



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:41 AM UTC

PDB ID : 2DXN / pdb_00002dxn
Title : Glycerophosphodiesterase from Enterobacter aerogenes
Authors : Jackson, C.J.; Carr, P.D.; Ollis, D.L.
Deposited on : 2006-08-28
Resolution : 2.92 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
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

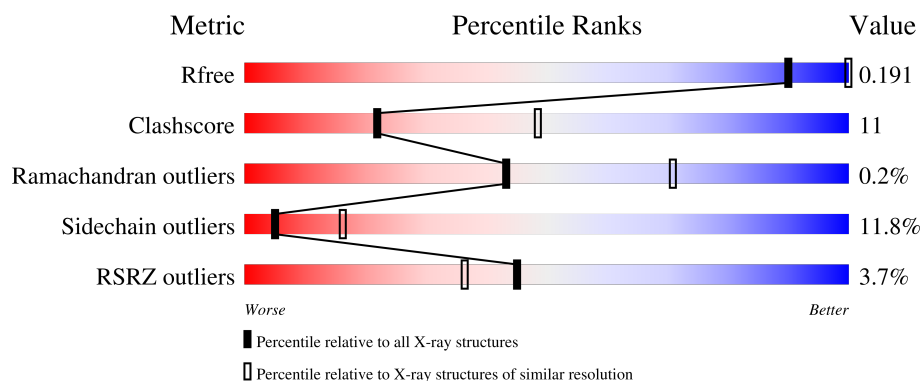
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.92 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	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

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 $\leq 5\%$. 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	274	2% 76% 20% ..
1	B	274	5% 73% 22% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4354 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 Phosphohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	0	0	0
			2137	1350	372	401	14			
1	B	271	Total	C	N	O	S	0	0	0
			2131	1347	369	401	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	227	ASP	ARG	SEE REMARK 999	UNP Q6XBH1
B	227	ASP	ARG	SEE REMARK 999	UNP Q6XBH1

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

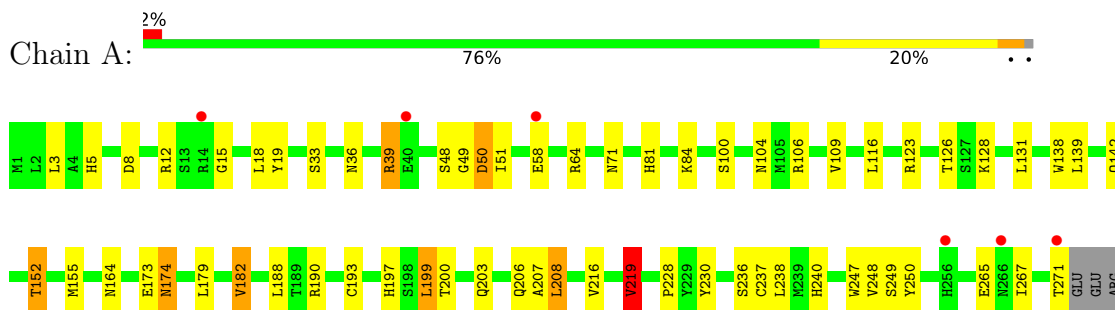
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	40	Total	O	0	0
			40	40		
3	B	42	Total	O	0	0
			42	42		

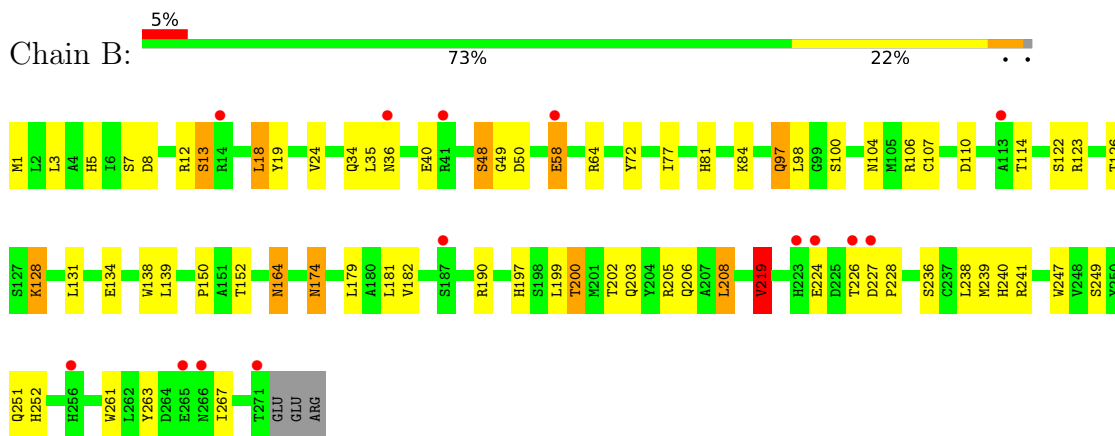
3 Residue-property plots [i](#)

