Full wwPDB X-ray Structure Validation Report (i)

May 15, 2020 – 10:15 am BST

PDB ID	:	3HGV
Title	:	Structure of Phenazine Antibiotic Biosynthesis Protein
Authors	:	Bera, A.K.; Atanasova, V.; Parsons, J.F.
Deposited on	:	2009-05-14
Resolution	:	2.30 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 following versions of software and data (see references (1)) were used in the production of this report:

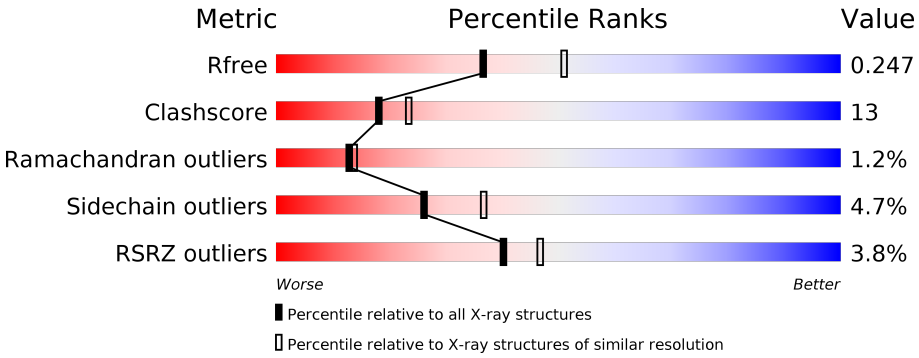
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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	369	4% 77% 14% • 6%
1	B	369	4% 71% 18% • • 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5804 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 EhpF.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	346	Total	C	N	O	S	Se	0	3	0
			2737	1741	470	517	2	7			
1	B	345	Total	C	N	O	S	Se	0	0	0
			2712	1723	465	515	2	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q8GPH0
A	-1	SER	-	EXPRESSION TAG	UNP Q8GPH0
A	0	HIS	-	EXPRESSION TAG	UNP Q8GPH0
B	-2	GLY	-	EXPRESSION TAG	UNP Q8GPH0
B	-1	SER	-	EXPRESSION TAG	UNP Q8GPH0
B	0	HIS	-	EXPRESSION TAG	UNP Q8GPH0

- Molecule 2 is water.

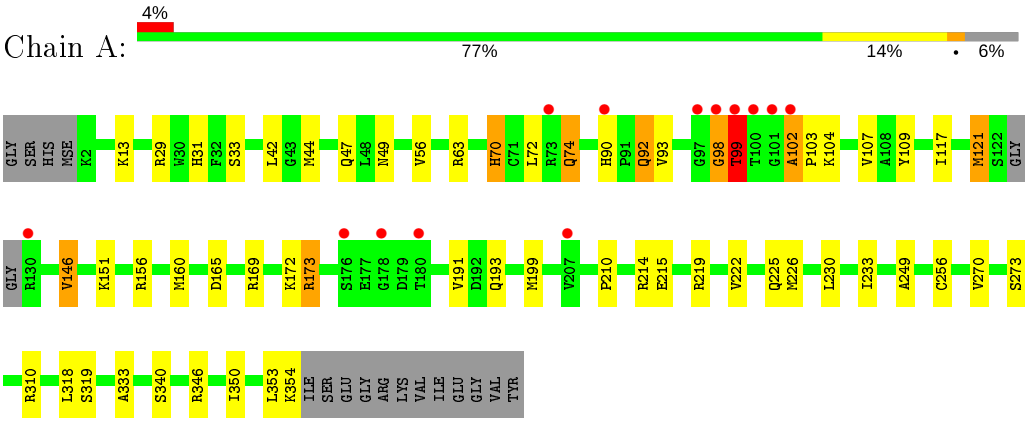
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	201	Total	O	0	0
			201	201		
2	B	154	Total	O	0	0
			154	154		

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.

