



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 02:30 am GMT

PDB ID : 4LTE
Title : Structure of Cysteine-free Human Insulin Degrading Enzyme in Complex with
Macrocyclic Inhibitor
Authors : Foda, Z.H.; Seeliger, M.A.; Saghatelian, A.; Liu, D.R.
Deposited on : 2013-07-23
Resolution : 2.71 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
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28683
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

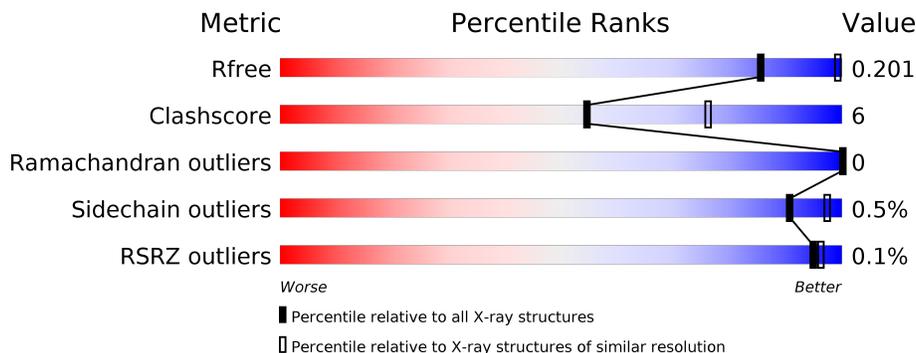
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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	978	
1	B	978	
2	M	5	
2	N	5	

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
2	LYN	M	3	-	-	X	-
2	LYN	N	3	-	-	X	-
4	EPE	A	1102	-	-	-	X
4	EPE	B	1102	-	-	-	X

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 16250 atoms, of which 34 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
			Total	C	N	O	S			
1	A	954	7771	5005	1304	1440	22	0	0	0
1	B	954	7760	5002	1302	1434	22	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	110	LEU	CYS	ENGINEERED MUTATION	UNP P14735
A	111	GLN	GLU	ENGINEERED MUTATION	UNP P14735
A	171	SER	CYS	ENGINEERED MUTATION	UNP P14735
A	178	ALA	CYS	ENGINEERED MUTATION	UNP P14735
A	257	VAL	CYS	ENGINEERED MUTATION	UNP P14735
A	414	LEU	CYS	ENGINEERED MUTATION	UNP P14735
A	573	ASN	CYS	ENGINEERED MUTATION	UNP P14735
A	590	SER	CYS	ENGINEERED MUTATION	UNP P14735
A	789	SER	CYS	ENGINEERED MUTATION	UNP P14735
A	812	ALA	CYS	ENGINEERED MUTATION	UNP P14735
A	819	ALA	CYS	ENGINEERED MUTATION	UNP P14735
A	904	SER	CYS	ENGINEERED MUTATION	UNP P14735
A	966	ASN	CYS	ENGINEERED MUTATION	UNP P14735
A	974	ALA	CYS	ENGINEERED MUTATION	UNP P14735
B	110	LEU	CYS	ENGINEERED MUTATION	UNP P14735
B	111	GLN	GLU	ENGINEERED MUTATION	UNP P14735
B	171	SER	CYS	ENGINEERED MUTATION	UNP P14735
B	178	ALA	CYS	ENGINEERED MUTATION	UNP P14735
B	257	VAL	CYS	ENGINEERED MUTATION	UNP P14735
B	414	LEU	CYS	ENGINEERED MUTATION	UNP P14735
B	573	ASN	CYS	ENGINEERED MUTATION	UNP P14735
B	590	SER	CYS	ENGINEERED MUTATION	UNP P14735
B	789	SER	CYS	ENGINEERED MUTATION	UNP P14735
B	812	ALA	CYS	ENGINEERED MUTATION	UNP P14735
B	819	ALA	CYS	ENGINEERED MUTATION	UNP P14735

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Chain	Residue	Modelled	Actual	Comment	Reference
B	904	SER	CYS	ENGINEERED MUTATION	UNP P14735
B	966	ASN	CYS	ENGINEERED MUTATION	UNP P14735
B	974	ALA	CYS	ENGINEERED MUTATION	UNP P14735

