Full wwPDB X-ray Structure Validation Report (i)

Oct 10, 2021 – 05:08 PM EDT

PDB ID	:	3CWX
Title	:	Crystal structure of cagd from helicobacter pylori pathogenicity island
Authors	:	Cendron, L.; Zanotti, G.; Angelini, A.; Barison, N.; Couturier, M.; Stein, M.
Deposited on	:	2008-04-23
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:

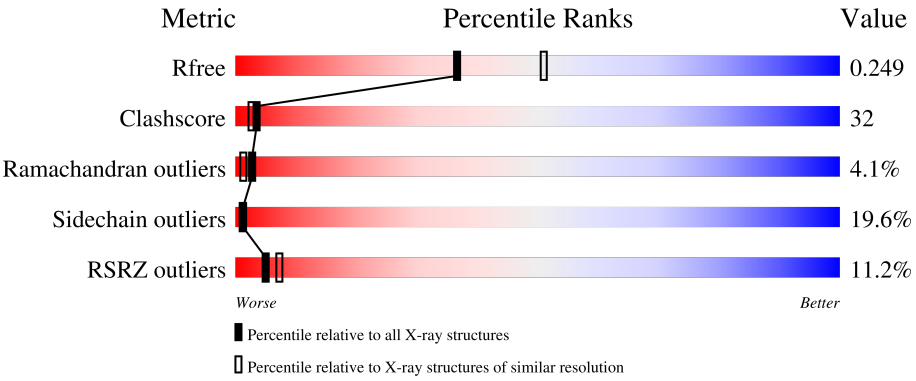
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 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	176	8% 30% 31% 10% 29%
1	B	176	4% 37% 26% 7% • 29%
1	C	176	11% 23% 34% 14% • 29%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3263 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 protein CagD.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	125	Total	C	N	O	S	Se	0	0	0
			1035	672	165	192	3	3			
1	B	125	Total	C	N	O	S	Se	0	0	0
			1035	672	165	192	3	3			
1	C	125	Total	C	N	O	S	Se	0	0	0
			1035	672	165	192	3	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	79	MSE	VAL	engineered mutation	UNP P94837
A	97	ILE	LEU	engineered mutation	UNP P94837
A	135	ASN	ASP	engineered mutation	UNP P94837
A	140	MSE	VAL	engineered mutation	UNP P94837
B	79	MSE	VAL	engineered mutation	UNP P94837
B	97	ILE	LEU	engineered mutation	UNP P94837
B	135	ASN	ASP	engineered mutation	UNP P94837
B	140	MSE	VAL	engineered mutation	UNP P94837
C	79	MSE	VAL	engineered mutation	UNP P94837
C	97	ILE	LEU	engineered mutation	UNP P94837
C	135	ASN	ASP	engineered mutation	UNP P94837
C	140	MSE	VAL	engineered mutation	UNP P94837

- Molecule 2 is water.

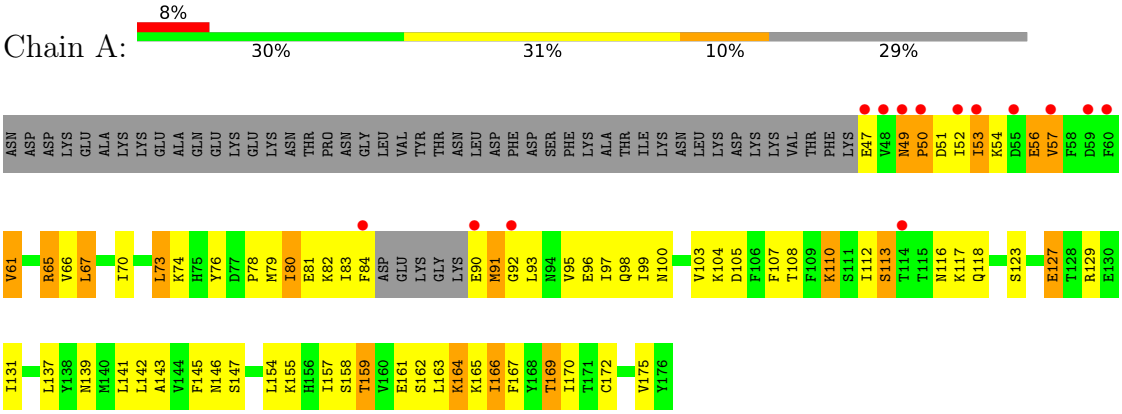
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	45	Total	O	0	0
			45	45		
2	B	80	Total	O	0	0
			80	80		
2	C	33	Total	O	0	0
			33	33		

3 Residue-property plots

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.

