



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:22 PM UTC

PDB ID : 3F8N / pdb_00003f8n
Title : Crystal structure of PerR-Zn-Mn
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Deposited on : 2008-11-13
Resolution : 3.15 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

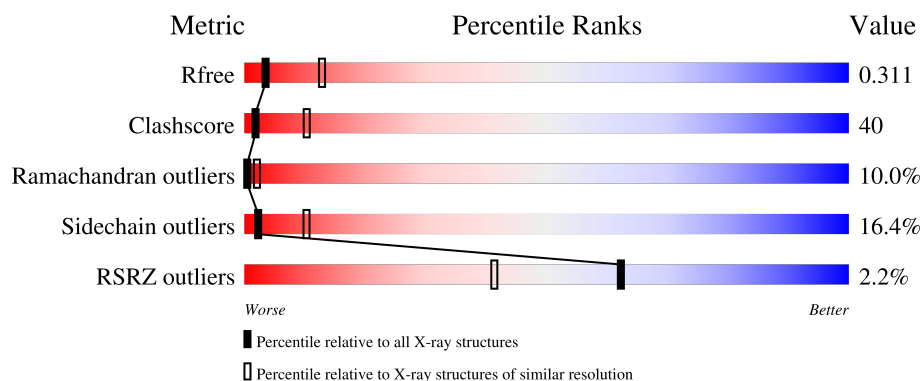
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	145	55% 23% 12% • 6%
1	B	145	3% 53% 23% 13% • 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2166 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 Peroxide operon regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	137	Total	C	N	O	S	37	0	0
			1086	686	187	207	6			
1	B	136	Total	C	N	O	S	7	0	0
			1075	680	187	202	6			

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		
2	B	1	Total	Mn	0	0
			1	1		

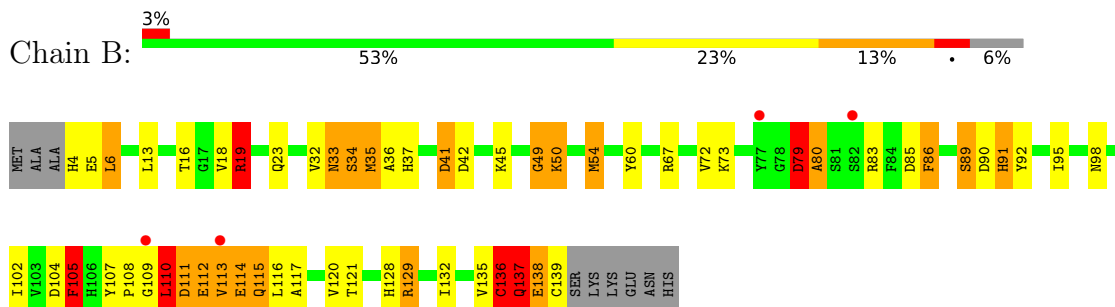
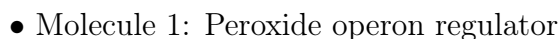
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O	0	0
			1	1		

- Molecule 1: Peroxide operon regulator



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.30Å 63.34Å 66.73Å 90.00° 80.41° 90.00°	Depositor
Resolution (Å)	45.64 – 3.15 45.64 – 3.15	Depositor EDS
% Data completeness (in resolution range)	100.0 (45.64-3.15) 99.1 (45.64-3.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.275 , 0.315 0.266 , 0.311	Depositor DCC
R_{free} test set	354 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	70.0	Xtriage
Anisotropy	0.838	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2166	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.18% 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: MN, 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	1.27	4/1111 (0.4%)	1.21	14/1506 (0.9%)
1	B	1.16	3/1100 (0.3%)	1.19	7/1490 (0.5%)
All	All	1.22	7/2211 (0.3%)	1.20	21/2996 (0.7%)