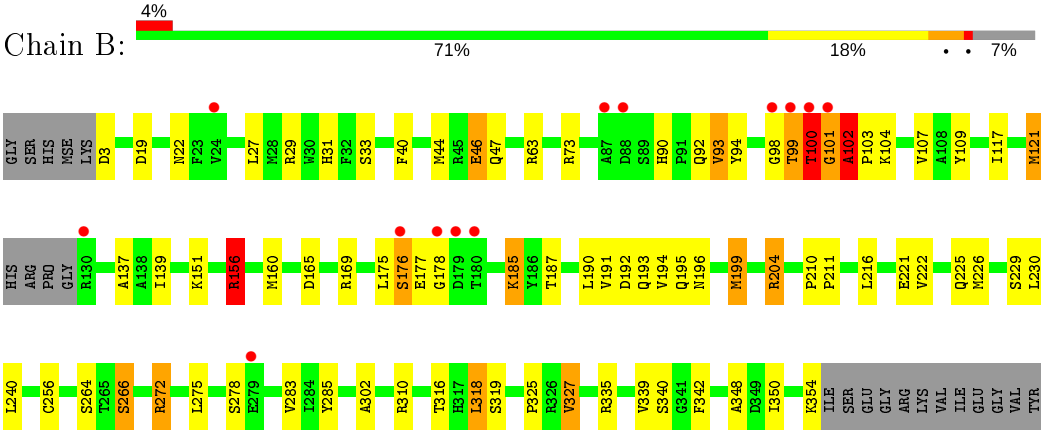
- Molecule 1: EhpF

Chain A:



- Molecule 1: EhpF

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	68.84Å 110.14Å 112.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.34 – 2.30 28.34 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (28.34-2.30) 99.7 (28.34-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.46 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.180 , 0.249 0.179 , 0.247	Depositor DCC
R_{free} test set	1934 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	39.9	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 37.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.012 for -h,l,k	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5804	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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

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	1.18	7/2801 (0.2%)	1.10	10/3797 (0.3%)
1	B	1.13	5/2766 (0.2%)	0.98	7/3752 (0.2%)
All	All	1.15	12/5567 (0.2%)	1.04	17/7549 (0.2%)

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
1	B	0	1
All	All	0	2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	146	VAL	CB-CG1	10.66	1.75	1.52
1	B	156	ARG	CG-CD	6.47	1.68	1.51
1	B	93	VAL	CB-CG2	-5.98	1.40	1.52
1	B	302	ALA	CA-CB	5.94	1.65	1.52
1	B	327	VAL	CB-CG2	5.42	1.64	1.52
1	A	333	ALA	CA-CB	5.41	1.63	1.52
1	A	109	TYR	CD1-CE1	5.33	1.47	1.39
1	A	56	VAL	CA-CB	5.32	1.66	1.54
1	A	13	LYS	CG-CD	5.30	1.70	1.52
1	A	270	VAL	CB-CG2	5.24	1.63	1.52
1	A	249	ALA	CA-CB	5.14	1.63	1.52
1	B	94	TYR	CD1-CE1	5.04	1.47	1.39

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	63	ARG	NE-CZ-NH2	-18.13	111.23	120.30
1	A	156	ARG	NE-CZ-NH2	-13.67	113.47	120.30
1	A	63	ARG	NE-CZ-NH1	11.39	126.00	120.30
1	B	204	ARG	NE-CZ-NH2	-7.66	116.47	120.30
1	B	156	ARG	NE-CZ-NH1	-7.22	116.69	120.30
1	A	346	ARG	NE-CZ-NH2	-6.68	116.96	120.30
1	A	156	ARG	CA-CB-CG	-5.96	100.30	113.40
1	B	310	ARG	NE-CZ-NH1	5.89	123.25	120.30
1	A	63	ARG	CG-CD-NE	-5.87	99.48	111.80
1	A	219	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	B	335	ARG	NE-CZ-NH2	-5.83	117.38	120.30
1	B	318	LEU	CB-CG-CD2	5.57	120.46	111.00
1	A	310	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	A	156	ARG	NE-CZ-NH1	5.53	123.07	120.30
1	B	33	SER	CB-CA-C	-5.38	99.89	110.10
1	A	49	ASN	CB-CA-C	-5.26	99.88	110.40
1	B	204	ARG	NE-CZ-NH1	5.18	122.89	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	102	ALA	Peptide
1	B	102	ALA	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	2737	0	2724	69	0
1	B	2712	0	2686	102	0
2	A	201	0	0	4	0
2	B	154	0	0	12	0
All	All	5804	0	5410	145	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 13.

