Full wwPDB X-ray Structure Validation Report (i)

Jan 30, 2021 – 08:27 PM EST

PDB ID	:	3PZL
Title	:	The crystal structure of agmatine ureohydrolase of Thermoplasma volcanium
Authors	:	Zhang, Z.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on	:	2010-12-14
Resolution	:	2.70 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 (i)) were used in the production of this report:

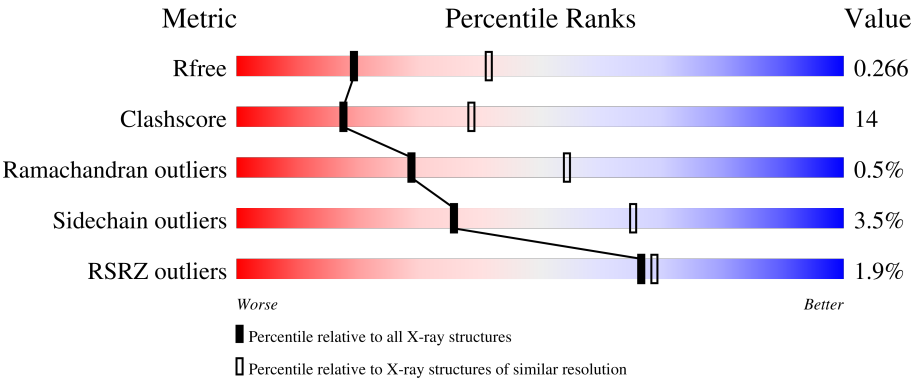
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.16
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.16

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	313	71% 20% • 7%
1	B	313	% 67% 25% • 6%
1	C	313	4% 63% 27% • 7%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6896 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 Agmatine ureohydrolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	290	Total	C	N	O	S	Se	0	0	0
			2272	1437	378	449	1	7			
1	B	293	Total	C	N	O	S	Se	0	0	0
			2296	1451	383	454	1	7			
1	C	290	Total	C	N	O	S	Se	0	0	0
			2272	1437	378	449	1	7			

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP Q97BB8
A	2	SER	-	expression tag	UNP Q97BB8
A	3	LEU	-	expression tag	UNP Q97BB8
A	306	GLU	-	expression tag	UNP Q97BB8
A	307	GLY	-	expression tag	UNP Q97BB8
A	308	HIS	-	expression tag	UNP Q97BB8
A	309	HIS	-	expression tag	UNP Q97BB8
A	310	HIS	-	expression tag	UNP Q97BB8
A	311	HIS	-	expression tag	UNP Q97BB8
A	312	HIS	-	expression tag	UNP Q97BB8
A	313	HIS	-	expression tag	UNP Q97BB8
B	1	MSE	-	expression tag	UNP Q97BB8
B	2	SER	-	expression tag	UNP Q97BB8
B	3	LEU	-	expression tag	UNP Q97BB8
B	306	GLU	-	expression tag	UNP Q97BB8
B	307	GLY	-	expression tag	UNP Q97BB8
B	308	HIS	-	expression tag	UNP Q97BB8
B	309	HIS	-	expression tag	UNP Q97BB8
B	310	HIS	-	expression tag	UNP Q97BB8
B	311	HIS	-	expression tag	UNP Q97BB8
B	312	HIS	-	expression tag	UNP Q97BB8
B	313	HIS	-	expression tag	UNP Q97BB8
C	1	MSE	-	expression tag	UNP Q97BB8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	2	SER	-	expression tag	UNP Q97BB8
C	3	LEU	-	expression tag	UNP Q97BB8
C	306	GLU	-	expression tag	UNP Q97BB8
C	307	GLY	-	expression tag	UNP Q97BB8
C	308	HIS	-	expression tag	UNP Q97BB8
C	309	HIS	-	expression tag	UNP Q97BB8
C	310	HIS	-	expression tag	UNP Q97BB8
C	311	HIS	-	expression tag	UNP Q97BB8
C	312	HIS	-	expression tag	UNP Q97BB8
C	313	HIS	-	expression tag	UNP Q97BB8

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

- Molecule 3 is water.