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	3
1	B	1	4
All	All	1	7

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	7	LYS	CA-CB	33.43	2.06	1.53
1	B	19	ARG	CD-NE	29.78	1.88	1.46
1	B	73	LYS	CB-CG	11.73	1.87	1.52
1	A	45	LYS	CB-CG	-10.08	1.22	1.52
1	A	112	GLU	CA-CB	9.78	1.73	1.53
1	B	19	ARG	CA-CB	-8.89	1.40	1.53
1	A	45	LYS	CE-NZ	-5.64	1.32	1.49

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	19	ARG	CG-CD-NE	15.83	146.82	112.00
1	B	19	ARG	N-CA-CB	12.38	130.29	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	45	LYS	CD-CE-NZ	10.50	145.51	111.90
1	A	7	LYS	CB-CA-C	-9.81	94.45	110.74
1	A	112	GLU	N-CA-CB	9.02	125.83	110.50
1	B	19	ARG	CA-CB-CG	8.13	130.37	114.10
1	B	79	ASP	CA-C-N	7.86	135.85	121.70
1	B	79	ASP	C-N-CA	7.86	135.85	121.70
1	A	105	PHE	N-CA-C	7.01	121.52	112.12
1	A	5	GLU	CA-CB-CG	6.50	127.11	114.10
1	A	138	GLU	N-CA-C	6.36	124.34	110.80
1	B	19	ARG	CB-CA-C	6.15	119.68	109.53
1	B	115	GLN	N-CA-C	5.86	117.34	111.07
1	A	110	LEU	CA-C-N	5.85	132.23	121.70
1	A	110	LEU	C-N-CA	5.85	132.23	121.70
1	A	92	TYR	N-CA-C	5.45	118.11	109.50
1	A	90	ASP	CA-C-N	5.36	131.34	121.70
1	A	90	ASP	C-N-CA	5.36	131.34	121.70
1	A	113	VAL	CA-C-N	5.05	130.79	121.70
1	A	113	VAL	C-N-CA	5.05	130.79	121.70
1	A	124	LYS	CA-CB-CG	-5.03	104.04	114.10

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	19	ARG	CA

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	136	CYS	Peptide
1	A	137	GLN	Peptide
1	A	138	GLU	Peptide
1	B	136	CYS	Peptide
1	B	137	GLN	Peptide
1	B	19	ARG	Sidechain
1	B	79	ASP	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	1086	0	1032	65	0
1	B	1075	0	1027	102	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	1	0
4	A	1	0	0	0	0
All	All	2166	0	2059	163	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 40.

