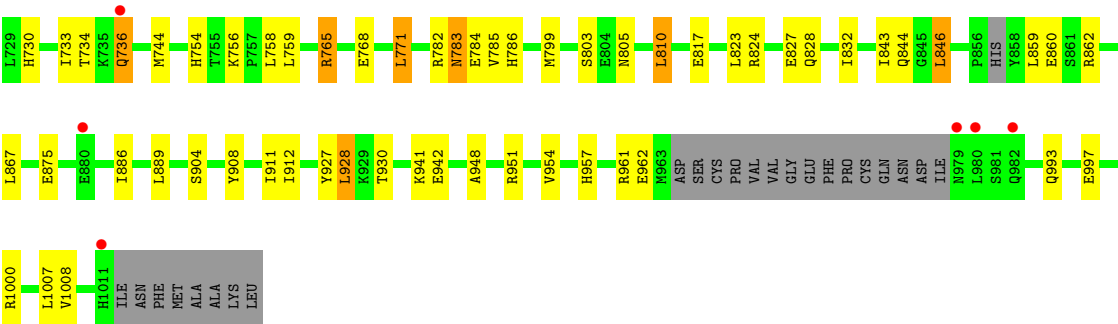
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Insulin-degrading enzyme

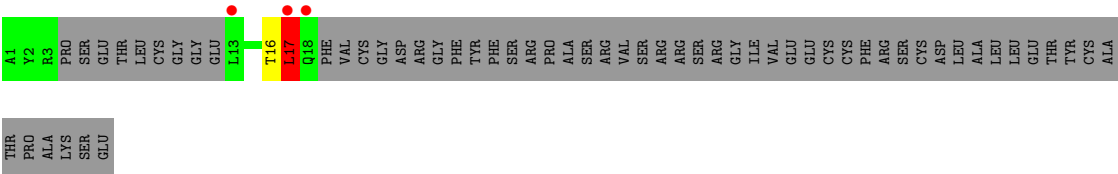


• Molecule 1: Insulin-degrading enzyme

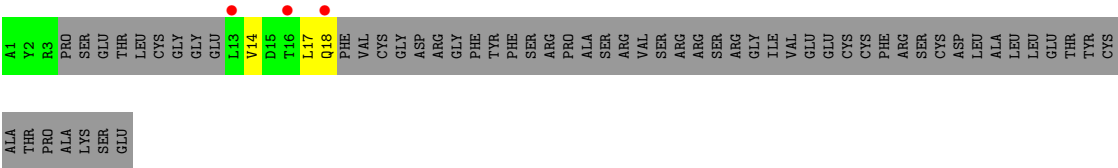




● Molecule 2: Insulin-like growth factor II



● Molecule 2: Insulin-like growth factor II



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	263.03Å 263.03Å 90.82Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.28 49.71 – 2.28	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-2.28) 99.7 (49.71-2.28)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.196 , 0.230 0.206 , 0.237	Depositor DCC
R_{free} test set	8139 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	35.4	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16411	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.86% 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, 0.333 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: ZN

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	1/7975 (0.0%)	0.68	6/10787 (0.1%)
1	B	0.57	0/7969	0.66	4/10777 (0.0%)
2	C	0.68	0/60	1.15	1/80 (1.2%)
2	D	0.61	0/60	0.79	0/80
All	All	0.58	1/16064 (0.0%)	0.67	11/21724 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	908	TYR	CD1-CE1	-5.36	1.31	1.39

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	LEU	CA-CB-CG	6.59	130.46	115.30
1	B	67	LEU	CA-CB-CG	6.34	129.88	115.30
1	B	311	ARG	NE-CZ-NH2	-5.75	117.42	120.30
2	C	17	LEU	CA-CB-CG	5.64	128.27	115.30
1	B	311	ARG	NE-CZ-NH1	5.51	123.06	120.30

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	7783	0	7721	106	1
1	B	7778	0	7718	111	0
2	C	62	0	60	4	0
2	D	62	0	60	4	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	384	0	0	30	0
4	B	338	0	0	23	0
4	C	2	0	0	0	0
All	All	16411	0	15559	221	1

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 7.

The worst 5 of 221 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:908:TYR:HE1	4:A:1368:HOH:O	1.18	1.23
1:A:667:MET:HG3	4:A:1031:HOH:O	1.39	1.22
1:A:908:TYR:CE1	4:A:1368:HOH:O	1.94	1.10
4:A:1311:HOH:O	2:C:17:LEU:HB3	1.53	1.08
1:B:154:SER:HB3	4:B:1351:HOH:O	1.53	1.08

All (1) 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)
1:A:460:ARG:NH2	1:A:747:ASP:OD1[3_655]	2.05	0.15

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	947/990 (96%)	924 (98%)	23 (2%)	0	100	100
1	B	944/990 (95%)	925 (98%)	19 (2%)	0	100	100
2	C	5/67 (8%)	3 (60%)	2 (40%)	0	100	100
2	D	5/67 (8%)	5 (100%)	0	0	100	100
All	All	1901/2114 (90%)	1857 (98%)	44 (2%)	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	846/880 (96%)	783 (93%)	63 (7%)	16	19
1	B	846/880 (96%)	787 (93%)	59 (7%)	18	21
2	C	6/57 (10%)	5 (83%)	1 (17%)	2	2
2	D	6/57 (10%)	6 (100%)	0	100	100
All	All	1704/1874 (91%)	1581 (93%)	123 (7%)	17	20

5 of 123 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	867	LEU
1	B	125	ASN
1	B	823	LEU
1	A	928	LEU
1	A	1007	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	957	HIS
1	B	184	ASN
1	B	828	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	52	ASN
1	B	102	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, 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	953/990 (96%)	-0.27	6 (0%) 89 91	20, 32, 47, 62	0
1	B	952/990 (96%)	-0.22	10 (1%) 80 84	25, 37, 50, 71	0
2	C	9/67 (13%)	1.58	3 (33%) 0 0	37, 66, 67, 67	0
2	D	9/67 (13%)	1.27	3 (33%) 0 0	36, 73, 75, 75	0
All	All	1923/2114 (90%)	-0.23	22 (1%) 80 84	20, 35, 49, 75	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	979	ASN	3.9
1	B	43	ASN	3.6
2	C	17	LEU	3.1
2	C	18	GLN	3.0
1	B	52	ASN	2.9

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
3	ZN	B	2	1/1	0.99	0.28	2.17	2,2,2,2	0
3	ZN	C	68	1/1	0.99	0.26	1.40	2,2,2,2	0

6.5 Other polymers [i](#)

There are no such residues in this entry.