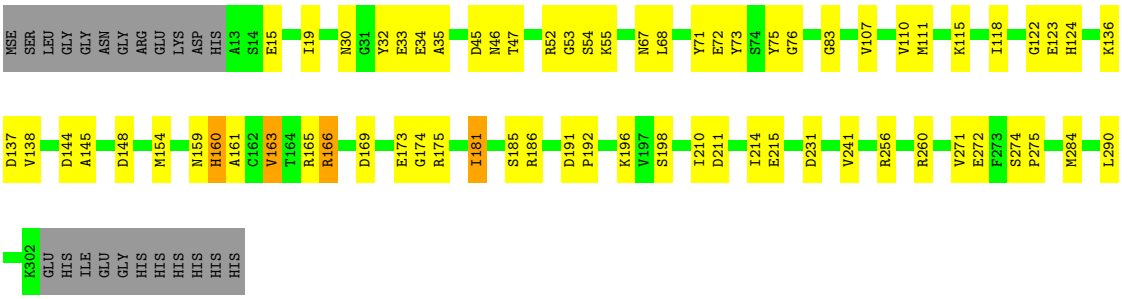
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	25	Total O 25 25	0	0
3	B	10	Total O 10 10	0	0
3	C	15	Total O 15 15	0	0

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.

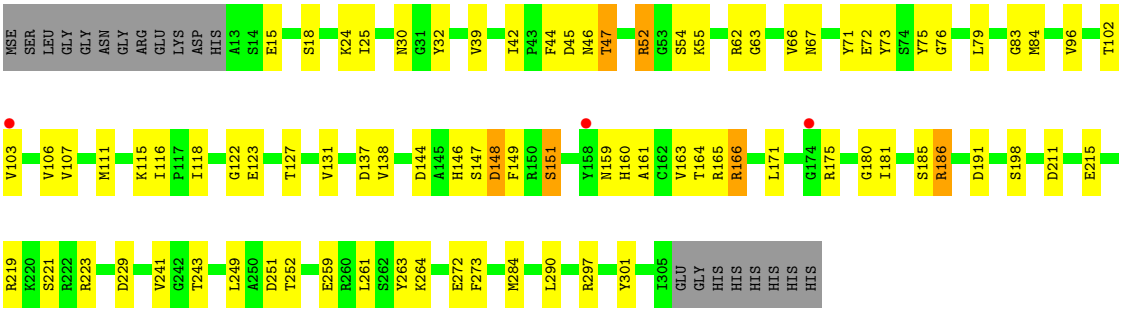
• Molecule 1: Agmatine ureohydrolase

Chain A:



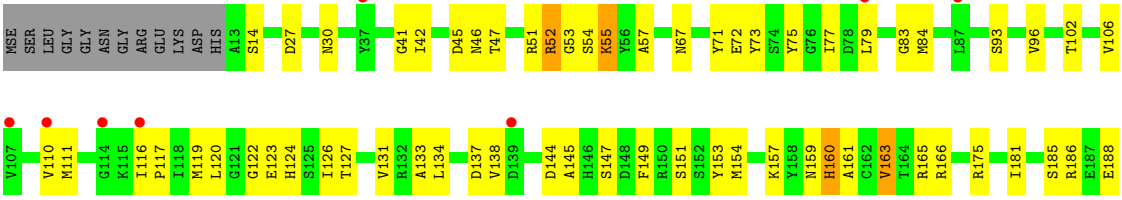
• Molecule 1: Agmatine ureohydrolase

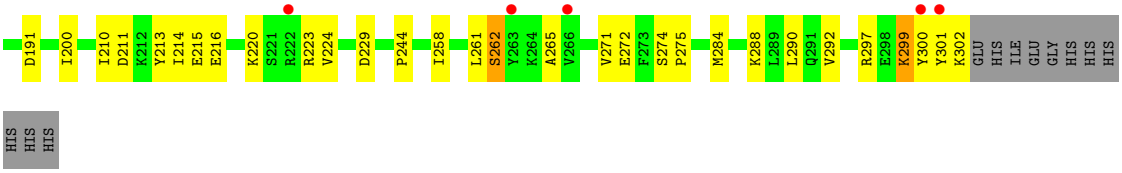
Chain B:



• Molecule 1: Agmatine ureohydrolase

Chain C:




D191
I200
I210
D211
K212
Y213
I214
E215
E216
K220
S221
R222
R223
V224
D229
P244
I258
L261
S262
Y263
K264
A265
V266
V271
E272
F273
S274
P275
M284
K288
L289
L290
Q291
V292
R297
E298
K299
Y300
Y301
K302
GLU
HIS
ILE
GLU
GLY
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	95.14Å 95.14Å 198.38Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	82.39 – 2.70 63.38 – 2.70	Depositor EDS
% Data completeness (in resolution range)	93.9 (82.39-2.70) 94.0 (63.38-2.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.66 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.220 , 0.271 0.210 , 0.266	Depositor DCC
R_{free} test set	1398 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	59.4	Xtriage
Anisotropy	0.479	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 27.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6896	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% 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: MN

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	0.76	0/2307	0.70	0/3104
1	B	0.73	0/2332	0.72	0/3138
1	C	0.74	1/2307 (0.0%)	0.72	0/3104
All	All	0.74	1/6946 (0.0%)	0.71	0/9346

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	216	GLU	CG-CD	5.04	1.59	1.51

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2272	0	2231	49	0
1	B	2296	0	2246	75	0
1	C	2272	0	2231	66	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	25	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	0	1	0
3	C	15	0	0	1	0
All	All	6896	0	6708	185	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 14.