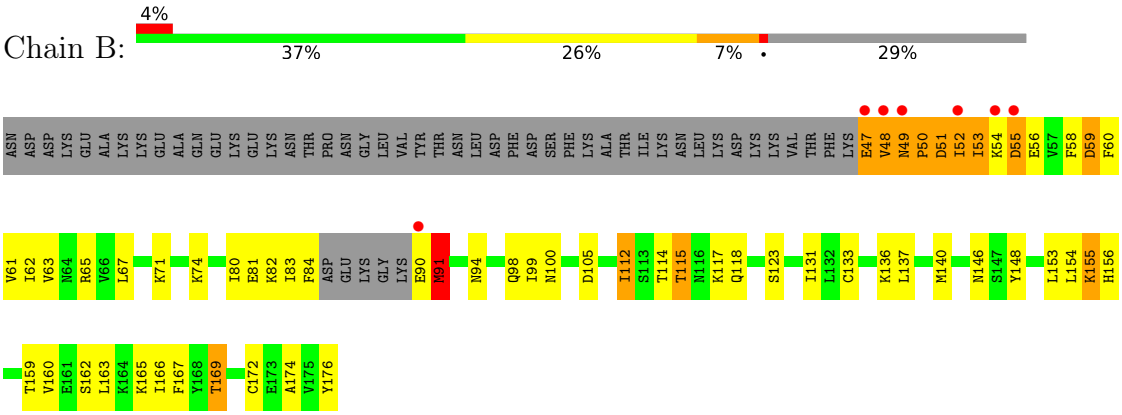
• Molecule 1: protein CagD

Chain A:



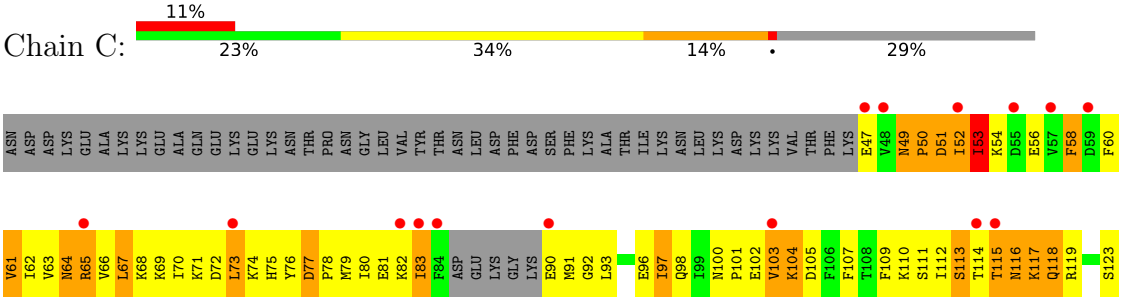
• Molecule 1: protein CagD

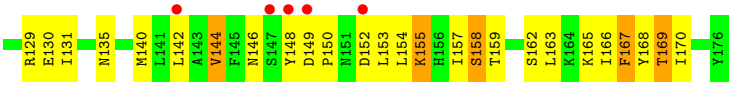
Chain B:



• Molecule 1: protein CagD

Chain C:




R129
E130
I131
N135
M140
L141
L142
A143
V144
F145
N146
S147
Y148
D149
P150
N151
D152
L153
L154
K155
H156
I157
S158
T159
S162
L163
K164
K165
I166
F167
Y168
T169
I170
Y176

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	78.18Å 117.96Å 65.16Å 90.00° 110.26° 90.00°	Depositor
Resolution (Å)	62.26 – 2.30 42.44 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (62.26-2.30) 96.1 (42.44-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.71 (at 2.00Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.242 , 0.288 0.246 , 0.249	Depositor DCC
R_{free} test set	1790 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	34.9	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 100.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	3263	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.75% 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	0.41	0/1050	0.88	1/1409 (0.1%)
1	B	0.43	0/1050	0.94	1/1409 (0.1%)
1	C	0.41	0/1050	0.85	1/1409 (0.1%)
All	All	0.42	0/3150	0.89	3/4227 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	129	ARG	NE-CZ-NH1	-6.28	117.16	120.30
1	B	167	PHE	CB-CG-CD2	5.44	124.61	120.80
1	C	167	PHE	CB-CG-CD2	5.05	124.33	120.80

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	1035	0	1052	64	0
1	B	1035	0	1052	54	0
1	C	1035	0	1053	88	0
2	A	45	0	0	2	0
2	B	80	0	0	10	0
2	C	33	0	0	1	0
All	All	3263	0	3157	201	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 32.

