Full wwPDB X-ray Structure Validation Report (i)

Mar 9, 2026 – 04:08 AM UTC

PDB ID	:	2VJN / pdb_00002vjn
Title	:	Formyl-CoA transferase mutant variant G260A
Authors	:	Berthold, C.L.; Toyota, C.G.; Richards, N.G.J.; Lindqvist, Y.
Deposited on	:	2007-12-11
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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

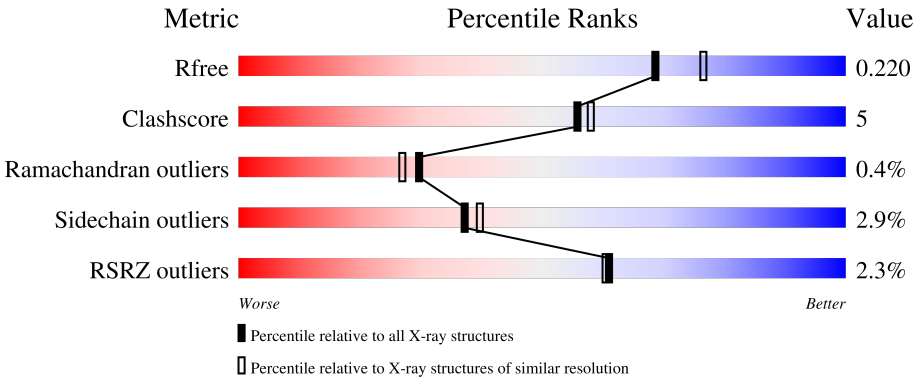
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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 of the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	428	2% 90% 9%
1	B	428	3% 90% 9%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7552 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.

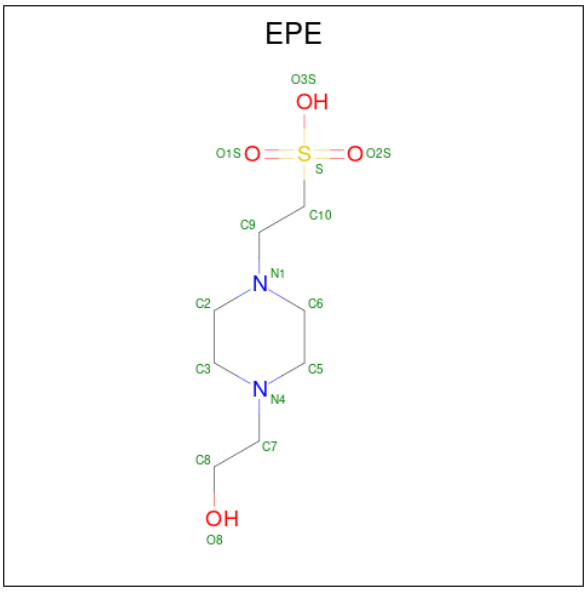
- Molecule 1 is a protein called FORMYL-COENZYME A TRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	2	0
			3324	2103	569	629	23			
1	B	427	Total	C	N	O	S	0	5	0
			3340	2114	568	635	23			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	186	ILE	MET	conflict	UNP O06644
B	186	ILE	MET	conflict	UNP O06644
A	260	ALA	GLY	engineered mutation	UNP O06644
B	260	ALA	GLY	engineered mutation	UNP O06644

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is water.

