



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:50 am GMT

PDB ID : 2AZ4
Title : Crystal Structure of a Protein of Unknown Function from *Enterococcus faecalis* V583
Authors : Zhang, R.; Maltseva, N.; Moy, S.; Collart, F.; Cymborowski, M.; Minor, W.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2005-09-09
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

<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

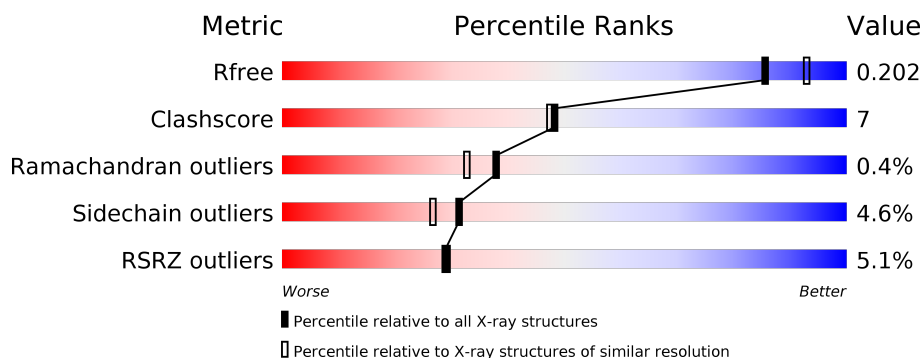
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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 ≥ 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	429	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 13%, green 84%, grey 12%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 84% 13% ... </div> </div>
1	B	429	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 9%, orange 1%, yellow 15%, green 82%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 9% 82% 15% .. </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7404 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 hypothetical protein EF2904.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	425	Total	C	N	O	S	0	0	0
			3427	2201	568	650	8			
1	B	426	Total	C	N	O	S	0	0	0
			3436	2207	570	651	8			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		

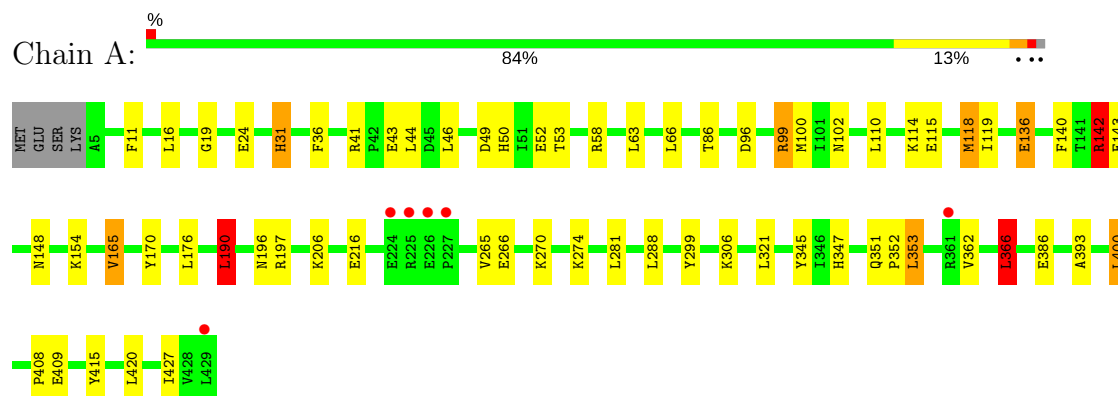
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	341	Total	O	0	0
			341	341		
3	B	196	Total	O	0	0
			196	196		

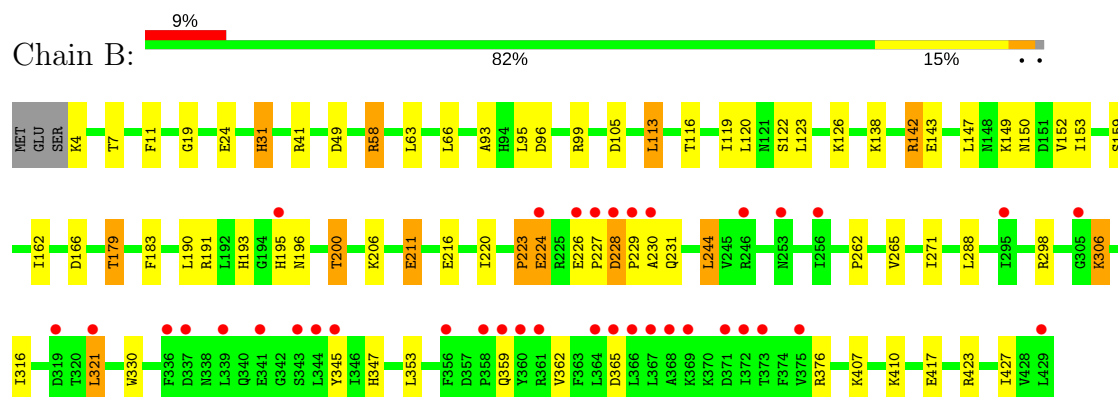
3 Residue-property plots [i](#)