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: Phosphohydrolase



• Molecule 1: Phosphohydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	164.27 Å 164.27 Å 164.27 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.92 50.00 – 2.92	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.00-2.92) 99.6 (50.00-2.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.39 (at 2.91 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.162 , 0.195 0.163 , 0.191	Depositor DCC
R_{free} test set	1668 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	70.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 75.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4354	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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	0.62	1/2196 (0.0%)	0.87	2/2996 (0.1%)
1	B	0.65	1/2190 (0.0%)	0.91	3/2989 (0.1%)
All	All	0.64	2/4386 (0.0%)	0.89	5/5985 (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	A	0	2
1	B	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	219	VAL	CA-CB	7.16	1.59	1.54
1	B	219	VAL	CA-CB	6.61	1.59	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	50	ASP	N-CA-C	-5.69	98.45	108.23
1	A	219	VAL	CB-CA-C	5.29	115.26	110.13
1	B	35	LEU	CA-C-N	-5.28	113.89	122.65
1	B	35	LEU	C-N-CA	-5.28	113.89	122.65
1	B	219	VAL	CB-CA-C	5.14	115.12	110.13

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	15	GLY	Peptide
1	A	48	SER	Peptide
1	B	48	SER	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	2137	0	2047	45	0
1	B	2131	0	2036	55	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	40	0	0	1	0
3	B	42	0	0	4	0
All	All	4354	0	4083	89	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 11.