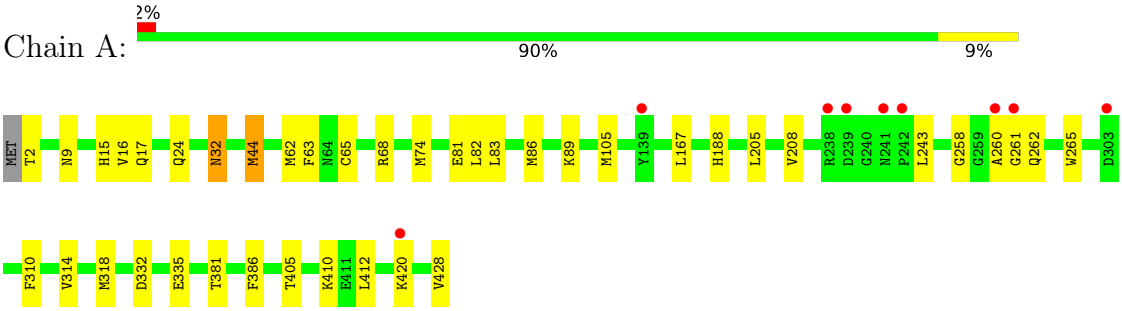
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	415	Total	O	0	0
			415	415		
3	B	458	Total	O	0	0
			458	458		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

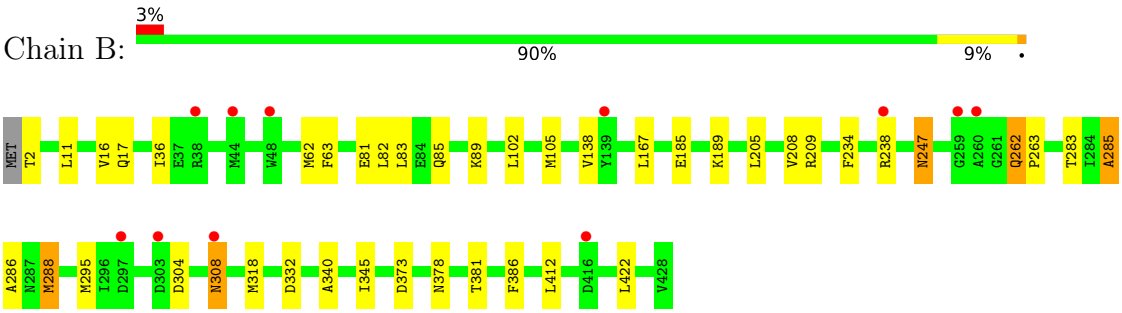
• Molecule 1: FORMYL-COENZYME A TRANSFERASE

Chain A:



• Molecule 1: FORMYL-COENZYME A TRANSFERASE

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	97.26Å 97.26Å 193.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 30.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (30.00-2.00) 99.3 (30.00-2.00)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.30 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.169 , 0.215 0.175 , 0.220	Depositor DCC
R_{free} test set	3207 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	13.6	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 44.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7552	wwPDB-VP
Average B, all atoms (Å^2)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: EPE

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	0.56	0/3404	0.75	1/4604 (0.0%)
1	B	0.62	3/3429 (0.1%)	0.76	0/4638
All	All	0.59	3/6833 (0.0%)	0.76	1/9242 (0.0%)

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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	286	ALA	CA-CB	-6.66	1.43	1.53
1	B	285	ALA	CA-CB	-6.60	1.43	1.53
1	B	286	ALA	C-O	-5.98	1.17	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	258	GLY	N-CA-C	5.10	119.92	113.24

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	261	GLY	Peptide

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	3324	0	3264	31	0
1	B	3340	0	3281	36	0
2	B	15	0	17	0	0
3	A	415	0	0	2	0
3	B	458	0	0	3	0
All	All	7552	0	6562	62	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 5.