All (185) 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:67:ASN:HD22	1:B:284:MSE:HE2	1.37	0.89
1:C:45:ASP:HB2	1:C:55:LYS:HG3	1.55	0.88
1:A:137:ASP:HB2	3:A:322:HOH:O	1.76	0.86
1:C:211:ASP:O	1:C:215:GLU:HG2	1.79	0.83
1:A:45:ASP:HB2	1:A:55:LYS:HG3	1.62	0.81
1:A:54:SER:HB3	1:A:122:GLY:CA	2.09	0.81
1:B:79:LEU:HB3	1:B:84:MSE:CE	2.10	0.80
1:C:54:SER:HB3	1:C:122:GLY:CA	2.12	0.79
1:C:67:ASN:HB3	1:C:284:MSE:HE1	1.64	0.78
1:A:159:ASN:HD22	1:A:161:ALA:H	1.32	0.77
1:B:72:GLU:HG2	1:B:75:TYR:HD2	1.48	0.76
1:A:54:SER:HB3	1:A:122:GLY:HA2	1.68	0.75
1:B:54:SER:HB3	1:B:122:GLY:CA	2.17	0.75
1:C:185:SER:HB3	1:C:188:GLU:OE1	1.85	0.75
1:B:47:THR:HG21	1:B:160:HIS:H	1.53	0.74
1:A:136:LYS:HA	1:A:175:ARG:NH2	2.02	0.74
1:A:256:ARG:NH2	1:A:260:ARG:HD3	2.03	0.73
1:C:138:VAL:O	1:C:175:ARG:NH1	2.23	0.72
1:A:136:LYS:HA	1:A:175:ARG:HH22	1.55	0.71
1:B:45:ASP:HB2	1:B:55:LYS:HG3	1.73	0.70
1:B:45:ASP:HB2	1:B:55:LYS:CG	2.22	0.69
1:B:159:ASN:HD22	1:B:161:ALA:H	1.40	0.69
1:B:159:ASN:ND2	1:B:161:ALA:H	1.91	0.69
1:B:42:ILE:HD13	1:B:103:VAL:HG22	1.75	0.67
1:C:72:GLU:HG2	1:C:75:TYR:HD2	1.60	0.66
1:B:147:SER:O	1:B:149:PHE:N	2.29	0.65
1:A:211:ASP:O	1:A:215:GLU:HG2	1.97	0.65
1:B:151:SER:O	1:B:166:ARG:NH2	2.30	0.65
1:A:165:ARG:NH2	1:A:191:ASP:OD2	2.29	0.64
1:C:54:SER:HB3	1:C:122:GLY:HA3	1.80	0.64
1:B:67:ASN:ND2	1:B:284:MSE:HE2	2.10	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:165:ARG:NH2	1:C:191:ASP:OD2	2.31	0.63
1:C:46:ASN:HA	1:C:52:ARG:HH22	1.61	0.63
1:C:106:VAL:O	1:C:110:VAL:HG23	1.97	0.63
1:C:119:MSE:SE	1:C:126:ILE:HD12	2.48	0.63
1:B:211:ASP:O	1:B:215:GLU:HG2	1.99	0.62
1:A:173:GLU:HG2	1:A:174:GLY:N	2.15	0.62
1:C:46:ASN:HA	1:C:52:ARG:NH2	2.15	0.61
1:B:42:ILE:HD13	1:B:103:VAL:CG2	2.29	0.61
1:C:220:LYS:O	1:C:220:LYS:HG2	2.00	0.61
1:B:67:ASN:HD22	1:B:284:MSE:CE	2.11	0.61
1:B:67:ASN:HB3	1:B:284:MSE:HE1	1.80	0.61
1:A:33:GLU:HG3	1:A:34:GLU:HG3	1.81	0.60
1:A:30:ASN:ND2	1:A:83:GLY:HA2	2.17	0.60
1:B:118:ILE:HG21	1:B:290:LEU:HD13	1.83	0.60
1:B:54:SER:HB3	1:B:122:GLY:HA3	1.82	0.60
1:B:44:PHE:HZ	1:B:96:VAL:HG22	1.68	0.59
1:A:72:GLU:HG2	1:A:75:TYR:HD2	1.67	0.59
1:C:67:ASN:HD22	1:C:284:MSE:HE2	1.68	0.59
1:A:181:ILE:HD11	1:B:73:TYR:CE1	2.38	0.58
1:C:157:LYS:HB3	1:C:166:ARG:HH21	1.68	0.58
1:B:221:SER:O	1:B:264:LYS:NZ	2.36	0.58
1:B:42:ILE:CD1	1:B:103:VAL:HG22	2.33	0.58
1:B:137:ASP:OD2	1:B:223:ARG:HD3	2.04	0.57
1:C:200:ILE:HD13	1:C:213:TYR:CD1	2.40	0.57
1:A:173:GLU:HG2	1:A:174:GLY:H	1.69	0.57
1:A:210:ILE:O	1:A:214:ILE:HG13	2.05	0.56
1:B:79:LEU:HB3	1:B:84:MSE:HE1	1.86	0.56
1:A:35:ALA:O	1:A:115:LYS:HE3	2.06	0.56
1:A:166:ARG:NH1	1:A:169:ASP:OD2	2.38	0.56
1:B:47:THR:CG2	1:B:160:HIS:H	2.16	0.55
1:C:102:THR:O	1:C:106:VAL:HG22	2.07	0.55
1:C:53:GLY:HA3	1:C:274:SER:OG	2.07	0.55
1:C:72:GLU:CG	1:C:75:TYR:HD2	2.20	0.55