All (145) 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:146:VAL:CG1	1:A:146:VAL:CB	1.75	1.65
1:A:160:MSE:CE	1:B:93:VAL:HG22	1.47	1.43
1:B:156:ARG:CG	1:B:156:ARG:HH11	1.41	1.31
1:A:160:MSE:HE2	1:B:93:VAL:CG2	1.71	1.20
1:A:160:MSE:CE	1:B:93:VAL:CG2	2.21	1.17
1:B:156:ARG:HG3	1:B:156:ARG:HH11	1.09	1.13
1:B:199:MSE:HE1	1:B:225:GLN:HB2	1.21	1.10
1:A:160:MSE:HE2	1:B:93:VAL:HG22	1.01	1.00
1:A:74:GLN:HG3	2:A:405:HOH:O	1.64	0.98
1:B:199:MSE:HE1	1:B:225:GLN:CB	1.95	0.97
1:A:102:ALA:HB3	1:B:196:ASN:ND2	1.80	0.96
1:B:156:ARG:NH1	1:B:156:ARG:HG3	1.75	0.94
1:A:93:VAL:CG2	1:B:160:MSE:HE2	1.97	0.94
1:A:72:LEU:HD12	1:A:104[B]:LYS:HD2	1.46	0.93
1:B:156:ARG:HG2	1:B:156:ARG:HH11	1.35	0.90
1:A:93:VAL:HG23	1:B:160:MSE:HE2	1.50	0.90
1:A:193:GLN:HE21	1:B:169:ARG:HH11	1.19	0.90
1:A:169:ARG:HH11	1:B:193:GLN:HE21	1.23	0.87
1:A:160:MSE:HE3	1:B:93:VAL:CG2	2.03	0.85
1:B:156:ARG:NH1	1:B:156:ARG:CG	2.21	0.85
1:B:99:THR:HG23	1:B:100:THR:H	1.41	0.85
1:A:99:THR:HG21	1:A:172:LYS:HD2	1.61	0.83
1:B:187:THR:O	1:B:191:VAL:HG23	1.80	0.81
1:B:102:ALA:HB3	1:B:103:PRO:HA	1.63	0.80
1:B:102:ALA:CB	1:B:103:PRO:HA	2.12	0.79
1:B:199:MSE:CE	1:B:225:GLN:CB	2.64	0.76
1:B:199:MSE:HE2	1:B:199:MSE:HA	1.67	0.75
1:B:137:ALA:HB1	1:B:139:ILE:HG12	1.69	0.74
1:A:72:LEU:HB2	1:A:104[B]:LYS:HG3	1.72	0.71
1:A:31:HIS:HE1	1:A:319:SER:O	1.73	0.71
1:B:46:GLU:HG2	1:B:47:GLN:HE21	1.56	0.69
1:A:93:VAL:HG22	1:B:160:MSE:HE2	1.74	0.69
1:A:160:MSE:HE3	1:B:93:VAL:HG23	1.72	0.69
1:A:193:GLN:NE2	1:B:169:ARG:HH11	1.90	0.68
1:A:353:LEU:O	1:A:354:LYS:HG2	1.94	0.68
1:A:102:ALA:CB	1:B:196:ASN:ND2	2.57	0.68
1:B:199:MSE:CE	1:B:225:GLN:HB2	2.10	0.67
1:B:272:ARG:NH2	2:B:471:HOH:O	2.23	0.67
1:A:193:GLN:HE21	1:B:169:ARG:NH1	1.91	0.67
1:B:73:ARG:CZ	1:B:104:LYS:HG3	2.26	0.66
1:B:46:GLU:CG	1:B:47:GLN:HE21	2.08	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:MSE:HE3	1:A:230:LEU:HD11	1.77	0.65
1:A:160:MSE:CE	1:B:93:VAL:HG23	2.21	0.65
1:A:226:MSE:HE3	1:A:230:LEU:CD1	2.26	0.65
1:B:199:MSE:HE3	1:B:225:GLN:HG2	1.79	0.65
1:B:29:ARG:HD3	2:B:511:HOH:O	1.97	0.65
1:B:199:MSE:CE	1:B:199:MSE:HA	2.27	0.64
1:A:93:VAL:HG22	1:B:160:MSE:CE	2.27	0.64