All (163) 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:109:GLY:HA2	1:B:110:LEU:CB	1.76	1.14
1:B:109:GLY:CA	1:B:110:LEU:HB2	1.77	1.14
1:B:49:GLY:HA3	1:B:50:LYS:CB	1.78	1.12
1:A:49:GLY:HA3	1:A:50:LYS:CB	1.78	1.12
1:B:90:ASP:CA	1:B:91:HIS:HB2	1.80	1.11
1:A:49:GLY:HA3	1:A:50:LYS:HB3	1.11	1.05
1:B:92:TYR:OH	1:B:110:LEU:HD21	1.55	1.05
1:A:113:VAL:HG23	1:A:117:ALA:H	1.17	1.05
1:B:49:GLY:HA3	1:B:50:LYS:HB2	1.37	1.05
1:B:90:ASP:HA	1:B:91:HIS:HB2	1.05	1.02
1:B:89:SER:HA	1:B:90:ASP:HB3	1.42	1.01
1:B:136:CYS:HB2	1:B:138:GLU:H	1.23	1.00
1:B:90:ASP:HA	1:B:91:HIS:CB	1.94	0.97
1:B:113:VAL:HA	1:B:114:GLU:C	1.88	0.97
1:A:136:CYS:HB3	1:A:137:GLN:HB2	1.47	0.94
1:B:136:CYS:HB3	1:B:137:GLN:HB2	1.48	0.94
1:B:79:ASP:HB2	1:B:80:ALA:CB	1.98	0.93
1:B:79:ASP:CB	1:B:80:ALA:HB2	1.99	0.91
1:B:136:CYS:HB2	1:B:139:CYS:HA	1.51	0.91
1:A:111:ASP:HA	1:A:112:GLU:C	1.93	0.90
1:B:79:ASP:CB	1:B:80:ALA:CB	2.49	0.90
1:B:113:VAL:HG13	1:B:117:ALA:HB3	1.54	0.90
1:B:113:VAL:CG1	1:B:117:ALA:HB3	2.01	0.90
1:B:79:ASP:HB3	1:B:80:ALA:HB2	1.54	0.89
1:B:113:VAL:CG1	1:B:117:ALA:CB	2.49	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:VAL:CG2	1:A:117:ALA:H	1.85	0.88
1:B:79:ASP:HB2	1:B:80:ALA:HB3	1.55	0.87
1:A:89:SER:HA	1:A:90:ASP:HB2	1.56	0.87
1:A:136:CYS:HB2	1:A:138:GLU:H	1.39	0.86
1:B:109:GLY:CA	1:B:110:LEU:CB	2.41	0.86
1:B:113:VAL:HG11	1:B:117:ALA:HB2	1.56	0.86
1:B:92:TYR:O	1:B:104:ASP:O	1.94	0.86
1:B:92:TYR:OH	1:B:110:LEU:CD2	2.22	0.86
1:B:109:GLY:HA2	1:B:110:LEU:HB2	0.90	0.86
1:A:110:LEU:HB3	1:A:111:ASP:CG	2.01	0.86
1:A:136:CYS:HB2	1:A:139:CYS:HA	1.58	0.85
1:B:113:VAL:HG22	1:B:116:LEU:HB3	1.59	0.84
1:B:49:GLY:CA	1:B:50:LYS:HB2	2.08	0.84
1:B:113:VAL:HG13	1:B:117:ALA:CB	2.08	0.83
1:A:136:CYS:CB	1:A:138:GLU:H	1.91	0.82
1:B:113:VAL:HG11	1:B:117:ALA:CB	2.11	0.80
1:A:113:VAL:HG23	1:A:117:ALA:N	1.98	0.77
1:B:136:CYS:CB	1:B:138:GLU:H	1.96	0.76
1:B:136:CYS:HB2	1:B:138:GLU:N	1.99	0.76
1:A:136:CYS:HB3	1:A:137:GLN:CB	2.15	0.76
1:B:49:GLY:HA3	1:B:50:LYS:HB3	1.65	0.76
1:A:136:CYS:CB	1:A:137:GLN:HB2	2.17	0.75
1:A:95:ILE:HD11	1:A:131:GLU:HG2	1.69	0.74
1:B:113:VAL:CG2	1:B:116:LEU:HB3	2.20	0.71
1:A:103:VAL:O	1:A:104:ASP:HB2	1.90	0.70
1:B:136:CYS:SG	3:B:204:ZN:ZN	1.83	0.68
1:B:113:VAL:HG22	1:B:117:ALA:H	1.59	0.67
1:A:116:LEU:HD23	1:B:107:TYR:HD1	1.60	0.67
1:A:113:VAL:HA	1:A:114:GLU:C	2.19	0.67
1:B:72:VAL:HG23	1:B:86:PHE:HA	1.77	0.66