All (89) 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:190:ARG:NH2	1:B:203:GLN:HB3	1.81	0.94
1:A:39:ARG:HH11	1:A:39:ARG:HG2	1.39	0.86
1:A:50:ASP:HB3	1:A:81:HIS:HB2	1.58	0.86
1:A:152:THR:HB	1:A:190:ARG:HB2	1.60	0.84
1:A:39:ARG:HH11	1:A:39:ARG:CG	1.91	0.84
1:B:131:LEU:H	1:B:174:ASN:HD21	1.31	0.78
1:A:197:HIS:HB2	1:A:219:VAL:HG13	1.67	0.77
1:A:131:LEU:H	1:A:174:ASN:HD21	1.32	0.75
1:B:197:HIS:HB2	1:B:219:VAL:HG13	1.72	0.72
1:B:240:HIS:HD2	1:B:249:SER:OG	1.73	0.72
1:B:104:ASN:HD22	1:B:106:ARG:NH2	1.89	0.70
1:B:152:THR:HB	1:B:190:ARG:HB2	1.76	0.67
1:A:39:ARG:HG2	1:A:39:ARG:NH1	2.10	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:LEU:HD22	1:B:199:LEU:HD21	1.80	0.64
1:A:182:VAL:HG12	1:A:188:LEU:HD23	1.79	0.63
1:A:240:HIS:HD2	1:A:249:SER:OG	1.83	0.61
1:B:104:ASN:HD22	1:B:106:ARG:HH22	1.46	0.61
1:A:174:ASN:H	1:A:174:ASN:HD22	1.48	0.60
1:A:5:HIS:CD2	1:A:240:HIS:HE1	2.19	0.60
1:B:58:GLU:HB2	3:B:1009:HOH:O	2.02	0.60
1:A:250:TYR:HB3	1:B:200:THR:HB	1.82	0.60
1:A:5:HIS:HD2	1:A:240:HIS:HE1	1.50	0.59
1:B:190:ARG:NH1	1:B:247:TRP:HB3	2.20	0.57
1:B:13:SER:HB3	1:B:58:GLU:HB3	1.87	0.57
1:A:208:LEU:HD22	1:B:208:LEU:HD22	1.87	0.56
1:A:8:ASP:H	1:A:49:GLY:HA3	1.70	0.56
1:A:271:THR:HA	3:A:1018:HOH:O	2.07	0.55
1:A:203:GLN:HG3	1:B:208:LEU:HB2	1.89	0.55
1:B:240:HIS:CD2	1:B:249:SER:OG	2.59	0.55
1:B:106:ARG:HD2	1:B:138:TRP:CD2	2.43	0.54
1:A:182:VAL:HG12	1:A:188:LEU:CD2	2.38	0.54
1:B:8:ASP:H	1:B:49:GLY:HA3	1.72	0.54
1:B:7:SER:HB3	1:B:48:SER:OG	2.07	0.53
1:B:104:ASN:ND2	1:B:106:ARG:NH2	2.57	0.53
1:B:152:THR:HG22	3:B:1025:HOH:O	2.09	0.52
1:B:18:LEU:HD22	1:B:19:TYR:CE2	2.45	0.52
1:B:50:ASP:HB3	1:B:81:HIS:HB2	1.91	0.51
1:A:152:THR:CB	1:A:190:ARG:HB2	2.37	0.51
1:A:197:HIS:HB2	1:A:219:VAL:CG1	2.39	0.51
1:B:5:HIS:CD2	1:B:240:HIS:HE1	2.28	0.51
1:B:34:GLN:HG2	3:B:1021:HOH:O	2.11	0.51
1:A:109:VAL:HB	1:A:116:LEU:HB2	1.93	0.50
1:B:152:THR:CB	1:B:190:ARG:HB2	2.41	0.50
1:B:164:ASN:HD22	1:B:164:ASN:C	2.21	0.49
1:B:239:MET:O	1:B:249:SER:HA	2.12	0.49
1:A:128:LYS:HE2	1:A:173:GLU:OE2	2.13	0.49
1:B:106:ARG:HD2	1:B:138:TRP:CG	2.48	0.48
1:A:104:ASN:HD22	1:A:106:ARG:HH12	1.59	0.48
1:B:152:THR:CG2	1:B:190:ARG:HB2	2.44	0.48
1:A:138:TRP:O	1:A:142:GLN:HG2	2.14	0.47
1:B:84:LYS:NZ	1:B:122:SER:O	2.45	0.47
1:B:252:HIS:HE1	3:B:1021:HOH:O	1.96	0.47
1:A:131:LEU:H	1:A:174:ASN:ND2	2.07	0.47
1:A:8:ASP:H	1:A:49:GLY:CA	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:ASN:HD22	1:A:71:ASN:H	1.62	0.46
1:B:5:HIS:HD2	1:B:240:HIS:HE1	1.63	0.46
1:A:126:THR:OG1	1:A:128:LYS:HG2	2.16	0.46
1:A:203:GLN:HB2	1:B:190:ARG:NH2	2.31	0.46
1:B:97:GLN:NE2	1:B:97:GLN:H	2.13	0.46
1:A:104:ASN:HB3	1:A:106:ARG:NH2	2.31	0.46
1:B:36:ASN:HB3	1:B:72:TYR:HE2	1.80	0.46
1:B:48:SER:HA	1:B:77:ILE:CG1	2.47	0.45
1:B:236:SER:OG	1:B:251:GLN:HG3	2.16	0.45
1:A:203:GLN:HG2	1:A:207:ALA:O	2.17	0.45
1:B:36:ASN:HB3	1:B:72:TYR:CE2	2.52	0.44
1:A:174:ASN:HD22	1:A:174:ASN:N	2.08	0.44
1:B:8:ASP:H	1:B:49:GLY:CA	2.30	0.44
1:A:203:GLN:HG2	1:A:208:LEU:HA	1.99	0.43
1:A:203:GLN:HE22	1:B:203:GLN:CG	2.31	0.43
1:A:190:ARG:NH1	1:A:247:TRP:HB3	2.33	0.43
1:B:97:GLN:H	1:B:97:GLN:HE21	1.67	0.43
1:A:267:ILE:HG22	1:B:19:TYR:HA	2.01	0.43
1:B:1:MET:O	1:B:241:ARG:HA	2.19	0.43
1:B:114:THR:HG23	1:B:150:PRO:HB2	2.00	0.42
1:A:228:PRO:HB2	1:B:263:TYR:HB3	2.02	0.42
1:B:126:THR:OG1	1:B:128:LYS:HG3	2.19	0.42
1:A:155:MET:O	1:A:193:CYS:HA	2.20	0.42
1:B:227:ASP:HA	1:B:228:PRO:HD3	1.95	0.42
1:A:174:ASN:H	1:A:174:ASN:ND2	2.15	0.41
1:B:8:ASP:HB3	1:B:197:HIS:CE1	2.55	0.41
1:B:98:LEU:HD23	1:B:98:LEU:HA	1.93	0.41
1:A:5:HIS:O	1:A:237:CYS:HB2	2.20	0.41
1:A:19:TYR:HA	1:B:267:ILE:HG22	2.03	0.41
1:B:97:GLN:O	1:B:107:CYS:HB3	2.21	0.41
1:B:18:LEU:HD22	1:B:19:TYR:CD2	2.55	0.41
1:A:39:ARG:CG	1:A:39:ARG:NH1	2.61	0.40
1:B:7:SER:CB	1:B:48:SER:OG	2.70	0.40
1:B:174:ASN:H	1:B:174:ASN:HD22	1.69	0.40
1:A:230:TYR:CZ	1:B:261:TRP:HB2	2.56	0.40