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: hypothetical protein EF2904



• Molecule 1: hypothetical protein EF2904



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.00Å 74.18Å 214.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 42.04 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.8 (50.00-2.00) 96.8 (42.04-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.198 , 0.244 0.202 , 0.202	Depositor DCC
R_{free} test set	3085 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.510	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7404	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% 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

5.1 Standard geometry

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	0.58	0/3509	0.72	7/4771 (0.1%)
1	B	0.52	0/3518	0.65	0/4782
All	All	0.55	0/7027	0.69	7/9553 (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
1	B	0	1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	142	ARG	NE-CZ-NH2	-8.02	116.29	120.30
1	A	99	ARG	NE-CZ-NH2	-6.93	116.83	120.30
1	A	142	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	A	118	MET	CG-SD-CE	-5.88	90.78	100.20
1	A	190	LEU	CA-CB-CG	5.51	127.98	115.30
1	A	400	LEU	CA-CB-CG	5.41	127.73	115.30
1	A	366	LEU	CA-CB-CG	5.11	127.06	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	223	PRO	Peptide

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	3427	0	3390	38	0
1	B	3436	0	3403	56	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	341	0	0	4	0
3	B	196	0	0	8	0
All	All	7404	0	6793	94	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 7.

All (94) 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:223:PRO:HA	1:B:224:GLU:HB2	1.29	1.12
1:B:228:ASP:HB3	1:B:229:PRO:HA	1.44	0.98
1:A:41:ARG:NE	1:A:43:GLU:OE2	2.09	0.86
1:B:191:ARG:O	1:B:200:THR:HG21	1.77	0.84
1:B:223:PRO:CA	1:B:224:GLU:HB2	2.06	0.83
1:B:223:PRO:HA	1:B:224:GLU:CB	2.08	0.81
1:B:7:THR:OG1	1:B:179:THR:HG21	1.83	0.79
1:B:119:ILE:HD11	1:B:265:VAL:HG21	1.66	0.77
1:B:195:HIS:O	1:B:196:ASN:HB2	1.85	0.75
1:B:228:ASP:HB3	1:B:229:PRO:CA	2.16	0.74
1:B:147:LEU:HD13	1:B:153:ILE:HD11	1.70	0.73
1:B:229:PRO:CB	1:B:230:ALA:HA	2.17	0.73
1:A:50:HIS:HD2	1:A:52:GLU:H	1.34	0.72
1:A:49:ASP:OD2	1:A:99:ARG:NH2	2.24	0.71
1:B:229:PRO:HB2	1:B:230:ALA:HA	1.75	0.68
1:B:119:ILE:HD13	1:B:288:LEU:HD11	1.78	0.65
1:A:345:TYR:OH	1:A:347:HIS:HD2	1.78	0.65
1:B:147:LEU:CD1	1:B:153:ILE:HD11	2.29	0.62
1:B:58:ARG:HH11	1:B:423:ARG:NH2	1.97	0.62
1:B:116:THR:O	1:B:120:LEU:HD13	2.00	0.61
1:A:409:GLU:HG2	1:A:420:LEU:HD11	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:HIS:HD2	3:B:612:HOH:O	1.86	0.58
1:A:408:PRO:HB2	1:A:420:LEU:HD22	1.88	0.55
1:B:24:GLU:OE2	1:B:31:HIS:HD2	1.89	0.55
1:B:345:TYR:OH	1:B:347:HIS:HD2	1.91	0.54
1:A:351:GLN:HG2	1:A:353:LEU:HD13	1.88	0.54
1:B:41:ARG:HH22	1:B:58:ARG:HG3	1.72	0.54
1:A:176:LEU:HD11	1:A:206:LYS:HB3	1.90	0.54
1:B:138:LYS:HD2	3:B:763:HOH:O	2.06	0.54
1:B:149:LYS:O	1:B:150:ASN:HB2	2.08	0.53