1:B:79:LEU:HB3	1:B:84:MSE:HE2	1.86	0.54
1:B:63:GLY:O	1:B:66:VAL:HG22	2.07	0.54
1:A:138:VAL:O	1:A:175:ARG:NH1	2.40	0.54
1:B:32:TYR:O	1:B:115:LYS:HE3	2.08	0.54
1:C:41:GLY:O	1:C:42:ILE:HD13	2.09	0.53
1:B:186:ARG:HB3	1:C:71:TYR:CG	2.43	0.53
1:C:160:HIS:HD2	1:C:272:GLU:OE2	1.91	0.53
1:A:107:VAL:O	1:A:111:MSE:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:27:ASP:HB3	1:C:84:MSE:HE1	1.90	0.52
1:A:55:LYS:HD2	3:A:321:HOH:O	2.08	0.52
1:B:146:HIS:CE1	1:B:243:THR:OG1	2.63	0.52
1:A:186:ARG:HG2	1:A:186:ARG:HH21	1.74	0.52
1:A:124:HIS:HA	1:A:271:VAL:HG21	1.93	0.51
1:C:77:ILE:HD11	1:C:299:LYS:HA	1.92	0.51
1:C:30:ASN:ND2	1:C:83:GLY:HA2	2.25	0.51
1:B:146:HIS:HE1	1:B:243:THR:OG1	1.93	0.51
1:C:111:MSE:HE1	1:C:133:ALA:O	2.10	0.51
1:A:67:ASN:HD22	1:A:284:MSE:HE2	1.75	0.51
1:C:153:TYR:HD2	1:C:159:ASN:ND2	2.09	0.50
1:B:171:LEU:HD22	1:B:175:ARG:CZ	2.41	0.50
1:C:27:ASP:CB	1:C:84:MSE:HE1	2.42	0.50
1:A:118:ILE:HG21	1:A:290:LEU:CD1	2.41	0.50
1:C:14:SER:HB2	3:C:326:HOH:O	2.12	0.50
1:C:160:HIS:O	1:C:163:VAL:HG12	2.12	0.50
1:B:24:LYS:HA	1:B:62:ARG:HD3	1.94	0.49
1:B:75:TYR:OH	1:B:259:GLU:HG3	2.12	0.49
1:C:144:ASP:OD1	1:C:145:ALA:N	2.45	0.49
1:C:27:ASP:HB3	1:C:84:MSE:CE	2.42	0.49
1:B:181:ILE:C	1:B:181:ILE:HD12	2.33	0.49
1:B:180:GLY:HA2	1:B:249:LEU:HD21	1.94	0.49
1:B:46:ASN:HA	1:B:52:ARG:HH12	1.76	0.49
1:C:124:HIS:CD2	1:C:271:VAL:HG21	2.47	0.49
1:C:137:ASP:OD1	1:C:223:ARG:NH1	2.45	0.49
1:B:45:ASP:CB	1:B:55:LYS:HG3	2.41	0.49
1:C:229:ASP:OD2	1:C:272:GLU:HG3	2.13	0.49
1:C:54:SER:HB3	1:C:122:GLY:HA2	1.92	0.49
1:C:45:ASP:C	1:C:123:GLU:OE2	2.51	0.49
1:A:210:ILE:HG13	1:A:214:ILE:HD11	1.95	0.48
1:B:138:VAL:O	1:B:175:ARG:NH1	2.44	0.48
1:A:67:ASN:HD22	1:A:284:MSE:CE	2.26	0.48
1:B:263:TYR:OH	1:B:264:LYS:HE3	2.13	0.48
1:B:148:ASP:HB2	1:B:163:VAL:CG1	2.43	0.48
1:B:54:SER:HB3	1:B:122:GLY:HA2	1.95	0.48
1:C:57:ALA:HA	1:C:275:PRO:HG3	1.96	0.47
1:B:144:ASP:OD2	1:B:229:ASP:OD2	2.33	0.47
1:B:47:THR:HG22	1:B:123:GLU:CD	2.34	0.47
1:C:47:THR:N	1:C:123:GLU:OE2	2.37	0.47
1:C:79:LEU:HB3	1:C:84:MSE:CE	2.45	0.47
1:A:160:HIS:HD2	1:A:272:GLU:OE2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:131:VAL:HA	1:C:134:LEU:HD12	1.96	0.47
1:B:71:TYR:OH	1:B:76:GLY:HA2	2.15	0.47
1:C:159:ASN:HD22	1:C:161:ALA:H	1.61	0.46
1:C:75:TYR:O	1:C:77:ILE:HG12	2.15	0.46
1:B:148:ASP:HB2	1:B:163:VAL:HG13	1.97	0.46
1:A:186:ARG:HG2	1:A:186:ARG:NH2	2.29	0.46
1:B:165:ARG:NH1	1:B:191:ASP:OD2	2.48	0.46
1:A:32:TYR:O	1:A:115:LYS:HE2	2.14	0.46
1:A:231:ASP:HA	1:A:241:VAL:HG11	1.97	0.46
1:B:47:THR:HG21	1:B:160:HIS:N	2.25	0.46
1:A:71:TYR:OH	1:A:76:GLY:HA2	2.16	0.46
1:B:160:HIS:HD2	1:B:272:GLU:OE2	1.99	0.46
1:C:116:ILE:HA	1:C:117:PRO:HD3	1.78	0.45
1:A:15:GLU:O	1:A:19:ILE:HG13	2.16	0.45
1:B:30:ASN:ND2	1:B:83:GLY:HA2	2.32	0.45