1:B:40:PHE:CZ	1:B:44:MSE:HE3	2.33	0.63
2:A:562:HOH:O	1:B:151:LYS:HD3	1.98	0.63
1:B:31:HIS:HE1	1:B:319:SER:O	1.80	0.63
1:A:165:ASP:H	1:A:193:GLN:HE22	1.47	0.63
1:B:102:ALA:CB	1:B:103:PRO:CA	2.76	0.63
1:A:169:ARG:HH11	1:B:193:GLN:NE2	1.95	0.62
1:A:117:ILE:O	1:A:121:MSE:HB2	2.00	0.61
1:B:199:MSE:CE	1:B:225:GLN:HG2	2.32	0.60
1:B:63:ARG:NH1	2:B:508:HOH:O	2.33	0.60
1:B:199:MSE:CE	1:B:225:GLN:CG	2.79	0.60
1:A:146:VAL:CG2	1:A:146:VAL:CG1	2.72	0.59
1:A:226:MSE:CE	1:A:230:LEU:CD1	2.81	0.59
1:B:92:GLN:NE2	2:B:513:HOH:O	2.36	0.59
1:A:92:GLN:HG3	2:B:393:HOH:O	2.04	0.58
1:A:173:ARG:NH2	1:B:192:ASP:OD2	2.35	0.58
1:A:226:MSE:HE2	1:A:230:LEU:HD12	1.84	0.58
1:A:72:LEU:CD1	1:A:104[B]:LYS:HD2	2.29	0.58
1:B:98:GLY:HA3	1:B:102:ALA:HB2	1.86	0.58
1:A:160:MSE:HE3	1:B:93:VAL:N	2.19	0.57
1:B:102:ALA:HB3	1:B:103:PRO:CA	2.33	0.57
1:A:222:VAL:O	1:A:226:MSE:HG3	2.05	0.57
1:B:221:GLU:HG2	1:B:222:VAL:N	2.20	0.57
1:A:107:VAL:HG22	1:B:160:MSE:HE1	1.86	0.56
1:B:98:GLY:O	1:B:99:THR:HG22	2.04	0.56
1:A:199:MSE:HE3	1:A:222:VAL:HG13	1.88	0.56
1:B:73:ARG:HE	1:B:102:ALA:HB1	1.71	0.56
1:B:199:MSE:CE	1:B:225:GLN:HE21	2.19	0.55
1:A:121:MSE:HG2	2:A:536:HOH:O	2.06	0.55
1:B:199:MSE:HE2	1:B:225:GLN:HE21	1.71	0.54
1:B:40:PHE:CE1	1:B:44:MSE:HE3	2.43	0.53
1:B:121:MSE:HE1	2:B:461:HOH:O	2.08	0.53
1:A:146:VAL:CG1	1:A:146:VAL:CA	2.80	0.53
1:A:160:MSE:HE1	1:B:107:VAL:HG22	1.91	0.53
1:B:40:PHE:CE1	1:B:44:MSE:CE	2.92	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:LYS:CD	2:B:488:HOH:O	2.57	0.52
1:A:72:LEU:CB	1:A:104[B]:LYS:HG3	2.38	0.52
1:A:226:MSE:CE	1:A:230:LEU:HD12	2.38	0.52
1:B:99:THR:HG23	1:B:100:THR:N	2.19	0.52
1:B:175:LEU:O	1:B:178:GLY:N	2.33	0.52
1:A:160:MSE:HE1	1:B:93:VAL:HG22	1.74	0.52
1:B:121:MSE:CE	2:B:461:HOH:O	2.58	0.52
1:A:29:ARG:O	1:A:33[B]:SER:HB3	2.10	0.51
1:A:169:ARG:NH1	1:B:193:GLN:HE21	2.02	0.51
1:A:31:HIS:CE1	1:A:319:SER:O	2.61	0.50
1:B:165:ASP:H	1:B:193:GLN:HE22	1.58	0.50
1:A:151:LYS:HD2	2:B:488:HOH:O	2.11	0.50
1:B:102:ALA:HB1	1:B:103:PRO:HA	1.90	0.50
1:B:109:TYR:N	1:B:109:TYR:CD1	2.80	0.50
1:A:98:GLY:O	1:A:99:THR:C	2.50	0.49
1:A:199:MSE:HE1	1:A:222:VAL:HA	1.95	0.49