1:B:206:LYS:HD2	3:B:751:HOH:O	2.08	0.53
1:B:93:ALA:CB	1:B:120:LEU:HD11	2.39	0.53
1:A:119:ILE:HD11	1:A:265:VAL:HG21	1.91	0.53
1:B:244:LEU:HD12	1:B:271:ILE:HG12	1.92	0.52
1:B:138:LYS:CD	3:B:763:HOH:O	2.57	0.52
1:A:114:LYS:NZ	1:A:148:ASN:HD22	2.08	0.52
1:A:63:LEU:HD13	1:A:66:LEU:HD23	1.91	0.52
1:B:122:SER:HB2	1:B:288:LEU:HD13	1.91	0.51
1:A:347:HIS:HE1	1:A:352:PRO:O	1.94	0.51
1:B:166:ASP:HB3	1:B:200:THR:HG22	1.92	0.51
1:B:220:ILE:HD12	1:B:410:LYS:HB2	1.93	0.51
1:A:118:MET:HE2	3:A:877:HOH:O	2.10	0.50
1:A:142:ARG:HD3	1:A:143:GLU:O	2.11	0.49
1:B:19:GLY:HA3	1:B:96:ASP:HB2	1.95	0.49
1:A:136:GLU:HG2	1:A:140:PHE:CD1	2.48	0.49
1:B:231:GLN:NE2	1:B:376:ARG:HD3	2.28	0.49
1:A:266:GLU:O	1:A:270:LYS:HG2	2.13	0.48
1:A:409:GLU:HG2	1:A:420:LEU:CD1	2.44	0.48
1:B:113:LEU:HD13	1:B:162:ILE:HG12	1.96	0.48
1:B:122:SER:CB	1:B:288:LEU:HD13	2.44	0.48
1:B:63:LEU:HD13	1:B:66:LEU:HD23	1.95	0.48
1:B:195:HIS:O	1:B:196:ASN:CB	2.60	0.48
1:B:166:ASP:HB3	1:B:200:THR:CG2	2.44	0.48
1:B:359:GLN:HG3	1:B:362:VAL:HG22	1.96	0.47
1:B:228:ASP:CB	1:B:229:PRO:CA	2.89	0.46
1:A:386:GLU:HB2	3:A:650:HOH:O	2.13	0.46
1:B:417:GLU:OE1	1:B:417:GLU:HA	2.16	0.46
1:B:49:ASP:HB2	3:B:650:HOH:O	2.14	0.46
1:B:228:ASP:CB	1:B:229:PRO:HA	2.29	0.46
1:A:102:ASN:HD21	1:A:142:ARG:H	1.64	0.46
1:A:274:LYS:HE2	3:B:667:HOH:O	2.14	0.46
1:A:281:LEU:O	1:A:299:TYR:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:PHE:HE2	1:A:427:ILE:HD12	1.82	0.45
1:A:46:LEU:HD13	1:A:53:THR:HG22	1.97	0.45
1:B:306:LYS:HD3	3:B:753:HOH:O	2.15	0.45
1:A:165:VAL:HG13	1:A:190:LEU:HB3	1.98	0.45
1:A:19:GLY:HA2	1:A:96:ASP:HB2	1.98	0.45
1:A:119:ILE:HD13	1:A:288:LEU:HD11	1.98	0.45
1:B:93:ALA:CB	1:B:120:LEU:CD1	2.96	0.44
1:B:142:ARG:HD3	1:B:143:GLU:O	2.18	0.44
1:B:123:LEU:HD21	1:B:262:PRO:HB2	2.00	0.44
1:B:49:ASP:HB2	3:B:707:HOH:O	2.18	0.44
1:A:49:ASP:CG	1:A:99:ARG:HH22	2.21	0.44
1:A:110:LEU:HD23	1:A:142:ARG:HD2	2.00	0.43
1:B:58:ARG:NH1	1:B:423:ARG:NH2	2.63	0.43
1:A:196:ASN:HB2	3:A:800:HOH:O	2.18	0.43
1:A:24:GLU:OE2	1:A:31:HIS:HD2	2.01	0.43
1:B:93:ALA:HB2	1:B:120:LEU:CD1	2.48	0.43
1:B:321:LEU:HG	1:B:330:TRP:CG	2.54	0.42
1:B:95:LEU:O	1:B:99:ARG:HB2	2.19	0.42
1:A:154:LYS:HG2	3:A:936:HOH:O	2.18	0.42
1:A:393:ALA:HA	1:A:415:TYR:CE2	2.55	0.42
1:A:366:LEU:HD12	1:A:366:LEU:C	2.40	0.42
1:B:11:PHE:HE2	1:B:427:ILE:HD12	1.85	0.42
1:B:105:ASP:O	1:B:142:ARG:NH2	2.53	0.42
1:B:407:LYS:HB3	1:B:410:LYS:HG3	2.01	0.42
1:A:115:GLU:HG2	1:A:170:TYR:CE2	2.55	0.42
1:A:36:PHE:CD2	1:A:100:MET:HG3	2.55	0.42
1:B:183:PHE:O	1:B:211:GLU:HB2	2.20	0.42
1:A:165:VAL:CG1	1:A:190:LEU:HB3	2.50	0.41
1:A:102:ASN:ND2	1:A:142:ARG:H	2.18	0.41
1:B:93:ALA:HB2	1:B:120:LEU:HD11	2.02	0.41
1:B:298:ARG:HD3	1:B:316:ILE:HD11	2.01	0.41
1:A:31:HIS:HE1	1:A:86:THR:OG1	2.04	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	423/429 (99%)	408 (96%)	15 (4%)	0	100	100
1	B	424/429 (99%)	406 (96%)	15 (4%)	3 (1%)	25	18
All	All	847/858 (99%)	814 (96%)	30 (4%)	3 (0%)	38	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	227	PRO
1	B	228	ASP
1	B	224	GLU