1:A:89:SER:CA	1:A:90:ASP:HB2	2.24	0.66
1:A:136:CYS:CB	1:A:139:CYS:HA	2.24	0.66
1:A:113:VAL:HA	1:A:115:GLN:N	2.10	0.66
1:A:49:GLY:CA	1:A:50:LYS:CB	2.63	0.65
1:B:138:GLU:N	1:B:139:CYS:HA	2.10	0.64
1:B:111:ASP:HA	1:B:112:GLU:C	2.22	0.64
1:A:136:CYS:HB2	1:A:138:GLU:N	2.13	0.64
1:B:113:VAL:HG13	1:B:117:ALA:H	1.63	0.62
1:B:41:ASP:O	1:B:45:LYS:HG2	1.98	0.62
1:B:136:CYS:HB3	1:B:137:GLN:CB	2.24	0.62
1:A:136:CYS:CB	1:A:138:GLU:N	2.61	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:ASP:HB3	1:B:80:ALA:CB	2.25	0.61
1:A:103:VAL:HG11	1:B:121:THR:HG22	1.83	0.60
1:B:111:ASP:CA	1:B:112:GLU:HG3	2.32	0.60
1:A:105:PHE:O	1:A:106:HIS:HB2	2.01	0.60
1:B:111:ASP:HA	1:B:112:GLU:O	2.01	0.60
1:B:113:VAL:CG1	1:B:117:ALA:HB2	2.22	0.60
1:A:44:TYR:CD1	1:A:44:TYR:C	2.80	0.59
1:B:102:ILE:O	1:B:102:ILE:HG22	2.02	0.59
1:B:23:GLN:NE2	1:B:54:MET:HG3	2.18	0.59
1:A:110:LEU:HB3	1:A:111:ASP:OD1	2.03	0.58
1:B:117:ALA:HA	1:B:120:VAL:HG22	1.85	0.58
1:B:79:ASP:HB2	1:B:80:ALA:HB2	1.70	0.58
1:B:89:SER:CA	1:B:90:ASP:HB3	2.26	0.57
1:B:113:VAL:CA	1:B:114:GLU:C	2.69	0.57
1:B:79:ASP:CB	1:B:80:ALA:HB3	2.26	0.57
1:A:113:VAL:HB	1:A:116:LEU:HB3	1.87	0.57
1:B:113:VAL:HG22	1:B:117:ALA:N	2.19	0.57
1:A:49:GLY:CA	1:A:50:LYS:HB3	2.07	0.57
1:B:92:TYR:HH	1:B:110:LEU:HD21	1.64	0.56
1:B:136:CYS:C	1:B:138:GLU:N	2.64	0.56
1:B:111:ASP:CA	1:B:112:GLU:O	2.54	0.55
1:A:113:VAL:HG21	1:A:117:ALA:HB2	1.88	0.55
1:B:112:GLU:O	1:B:115:GLN:N	2.38	0.55
1:B:113:VAL:HG22	1:B:116:LEU:CB	2.35	0.55
1:B:89:SER:HA	1:B:90:ASP:CB	2.19	0.54
1:B:90:ASP:CB	1:B:91:HIS:HB2	2.36	0.54
1:A:137:GLN:HB3	1:A:140:SER:O	2.07	0.54
1:A:83:ARG:CZ	1:A:102:ILE:HD11	2.37	0.54
1:A:92:TYR:HB3	1:A:105:PHE:CE2	2.44	0.54
1:B:111:ASP:CB	1:B:112:GLU:O	2.57	0.54
1:A:116:LEU:CD2	1:B:107:TYR:HD1	2.20	0.53
1:A:92:TYR:HB3	1:A:105:PHE:CZ	2.45	0.52
1:B:109:GLY:CA	1:B:110:LEU:HB3	2.39	0.51
1:A:133:TYR:HE1	1:B:129:ARG:HB2	1.75	0.51
1:A:23:GLN:NE2	1:A:54:MET:HG3	2.27	0.50
1:A:136:CYS:C	1:A:138:GLU:H	2.19	0.50
1:B:6:LEU:HD22	1:B:32:VAL:HG21	1.93	0.50
1:B:113:VAL:HG13	1:B:117:ALA:N	2.27	0.50
1:A:110:LEU:N	1:A:111:ASP:O	2.45	0.49
1:B:37:HIS:HB2	1:B:83:ARG:HH11	1.77	0.49
1:A:35:MET:HE2	1:A:35:MET:H	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:SER:C	1:A:36:ALA:H	2.21	0.49
1:A:44:TYR:C	1:A:44:TYR:HD1	2.21	0.49
1:A:136:CYS:HB3	1:A:137:GLN:CA	2.43	0.49
1:B:4:HIS:HD2	1:B:5:GLU:H	1.61	0.48