1:A:191:VAL:HG21	1:A:215:GLU:HB2	1.95	0.49
1:A:102:ALA:HB3	1:B:196:ASN:HD21	1.71	0.48
1:B:3:ASP:N	2:B:497:HOH:O	2.46	0.48
1:A:146:VAL:HB	1:A:146:VAL:CG1	2.18	0.48
1:A:199:MSE:CE	1:A:222:VAL:HA	2.44	0.48
1:B:232:GLN:HG3	1:B:233:ILE:N	2.29	0.47
1:B:117:ILE:O	1:B:121:MSE:HB2	2.14	0.47
1:B:210:PRO:HG2	1:B:240:LEU:HD12	1.96	0.47
1:B:216:LEU:HD22	1:B:222:VAL:HG11	1.97	0.47
1:B:226:MSE:HE3	1:B:230:LEU:CD1	2.45	0.47
1:A:210:PRO:O	1:A:214:ARG:HB2	2.16	0.46
1:A:93:VAL:CG2	1:B:160:MSE:CE	2.78	0.46
1:A:121:MSE:CE	1:A:121:MSE:HA	2.46	0.46
1:B:19:ASP:OD2	1:B:22:ASN:ND2	2.33	0.45
1:B:100:THR:O	1:B:101:GLY:C	2.54	0.45
1:B:195:GLN:HG3	1:B:222:VAL:HG22	1.97	0.45
1:B:98:GLY:HA3	1:B:102:ALA:CB	2.47	0.44
1:B:90:HIS:HB3	2:B:499:HOH:O	2.16	0.44
1:A:44:MSE:HE2	1:A:44:MSE:HB2	1.62	0.44
1:B:185:LYS:HB2	1:B:185:LYS:HE3	1.78	0.44
1:B:226:MSE:HE3	1:B:230:LEU:HD12	1.99	0.44
1:A:273:SER:HA	1:A:284:ILE:O	2.17	0.44
1:B:99:THR:CG2	1:B:100:THR:H	2.21	0.44
1:B:195:GLN:HE21	1:B:222:VAL:CG2	2.30	0.44
1:A:121:MSE:HE3	1:A:121:MSE:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:THR:HG21	1:A:172:LYS:CD	2.40	0.43
1:B:99:THR:C	1:B:100:THR:O	2.56	0.43
1:B:210:PRO:HB2	1:B:211:PRO:HD3	2.00	0.43
1:A:199:MSE:HE1	1:A:225:GLN:HB3	2.01	0.43
1:A:285:TYR:CE1	1:A:350:ILE:HD12	2.52	0.43
1:B:283:VAL:O	1:B:348:ALA:HA	2.19	0.43
1:B:190:LEU:O	1:B:194:VAL:HG23	2.19	0.43
1:A:70[B]:HIS:CE1	2:A:556:HOH:O	2.70	0.43
1:A:233:ILE:HG13	1:A:256:CYS:SG	2.58	0.42
1:B:316:THR:HG23	1:B:325:PRO:HA	2.02	0.42
1:B:175:LEU:O	1:B:177:GLU:N	2.53	0.42
1:B:285:TYR:CE1	1:B:350:ILE:HD12	2.55	0.42
1:B:156:ARG:NH1	1:B:156:ARG:HG2	2.15	0.41
1:B:27:LEU:HA	1:B:27:LEU:HD23	1.89	0.41
1:B:195:GLN:HE21	1:B:222:VAL:HG23	1.86	0.41
1:B:204:ARG:HD3	1:B:229:SER:O	2.20	0.41
1:B:339:VAL:O	1:B:342:PHE:HB2	2.21	0.41
1:A:44:MSE:HG3	1:A:44:MSE:O	2.20	0.41
1:B:31:HIS:HD2	2:B:367:HOH:O	2.04	0.40
1:B:266:SER:OG	1:B:327:VAL:HG11	2.21	0.40
1:B:233:ILE:HG13	1:B:256:CYS:SG	2.61	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	345/369 (94%)	329 (95%)	13 (4%)	3 (1%)	17	20
1	B	341/369 (92%)	324 (95%)	12 (4%)	5 (2%)	10	10
All	All	686/738 (93%)	653 (95%)	25 (4%)	8 (1%)	13	14