1:C:165:ARG:CZ	1:C:191:ASP:OD2	2.65	0.45
1:A:68:LEU:HG	1:A:284:MSE:HE1	1.99	0.45
1:C:153:TYR:CZ	1:C:154:MSE:HE2	2.51	0.45
1:B:25:ILE:HD12	1:B:39:VAL:HG11	1.99	0.45
1:C:262:SER:OG	1:C:297:ARG:HB2	2.17	0.45
1:C:300:TYR:C	1:C:302:LYS:H	2.20	0.45
1:B:72:GLU:CG	1:B:75:TYR:HD2	2.25	0.45
1:A:47:THR:N	1:A:123:GLU:OE2	2.45	0.44
1:A:148:ASP:CB	1:A:163:VAL:HG13	2.48	0.44
1:B:165:ARG:NH2	1:B:191:ASP:OD2	2.49	0.44
1:C:51:ARG:NH1	1:C:244:PRO:HG3	2.33	0.44
1:B:116:ILE:CD1	1:B:297:ARG:CZ	2.95	0.44
1:C:41:GLY:HA2	1:C:120:LEU:O	2.17	0.44
1:B:45:ASP:HB2	1:B:55:LYS:HG2	1.96	0.44
1:B:148:ASP:O	1:B:164:THR:N	2.51	0.44
1:B:67:ASN:HB3	1:B:284:MSE:CE	2.48	0.43
1:A:173:GLU:HG3	1:A:196:LYS:HA	1.99	0.43
1:C:220:LYS:CG	1:C:220:LYS:O	2.65	0.43
1:B:116:ILE:HD11	1:B:297:ARG:CZ	2.49	0.43
1:B:215:GLU:HB3	1:B:219:ARG:NH1	2.33	0.43
1:B:241:VAL:HA	1:B:273:PHE:HA	2.01	0.43
1:C:258:ILE:HG22	1:C:292:VAL:HG12	2.00	0.43
1:B:32:TYR:CE1	1:B:115:LYS:HD3	2.53	0.43
1:B:107:VAL:HG12	1:B:111:MSE:HE2	2.00	0.43
1:B:186:ARG:HB3	1:C:71:TYR:CD2	2.53	0.43
1:A:166:ARG:HD3	1:A:166:ARG:HA	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:ASP:OD1	1:A:145:ALA:N	2.52	0.42
1:A:68:LEU:HG	1:A:284:MSE:CE	2.49	0.42
1:C:153:TYR:OH	1:C:154:MSE:HE2	2.20	0.42
1:A:110:VAL:HG13	1:A:115:LYS:HB2	2.01	0.42
1:A:210:ILE:CG1	1:A:214:ILE:HD11	2.49	0.42
1:C:127:THR:O	1:C:131:VAL:HG23	2.19	0.42
1:B:181:ILE:HD11	1:C:73:TYR:CE1	2.55	0.42
1:A:274:SER:HA	1:A:275:PRO:HD3	1.84	0.42
1:A:30:ASN:HD22	1:A:83:GLY:HA2	1.83	0.42
1:C:46:ASN:CA	1:C:52:ARG:HH22	2.31	0.42
1:B:47:THR:N	1:B:123:GLU:OE2	2.52	0.42
1:A:73:TYR:CE1	1:C:181:ILE:HD11	2.55	0.42
1:C:67:ASN:HD22	1:C:284:MSE:CE	2.32	0.42
1:B:297:ARG:O	1:B:301:TYR:HD2	2.03	0.42
1:C:224:VAL:O	1:C:265:ALA:HA	2.20	0.42
1:A:165:ARG:HD2	1:A:165:ARG:HA	1.85	0.41
1:B:15:GLU:O	1:B:18:SER:HB3	2.21	0.41
1:B:171:LEU:HD22	1:B:175:ARG:NH1	2.35	0.41
1:B:251:ASP:OD1	1:B:252:THR:N	2.50	0.41
1:B:84:MSE:HB2	3:B:324:HOH:O	2.20	0.41
1:B:102:THR:O	1:B:106:VAL:HG23	2.20	0.41
1:C:149:PHE:O	1:C:165:ARG:NH1	2.53	0.41
1:A:191:ASP:OD1	1:A:192:PRO:HD2	2.20	0.41
1:B:127:THR:O	1:B:131:VAL:HG23	2.19	0.41
1:C:163:VAL:CG2	1:C:163:VAL:O	2.69	0.41
1:A:52:ARG:HG3	1:A:53:GLY:H	1.85	0.41
1:B:45:ASP:OD2	1:B:55:LYS:HG3	2.21	0.40
1:C:210:ILE:O	1:C:214:ILE:HG13	2.20	0.40
1:B:67:ASN:ND2	1:B:284:MSE:CE	2.79	0.40
1:C:151:SER:O	1:C:166:ARG:NH2	2.54	0.40
1:C:288:LYS:HA	1:C:288:LYS:HD2	1.90	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	288/313 (92%)	272 (94%)	15 (5%)	1 (0%)	41	66
1	B	291/313 (93%)	276 (95%)	14 (5%)	1 (0%)	41	66
1	C	288/313 (92%)	269 (93%)	17 (6%)	2 (1%)	22	46
All	All	867/939 (92%)	817 (94%)	46 (5%)	4 (0%)	29	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	55	LYS
1	A	46	ASN
1	C	301	TYR
1	B	148	ASP