1:A:23:GLN:HB2	1:A:54:MET:HE2	1.95	0.48
1:B:110:LEU:HD21	1:B:128:HIS:CE1	2.48	0.48
1:A:90:ASP:O	1:A:90:ASP:CG	2.56	0.48
1:B:90:ASP:CA	1:B:91:HIS:CB	2.66	0.48
1:B:136:CYS:C	1:B:138:GLU:H	2.21	0.47
1:A:136:CYS:CA	1:A:137:GLN:HB2	2.44	0.47
1:B:37:HIS:HB2	1:B:83:ARG:NH1	2.29	0.47
1:B:110:LEU:HD21	1:B:128:HIS:NE2	2.29	0.47
1:A:136:CYS:C	1:A:138:GLU:N	2.73	0.47
1:A:103:VAL:O	1:A:104:ASP:CB	2.60	0.47
1:A:111:ASP:HA	1:A:112:GLU:O	2.13	0.46
1:B:112:GLU:CD	1:B:113:VAL:O	2.58	0.46
1:B:138:GLU:O	1:B:138:GLU:HG2	2.15	0.46
1:A:110:LEU:H	1:A:111:ASP:C	2.23	0.46
1:A:117:ALA:HA	1:A:120:VAL:HG22	1.96	0.46
1:A:62:ASN:O	1:A:65:VAL:HB	2.16	0.46
1:A:135:VAL:C	1:A:136:CYS:O	2.59	0.46
1:B:86:PHE:O	1:B:86:PHE:CG	2.69	0.46
1:A:136:CYS:HB3	1:A:137:GLN:C	2.41	0.45
1:B:136:CYS:CB	1:B:137:GLN:HB2	2.33	0.45
1:B:33:ASN:N	1:B:33:ASN:ND2	2.65	0.45
1:B:85:ASP:O	1:B:86:PHE:HB2	2.16	0.45
1:B:110:LEU:CD2	1:B:128:HIS:CE1	2.99	0.45
1:B:136:CYS:CB	1:B:139:CYS:HA	2.36	0.45
1:B:92:TYR:OH	1:B:110:LEU:HD23	2.14	0.44
1:B:34:SER:C	1:B:36:ALA:H	2.24	0.44
1:B:138:GLU:N	1:B:139:CYS:CA	2.79	0.44
1:B:111:ASP:HA	1:B:112:GLU:HG3	1.99	0.44
1:B:136:CYS:CB	1:B:138:GLU:N	2.71	0.43
1:A:89:SER:HA	1:A:90:ASP:CB	2.31	0.43
1:A:113:VAL:O	1:A:113:VAL:CG1	2.65	0.43
1:B:108:PRO:HA	1:B:109:GLY:HA2	1.83	0.43
1:B:113:VAL:HA	1:B:115:GLN:N	2.31	0.43
1:B:35:MET:H	1:B:35:MET:HG2	1.62	0.42
1:B:98:ASN:HB3	1:B:139:CYS:SG	2.59	0.42
1:A:136:CYS:HB3	1:A:138:GLU:N	2.35	0.42
1:B:113:VAL:CG1	1:B:117:ALA:H	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:LEU:C	1:A:49:GLY:N	2.77	0.42
1:A:93:HIS:CD2	1:A:102:ILE:HG22	2.54	0.42
1:A:113:VAL:CG2	1:A:117:ALA:CB	2.98	0.42
1:B:105:PHE:HZ	1:B:132:ILE:HD13	1.84	0.42
1:B:138:GLU:H	1:B:139:CYS:HA	1.82	0.42
1:B:23:GLN:HE22	1:B:54:MET:HG3	1.84	0.41
1:B:113:VAL:CG2	1:B:117:ALA:H	2.30	0.41
1:A:102:ILE:HD12	1:A:102:ILE:N	2.36	0.41
1:B:110:LEU:HD13	1:B:111:ASP:OD2	2.20	0.41
1:B:111:ASP:HB3	1:B:114:GLU:HG2	2.03	0.41
1:A:113:VAL:HG21	1:A:117:ALA:CB	2.50	0.41
1:A:138:GLU:N	1:A:139:CYS:HA	2.36	0.41
1:B:135:VAL:C	1:B:136:CYS:O	2.62	0.40
1:A:90:ASP:HA	1:A:91:HIS:HB2	2.03	0.40
1:B:111:ASP:N	1:B:112:GLU:HG3	2.36	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	135/145 (93%)	99 (73%)	22 (16%)	14 (10%)	0	2
1	B	134/145 (92%)	101 (75%)	20 (15%)	13 (10%)	0	2
All	All	269/290 (93%)	200 (74%)	42 (16%)	27 (10%)	0	2