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	100	THR
1	B	102	ALA
1	A	98	GLY
1	A	99	THR
1	B	99	THR
1	B	176	SER
1	B	101	GLY
1	A	103	PRO

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	303/310 (98%)	290 (96%)	13 (4%)	29	40
1	B	299/310 (96%)	283 (95%)	16 (5%)	22	30
All	All	602/620 (97%)	573 (95%)	29 (5%)	26	36

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	LEU
1	A	47	GLN
1	A	70[A]	HIS
1	A	70[B]	HIS
1	A	74	GLN
1	A	90	HIS
1	A	92	GLN
1	A	99	THR
1	A	121	MSE
1	A	173	ARG
1	A	275	LEU
1	A	318	LEU
1	A	340	SER
1	B	46	GLU
1	B	100	THR

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Mol	Chain	Res	Type
1	B	121	MSE
1	B	156	ARG
1	B	176	SER
1	B	185	LYS
1	B	199	MSE
1	B	232	GLN
1	B	264	SER
1	B	266	SER
1	B	272	ARG
1	B	275	LEU
1	B	278	SER
1	B	318	LEU
1	B	340	SER
1	B	354	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	31	HIS
1	A	47	GLN
1	A	79	ASN
1	A	92	GLN
1	A	193	GLN
1	B	25	GLN
1	B	31	HIS
1	B	47	GLN
1	B	74	GLN
1	B	79	ASN
1	B	188	HIS
1	B	193	GLN
1	B	195	GLN
1	B	225	GLN
1	B	232	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 carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	339/369 (91%)	-0.13	13 (3%) 40 47	23, 34, 61, 76	5 (1%)
1	B	338/369 (91%)	-0.03	13 (3%) 40 47	25, 40, 64, 77	6 (1%)
All	All	677/738 (91%)	-0.08	26 (3%) 40 47	23, 37, 62, 77	11 (1%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	100	THR	8.3
1	B	100	THR	6.9
1	A	99	THR	5.1
1	A	178	GLY	4.8
1	A	101	GLY	4.6
1	A	130	ARG	4.3
1	B	99	THR	3.4
1	B	87	ALA	3.3
1	B	130	ARG	3.2
1	B	101	GLY	3.2
1	A	180	THR	2.9
1	A	102	ALA	2.9
1	B	88	ASP	2.7
1	B	98	GLY	2.7
1	A	98	GLY	2.4
1	A	73	ARG	2.4
1	B	178	GLY	2.3
1	A	176	SER	2.3
1	A	207	VAL	2.3
1	A	97	GLY	2.2
1	B	176	SER	2.2
1	B	179	ASP	2.2
1	B	180	THR	2.2
1	A	90	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	24	VAL	2.1
1	B	279	GLU	2.1

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.