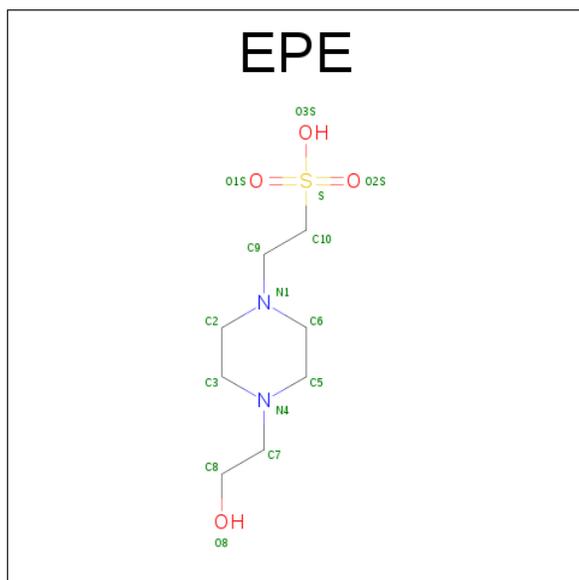
- Molecule 2 is a protein called Macrocytic Inhibitor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	M	4	Total	C	N	O	0	0	0
			45	35	4	6			
2	N	4	Total	C	N	O	0	0	0
			45	35	4	6			

- 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	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
4	A	1	Total	C	H	N	O	S	0	0
			32	8	17	2	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			S
4	B	1	32	8	17	2	4	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	297	Total 297	O 297	0	0
5	B	265	Total 265	O 265	0	0
5	M	1	Total 1	O 1	0	0



- Molecule 2: Macrocyclic Inhibitor



4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	261.97Å 261.97Å 90.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	130.99 – 2.71 226.88 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (130.99-2.71) 95.3 (226.88-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.69Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.158 , 0.200 0.160 , 0.201	Depositor DCC
R_{free} test set	2207 reflections (2.27%)	DCC
Wilson B-factor (Å ²)	31.8	Xtrriage
Anisotropy	0.020	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.028 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16250	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.93% 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: EPE, ZN, DFF, FUM, LYN

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	0.51	0/7966	0.63	1/10784 (0.0%)
1	B	0.53	0/7955	0.63	1/10770 (0.0%)
2	M	6.45	6/10 (60.0%)	8.01	6/11 (54.5%)
2	N	6.40	6/10 (60.0%)	8.90	6/11 (54.5%)
All	All	0.57	12/15941 (0.1%)	0.69	14/21576 (0.1%)

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	M	0	1
2	N	0	1
All	All	0	2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	1	PHE	CG-CD2	9.78	1.53	1.38
2	N	1	PHE	CG-CD2	9.30	1.52	1.38
2	M	1	PHE	CD2-CE2	9.12	1.57	1.39
2	N	1	PHE	CG-CD1	9.02	1.52	1.38
2	N	1	PHE	CD2-CE2	8.64	1.56	1.39

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	1	PHE	CB-CG-CD2	-16.78	109.06	120.80
2	N	1	PHE	CB-CG-CD1	-16.62	109.16	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	1	PHE	CB-CG-CD2	-16.23	109.44	120.80
2	M	1	PHE	CB-CG-CD1	-14.24	110.83	120.80
2	N	1	PHE	CG-CD2-CE2	-10.80	108.92	120.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	M	1	PHE	Sidechain
2	N	1	PHE	Sidechain

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	7771	0	7665	85	3
1	B	7760	0	7663	88	3
2	M	45	0	35	19	0
2	N	45	0	35	21	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	15	17	17	1	0
4	B	15	17	17	0	0
5	A	297	0	0	5	0
5	B	265	0	0	3	0
5	M	1	0	0	0	0
All	All	16216	34	15432	187	3

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 6.

The worst 5 of 187 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:M:3:LYN:HB2	2:M:4:FUM:H4	1.34	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:946:VAL:HA	1:A:951:ARG:NH1	1.70	1.06
1:A:780:GLN:HE21	1:A:959:LEU:HD11	1.32	0.95
2:M:3:LYN:HB2	2:M:4:FUM:C4	2.03	0.88
1:B:49:ARG:NH2	1:B:447:GLU:OE2	2.07	0.87

All (3) 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:934:GLU:OE2	1:B:53:HIS:CD2[6_554]	1.52	0.68
1:A:934:GLU:OE2	1:B:53:HIS:NE2[6_554]	1.66	0.54
1:A:878:THR:OG1	1:B:457:GLU:OE2[6_554]	2.09	0.11