All (62) 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:405:THR:HG21	1:A:428:VAL:CG1	1.90	1.01
1:B:234:PHE:CZ	1:B:318:MET:HE3	1.98	0.98
1:B:295:MET:CE	1:B:345:ILE:HD12	1.96	0.96
1:B:295:MET:HE3	1:B:345:ILE:HD12	1.49	0.90
1:A:260:ALA:HB2	3:B:2193:HOH:O	1.74	0.87
1:B:234:PHE:CE1	1:B:318:MET:HE3	2.12	0.84
1:A:405:THR:HG21	1:A:428:VAL:HG11	1.61	0.80
1:B:11:LEU:HD11	1:B:36:ILE:HD11	1.65	0.79
1:A:405:THR:CG2	1:A:428:VAL:HG11	2.16	0.75
1:A:44:MET:HE3	1:A:44:MET:H	1.51	0.74
1:A:405:THR:HG21	1:A:428:VAL:HG13	1.67	0.73
1:A:405:THR:CG2	1:A:428:VAL:CG1	2.67	0.72
1:B:318:MET:HA	1:B:318:MET:HE2	1.72	0.70
1:B:295:MET:HE1	1:B:345:ILE:HD12	1.77	0.66
1:A:44:MET:HE3	1:A:44:MET:N	2.12	0.65
1:B:288:MET:HA	1:B:288:MET:HE2	1.80	0.64
1:B:247:ASN:HD22	1:B:247:ASN:H	1.47	0.62
1:B:81[B]:GLU:OE2	1:B:85:GLN:NE2	2.34	0.60
1:A:83:LEU:HA	1:A:86:MET:HE3	1.82	0.60
1:B:262:GLN:HG3	1:B:263:PRO:HD2	1.84	0.59
1:A:167:LEU:HD21	1:B:167:LEU:HD21	1.85	0.58
1:B:17:GLN:HG3	1:B:63:PHE:CE2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:208:VAL:O	1:B:208:VAL:HG12	2.04	0.57
1:B:262:GLN:HB3	1:B:283[B]:THR:HG23	1.87	0.56
1:A:208:VAL:HG12	1:A:208:VAL:O	2.06	0.55
1:B:262:GLN:HG2	1:B:285:ALA:HA	1.87	0.55
1:A:44:MET:H	1:A:44:MET:CE	2.18	0.54
1:B:295:MET:CE	1:B:340:ALA:HA	2.37	0.54
1:A:32:ASN:HD22	1:A:32:ASN:C	2.15	0.53
1:A:24:GLN:HE21	1:A:65:CYS:H	1.55	0.53
1:A:167:LEU:CD2	1:B:167:LEU:HD21	2.40	0.52
1:A:89:LYS:HE2	1:A:412:LEU:HD23	1.91	0.51
1:B:283[A]:THR:HG22	3:B:2325:HOH:O	2.11	0.50
1:A:17:GLN:HG3	1:A:63:PHE:CE2	2.48	0.49
1:A:74:MET:HB3	1:A:105:MET:HE3	1.93	0.49
1:A:188:HIS:HE1	1:B:185:GLU:OE1	1.97	0.48
1:B:247:ASN:HD22	1:B:247:ASN:N	2.11	0.46
1:A:260:ALA:HB2	1:B:17:GLN:HE22	1.81	0.46
1:A:32:ASN:HD21	1:A:68:ARG:HH21	1.64	0.46
1:A:9:ASN:HD22	1:A:32:ASN:HB3	1.81	0.46
1:A:63:PHE:CZ	1:B:209:ARG:HD2	2.52	0.45
1:B:373:ASP:H	1:B:378:ASN:ND2	2.14	0.45
1:B:82:LEU:HD11	1:B:422:LEU:HD13	1.99	0.45
1:A:89:LYS:CE	1:A:412:LEU:HD23	2.47	0.45
1:A:243:LEU:HD11	3:A:2186:HOH:O	2.17	0.44
1:A:265:TRP:CD2	1:A:318:MET:HE1	2.52	0.44
1:B:247:ASN:H	1:B:247:ASN:ND2	2.14	0.44
1:B:89:LYS:HE2	1:B:412:LEU:HD23	1.99	0.43
1:B:262:GLN:HB3	1:B:283[B]:THR:CG2	2.48	0.43
1:B:295:MET:HE2	1:B:340:ALA:HA	1.99	0.43
1:B:288:MET:HE2	1:B:288:MET:CA	2.47	0.43
1:B:62:MET:HE3	1:B:381:THR:HA	2.01	0.42
1:A:420:LYS:HG3	3:A:2409:HOH:O	2.19	0.42
1:A:62:MET:HE3	1:A:381:THR:HA	2.02	0.42
1:B:304:ASP:O	1:B:308:ASN:HB2	2.19	0.42
1:A:405:THR:CG2	1:A:428:VAL:HG13	2.40	0.42
1:A:310:PHE:O	1:A:314:VAL:HG23	2.20	0.41
1:B:102:LEU:HA	1:B:105:MET:HG2	2.02	0.41
1:A:332:ASP:OD1	1:A:335:GLU:HG2	2.21	0.41
1:B:208:VAL:O	1:B:208:VAL:CG1	2.69	0.40
1:B:238:ARG:HG3	3:B:2458:HOH:O	2.20	0.40
1:B:11:LEU:CD1	1:B:36:ILE:HD11	2.43	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	427/428 (100%)	419 (98%)	6 (1%)	2 (0%)	24	21
1	B	430/428 (100%)	419 (97%)	10 (2%)	1 (0%)	43	42
All	All	857/856 (100%)	838 (98%)	16 (2%)	3 (0%)	30	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	16	VAL
1	A	16	VAL
1	A	262	GLN