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	378/382 (99%)	362 (96%)	16 (4%)	34	30
1	B	379/382 (99%)	360 (95%)	19 (5%)	28	23
All	All	757/764 (99%)	722 (95%)	35 (5%)	31	27

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LEU
1	A	31	HIS
1	A	44	LEU
1	A	58	ARG
1	A	136	GLU
1	A	142	ARG
1	A	165	VAL
1	A	190	LEU
1	A	197	ARG

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Mol	Chain	Res	Type
1	A	216	GLU
1	A	306	LYS
1	A	321	LEU
1	A	353	LEU
1	A	362	VAL
1	A	366	LEU
1	A	400	LEU
1	B	4	LYS
1	B	31	HIS
1	B	58	ARG
1	B	113	LEU
1	B	126	LYS
1	B	142	ARG
1	B	152	VAL
1	B	159	SER
1	B	179	THR
1	B	190	LEU
1	B	200	THR
1	B	211	GLU
1	B	216	GLU
1	B	226	GLU
1	B	244	LEU
1	B	306	LYS
1	B	321	LEU
1	B	353	LEU
1	B	365	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	HIS
1	A	50	HIS
1	A	102	ASN
1	A	121	ASN
1	A	148	ASN
1	A	347	HIS
1	A	359	GLN
1	B	31	HIS
1	B	84	GLN
1	B	193	HIS
1	B	231	GLN
1	B	347	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](#)

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 4 ligands modelled in this entry, 4 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

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, 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	425/429 (99%)	0.01	6 (1%) 75 75	14, 23, 36, 57	0
1	B	426/429 (99%)	0.51	37 (8%) 11 11	18, 34, 57, 71	0
All	All	851/858 (99%)	0.26	43 (5%) 29 29	14, 28, 50, 71	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	230	ALA	6.2
1	B	229	PRO	6.1
1	B	356	PHE	5.7
1	B	226	GLU	4.7
1	A	226	GLU	4.5
1	A	227	PRO	4.5
1	B	253	ASN	4.3
1	A	225	ARG	3.7
1	B	321	LEU	3.7
1	B	364	LEU	3.6
1	B	375	VAL	3.6
1	B	341	GLU	3.6
1	B	227	PRO	3.5
1	B	365	ASP	3.5
1	B	344	LEU	3.4
1	B	195	HIS	3.3
1	B	337	ASP	3.3
1	B	429	LEU	3.2
1	B	372	ILE	3.2
1	B	305	GLY	3.2
1	B	371	ASP	3.1
1	B	373	THR	3.1
1	A	224	GLU	2.9
1	B	256	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	361	ARG	2.8
1	A	361	ARG	2.8
1	B	339	LEU	2.7
1	B	369	LYS	2.7
1	B	336	PHE	2.7
1	B	367	LEU	2.7
1	B	224	GLU	2.6
1	B	368	ALA	2.5
1	B	295	ILE	2.5
1	B	345	TYR	2.4
1	B	366	LEU	2.4
1	B	228	ASP	2.3
1	A	429	LEU	2.2
1	B	343	SER	2.2
1	B	359	GLN	2.1
1	B	319	ASP	2.1
1	B	358	PRO	2.1
1	B	246	ARG	2.1
1	B	360	TYR	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 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(Å ²)	Q<0.9
2	ZN	B	603	1/1	0.99	0.11	-0.70	30,30,30,30	0
2	ZN	A	601	1/1	1.00	0.08	-1.81	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	A	602	1/1	1.00	0.08	-2.87	27,27,27,27	0
2	ZN	B	604	1/1	0.99	0.07	-3.21	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.