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	269/274 (98%)	256 (95%)	12 (4%)	1 (0%)	30	58
1	B	269/274 (98%)	260 (97%)	9 (3%)	0	100	100
All	All	538/548 (98%)	516 (96%)	21 (4%)	1 (0%)	43	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	VAL

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	233/236 (99%)	207 (89%)	26 (11%)	6	18
1	B	232/236 (98%)	203 (88%)	29 (12%)	4	14
All	All	465/472 (98%)	410 (88%)	55 (12%)	5	16

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	12	ARG
1	A	18	LEU
1	A	33	SER
1	A	39	ARG

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Mol	Chain	Res	Type
1	A	51	ILE
1	A	58	GLU
1	A	64	ARG
1	A	84	LYS
1	A	100	SER
1	A	123	ARG
1	A	139	LEU
1	A	152	THR
1	A	164	ASN
1	A	174	ASN
1	A	179	LEU
1	A	182	VAL
1	A	199	LEU
1	A	200	THR
1	A	206	GLN
1	A	208	LEU
1	A	219	VAL
1	A	236	SER
1	A	238	LEU
1	A	248	VAL
1	A	265	GLU
1	B	3	LEU
1	B	12	ARG
1	B	13	SER
1	B	18	LEU
1	B	24	VAL
1	B	40	GLU
1	B	58	GLU
1	B	64	ARG
1	B	97	GLN
1	B	100	SER
1	B	110	ASP
1	B	123	ARG
1	B	128	LYS
1	B	134	GLU
1	B	139	LEU
1	B	164	ASN
1	B	174	ASN
1	B	179	LEU
1	B	181	LEU
1	B	182	VAL
1	B	200	THR

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Mol	Chain	Res	Type
1	B	202	THR
1	B	205	ARG
1	B	206	GLN
1	B	208	LEU
1	B	219	VAL
1	B	224	GLU
1	B	226	THR
1	B	238	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	HIS
1	A	36	ASN
1	A	61	GLN
1	A	97	GLN
1	A	104	ASN
1	A	142	GLN
1	A	164	ASN
1	A	166	GLN
1	A	174	ASN
1	A	203	GLN
1	A	240	HIS
1	A	242	GLN
1	A	246	GLN
1	A	252	HIS
1	A	266	ASN
1	B	5	HIS
1	B	28	ASN
1	B	34	GLN
1	B	36	ASN
1	B	61	GLN
1	B	97	GLN
1	B	103	ASN
1	B	104	ASN
1	B	164	ASN
1	B	166	GLN
1	B	174	ASN
1	B	206	GLN
1	B	223	HIS
1	B	240	HIS
1	B	242	GLN

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Mol	Chain	Res	Type
1	B	246	GLN

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 oligosaccharides 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	271/274 (98%)	0.29	6 (2%) 62 53	66, 77, 87, 90	0
1	B	271/274 (98%)	0.43	14 (5%) 33 26	63, 76, 84, 91	0
All	All	542/548 (98%)	0.36	20 (3%) 45 36	63, 76, 86, 91	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	226	THR	3.8
1	B	271	THR	3.4
1	B	224	GLU	3.1
1	A	256	HIS	2.9
1	B	14	ARG	2.8
1	B	266	ASN	2.8
1	A	266	ASN	2.5
1	B	256	HIS	2.5
1	A	58	GLU	2.5
1	A	271	THR	2.5
1	B	223	HIS	2.4
1	B	187	SER	2.4
1	B	113	ALA	2.4
1	B	41	ARG	2.3
1	B	227	ASP	2.3
1	A	14	ARG	2.3
1	A	40	GLU	2.1
1	B	265	GLU	2.1
1	B	36	ASN	2.0
1	B	58	GLU	2.0

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, 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	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	A	1002	1/1	0.86	0.17	76,76,76,76	1
2	ZN	A	1001	1/1	0.90	0.13	81,81,81,81	1
2	ZN	B	1003	1/1	0.91	0.14	79,79,79,79	1
2	ZN	B	1004	1/1	0.93	0.12	73,73,73,73	1

6.5 Other polymers [i](#)

There are no such residues in this entry.