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	352/351 (100%)	343 (97%)	9 (3%)	40	44
1	B	355/351 (101%)	344 (97%)	11 (3%)	35	37
All	All	707/702 (101%)	687 (97%)	20 (3%)	37	41

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	15	HIS
1	A	32	ASN

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Mol	Chain	Res	Type
1	A	44	MET
1	A	81	GLU
1	A	82	LEU
1	A	205	LEU
1	A	386	PHE
1	A	410	LYS
1	B	2	THR
1	B	83	LEU
1	B	138	VAL
1	B	189	LYS
1	B	205	LEU
1	B	247	ASN
1	B	262	GLN
1	B	288	MET
1	B	308	ASN
1	B	332	ASP
1	B	386	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	17	GLN
1	A	24	GLN
1	A	32	ASN
1	A	54	ASN
1	A	113	GLN
1	A	188	HIS
1	A	206	ASN
1	B	17	GLN
1	B	135	HIS
1	B	206	ASN
1	B	231	GLN
1	B	233	ASN
1	B	241	ASN
1	B	247	ASN
1	B	308	ASN
1	B	342	GLN
1	B	378	ASN
1	B	426	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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	EPE	B	1429	-	15,15,15	0.68	1 (6%)	19,20,20	0.88	0

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	EPE	B	1429	-	-	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)
2	B	1429	EPE	C10-S	2.15	1.80	1.77

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

6.1 Protein, DNA and RNA chains

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^{th} 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	427/428 (99%)	-0.29	9 (2%)	63	63	4, 10, 26, 33	2 (0%)
1	B	427/428 (99%)	-0.31	11 (2%)	57	56	5, 10, 25, 31	5 (1%)
All	All	854/856 (99%)	-0.30	20 (2%)	61	60	4, 10, 26, 33	7 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	261	GLY	5.0
1	A	260	ALA	4.5
1	B	48	TRP	4.4
1	B	259	GLY	4.2
1	A	303	ASP	3.1
1	A	239	ASP	3.0
1	B	260	ALA	3.0
1	B	308	ASN	2.8
1	A	420	LYS	2.7
1	B	297	ASP	2.4
1	B	416	ASP	2.4
1	B	44	MET	2.4
1	B	303	ASP	2.4
1	A	139	TYR	2.3
1	B	139	TYR	2.3
1	B	38	ARG	2.3
1	A	242	PRO	2.3
1	A	241	ASN	2.3
1	B	238	ARG	2.3
1	A	238	ARG	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 oligosaccharides 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. The B-factors column lists the minimum, median, 95^{th} 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	B-factors(Å^2)	Q<0.9
2	EPE	B	1429	15/15	0.95	0.09	12,15,19,21	0

6.5 Other polymers (i)

There are no such residues in this entry.