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	950/978 (97%)	928 (98%)	22 (2%)	0	100	100
1	B	950/978 (97%)	928 (98%)	22 (2%)	0	100	100
All	All	1900/1956 (97%)	1856 (98%)	44 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	840/870 (97%)	836 (100%)	4 (0%)	91	97
1	B	838/870 (96%)	833 (99%)	5 (1%)	89	97
All	All	1678/1740 (96%)	1669 (100%)	9 (0%)	91	97

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	353	LYS
1	B	962	GLU
1	B	743	GLN
1	A	933	LYS
1	B	736	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	724	HIS
1	B	780	GLN
1	A	780	GLN
1	A	363	GLN
1	B	386	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

4 non-standard protein/DNA/RNA residues 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	DFP	M	2	2	20,20,21	1.03	2 (10%)	25,26,28	1.59	2 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	LYN	M	3	2	9,9,9	2.37	1 (11%)	8,10,10	1.83	2 (25%)
2	DFE	N	2	2	20,20,21	0.89	1 (5%)	25,26,28	1.75	4 (16%)
2	LYN	N	3	2	9,9,9	2.58	1 (11%)	8,10,10	2.25	2 (25%)

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	DFE	M	2	2	-	0/12/14/16	0/2/2/2
2	LYN	M	3	2	-	0/8/9/9	0/0/0/0
2	DFE	N	2	2	-	0/12/14/16	0/2/2/2
2	LYN	N	3	2	-	0/8/9/9	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	2	DFE	CZ-C7	2.05	1.53	1.49
2	M	2	DFE	C4-C7	2.14	1.53	1.49
2	M	2	DFE	CZ-C7	2.38	1.53	1.49
2	M	3	LYN	C-NT	6.95	1.46	1.32
2	N	3	LYN	C-NT	7.56	1.47	1.32

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	2	DFE	CG-CB-CA	-4.87	104.48	114.29
2	M	2	DFE	CG-CB-CA	-4.60	105.01	114.29
2	M	2	DFE	CB-CA-C	-4.14	103.43	111.41
2	N	3	LYN	O-C-NT	-4.10	116.78	123.06
2	N	2	DFE	CB-CA-C	-3.91	103.88	111.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	M	2	DFE	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	M	3	LYN	14	0
2	N	2	DFE	3	0
2	N	3	LYN	13	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are 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	$\# Z > 2$
4	EPE	A	1102	-	15,15,15	0.62	0	18,20,20	2.49	7 (38%)
4	EPE	B	1102	-	15,15,15	0.75	1 (6%)	18,20,20	2.47	5 (27%)

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
4	EPE	A	1102	-	-	0/9/19/19	0/1/1/1
4	EPE	B	1102	-	-	0/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1102	EPE	C10-S	2.48	1.81	1.77

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1102	EPE	C2-C3-N4	2.14	114.96	110.63
4	A	1102	EPE	C7-N4-C5	2.39	117.39	111.26
4	A	1102	EPE	C9-N1-C2	2.61	117.95	111.26
4	A	1102	EPE	O3S-S-C10	3.28	110.09	106.06
4	B	1102	EPE	C7-N4-C3	3.54	120.34	111.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1102	EPE	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, 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	954/978 (97%)	-0.17	0 100 100	17, 28, 49, 83	0
1	B	954/978 (97%)	-0.25	0 100 100	18, 29, 49, 84	0
2	M	1/5 (20%)	3.68	1 (100%) 0 0	79, 79, 79, 79	0
2	N	1/5 (20%)	3.42	1 (100%) 0 0	75, 75, 75, 75	0
All	All	1910/1966 (97%)	-0.21	2 (0%) 95 96	17, 29, 49, 84	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	M	1	PHE	3.7
2	N	1	PHE	3.4

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
2	DFD	M	2	19/20	0.88	0.35	-	34,67,96,97	0
2	LYN	N	3	10/10	0.80	0.56	-	73,85,103,113	0
2	LYN	M	3	10/10	0.76	0.56	-	68,87,101,101	0
2	DFD	N	2	19/20	0.89	0.34	-	31,61,104,109	0

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
4	EPE	B	1102	15/15	0.96	0.21	3.60	40,51,61,62	0
4	EPE	A	1102	15/15	0.98	0.19	2.10	29,47,56,66	0
3	ZN	A	1101	1/1	0.99	0.16	-	37,37,37,37	0
3	ZN	B	1101	1/1	0.98	0.14	-	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.