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	247/258 (96%)	240 (97%)	7 (3%)	43	73
1	B	249/258 (96%)	241 (97%)	8 (3%)	39	68
1	C	247/258 (96%)	236 (96%)	11 (4%)	27	55
All	All	743/774 (96%)	717 (96%)	26 (4%)	36	65

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	MSE
1	A	160	HIS
1	A	163	VAL
1	A	166	ARG
1	A	181	ILE
1	A	185	SER

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Mol	Chain	Res	Type
1	A	198	SER
1	B	47	THR
1	B	52	ARG
1	B	151	SER
1	B	166	ARG
1	B	185	SER
1	B	186	ARG
1	B	198	SER
1	B	261	LEU
1	C	52	ARG
1	C	93	SER
1	C	96	VAL
1	C	147	SER
1	C	160	HIS
1	C	163	VAL
1	C	186	ARG
1	C	261	LEU
1	C	262	SER
1	C	290	LEU
1	C	299	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN
1	A	159	ASN
1	A	160	HIS
1	B	30	ASN
1	B	67	ASN
1	B	146	HIS
1	B	159	ASN
1	B	160	HIS
1	B	304	HIS
1	C	30	ASN
1	C	67	ASN
1	C	159	ASN
1	C	160	HIS

5.3.3 RNA

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 6 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, 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	283/313 (90%)	-0.08	0 100 100	40, 53, 71, 82	0
1	B	286/313 (91%)	-0.03	3 (1%) 82 83	41, 57, 77, 84	0
1	C	283/313 (90%)	0.15	13 (4%) 32 31	44, 65, 82, 100	0
All	All	852/939 (90%)	0.01	16 (1%) 66 69	40, 58, 79, 100	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	103	VAL	4.5
1	C	222	ARG	4.1
1	C	37	TYR	3.4
1	C	114	GLY	3.1
1	B	158	TYR	3.0
1	C	107	VAL	2.8
1	C	300	TYR	2.8
1	C	266	VAL	2.7
1	C	263	TYR	2.6
1	C	87	LEU	2.5
1	B	174	GLY	2.5
1	C	301	TYR	2.5
1	C	116	ILE	2.2
1	C	79	LEU	2.1
1	C	110	VAL	2.1
1	C	139	ASP	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 (i)

There are no monosaccharides 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	MN	A	315	1/1	0.90	0.06	64,64,64,64	0
2	MN	C	314	1/1	0.90	0.04	62,62,62,62	0
2	MN	B	315	1/1	0.91	0.05	63,63,63,63	0
2	MN	C	315	1/1	0.93	0.14	56,56,56,56	0
2	MN	A	314	1/1	0.98	0.14	47,47,47,47	0
2	MN	B	314	1/1	0.98	0.11	56,56,56,56	0

6.5 Other polymers (i)

There are no such residues in this entry.