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	50	LYS
1	A	90	ASP
1	A	103	VAL

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Mol	Chain	Res	Type
1	A	104	ASP
1	A	111	ASP
1	A	136	CYS
1	B	50	LYS
1	B	80	ALA
1	B	86	PHE
1	B	91	HIS
1	A	18	VAL
1	A	112	GLU
1	A	114	GLU
1	A	138	GLU
1	B	18	VAL
1	B	105	PHE
1	B	110	LEU
1	B	112	GLU
1	B	136	CYS
1	B	137	GLN
1	A	5	GLU
1	B	49	GLY
1	A	49	GLY
1	A	79	ASP
1	A	106	HIS
1	B	138	GLU
1	B	89	SER

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	117/125 (94%)	98 (84%)	19 (16%)	2	11
1	B	115/125 (92%)	96 (84%)	19 (16%)	2	10
All	All	232/250 (93%)	194 (84%)	38 (16%)	2	10

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	THR
1	A	13	LEU
1	A	35	MET
1	A	42	ASP
1	A	44	TYR
1	A	60	TYR
1	A	64	ARG
1	A	67	ARG
1	A	71	LEU
1	A	81	SER
1	A	82	SER
1	A	88	THR
1	A	89	SER
1	A	95	ILE
1	A	102	ILE
1	A	110	LEU
1	A	111	ASP
1	A	131	GLU
1	A	132	ILE
1	B	6	LEU
1	B	13	LEU
1	B	16	THR
1	B	19	ARG
1	B	33	ASN
1	B	34	SER
1	B	35	MET
1	B	41	ASP
1	B	42	ASP
1	B	54	MET
1	B	60	TYR
1	B	67	ARG
1	B	95	ILE
1	B	105	PHE
1	B	110	LEU
1	B	111	ASP
1	B	113	VAL
1	B	114	GLU
1	B	129	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN

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Mol	Chain	Res	Type
1	A	106	HIS
1	A	137	GLN
1	B	4	HIS
1	B	23	GLN
1	B	33	ASN
1	B	106	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 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 [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	137/145 (94%)	0.42	2 (1%)	72 52	32, 70, 91, 100	10 (7%)
1	B	136/145 (93%)	0.55	4 (2%)	53 34	42, 67, 88, 100	3 (2%)
All	All	273/290 (94%)	0.48	6 (2%)	62 41	32, 69, 90, 100	13 (4%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	113	VAL	2.5
1	B	109	GLY	2.3
1	A	75	LEU	2.2
1	B	82	SER	2.0
1	B	77	TYR	2.0
1	A	102	ILE	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	MN	B	203	1/1	0.98	0.06	59,59,59,59	0
2	MN	A	201	1/1	0.99	0.03	70,70,70,70	0
3	ZN	B	204	1/1	0.99	0.03	81,81,81,81	0
3	ZN	A	202	1/1	1.00	0.03	65,65,65,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.