All (201) 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:53:ILE:HD13	1:B:80:ILE:HD13	1.52	0.92
1:B:98:GLN:HE22	1:B:105:ASP:H	1.20	0.89
1:B:98:GLN:NE2	1:B:105:ASP:H	1.84	0.76
1:C:155:LYS:O	1:C:159:THR:HG23	1.85	0.76
1:C:100:ASN:HB3	1:C:103:VAL:HG23	1.69	0.75
1:A:70:ILE:HA	1:A:146:ASN:HD21	1.51	0.73
1:B:49:ASN:OD1	1:B:81:GLU:HG2	1.89	0.72
1:B:155:LYS:O	1:B:159:THR:HG23	1.89	0.72
1:B:162:SER:O	1:B:166:ILE:HD12	1.89	0.72
1:C:61:VAL:O	1:C:65:ARG:HB2	1.91	0.70
1:A:98:GLN:HE22	1:A:105:ASP:H	1.39	0.69
1:A:50:PRO:HG3	1:A:82:LYS:HG3	1.73	0.69
1:C:117:LYS:HD2	1:C:118:GLN:H	1.58	0.68
1:C:98:GLN:HE22	1:C:105:ASP:H	1.42	0.68
1:B:71:LYS:H	1:B:146:ASN:HD21	1.41	0.67
1:B:59:ASP:HB2	2:B:256:HOH:O	1.94	0.67
1:C:50:PRO:HD2	1:C:81:GLU:HA	1.76	0.67
1:B:62:ILE:HB	1:B:118:GLN:OE1	1.95	0.67
1:A:98:GLN:NE2	1:A:105:ASP:H	1.92	0.67
1:A:155:LYS:O	1:A:159:THR:HG23	1.94	0.66
1:B:52:ILE:HA	2:B:238:HOH:O	1.95	0.66
1:A:73:LEU:O	1:A:78:PRO:HD3	1.96	0.66
1:C:71:LYS:HG3	1:C:146:ASN:OD1	1.96	0.66
1:A:83:ILE:HG22	1:A:91:MSE:SE	2.47	0.65
1:C:71:LYS:NZ	1:C:146:ASN:HB3	2.12	0.65
1:A:81:GLU:O	1:A:93:LEU:HD12	1.96	0.64
1:C:140:MSE:O	1:C:144:VAL:HG23	1.98	0.63
1:A:91:MSE:SE	1:A:91:MSE:C	2.87	0.63
1:C:60:PHE:CE2	1:C:93:LEU:HB2	2.34	0.63
1:A:143:ALA:O	1:A:147:SER:HB3	1.99	0.62
1:B:83:ILE:HG22	1:B:91:MSE:SE	2.50	0.62
1:C:47:GLU:O	1:C:47:GLU:HG2	2.00	0.62
1:B:131:ILE:HD13	1:B:137:LEU:HD13	1.80	0.62
1:B:118:GLN:HG2	1:B:133:CYS:SG	2.41	0.61
1:A:127:GLU:HG2	1:A:167:PHE:HZ	1.66	0.61
1:C:119:ARG:HG2	1:C:130:GLU:OE2	2.01	0.60
1:A:49:ASN:HB3	1:A:81:GLU:HG2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:GLN:HE22	1:B:105:ASP:N	1.96	0.60
1:C:76:TYR:HA	1:C:101:PRO:HG3	1.82	0.60
1:A:56:GLU:HG2	1:A:57:VAL:H	1.65	0.59
1:C:82:LYS:HD3	1:C:90:GLU:HB2	1.83	0.58
1:C:75:HIS:CE1	1:C:101:PRO:HG2	2.39	0.58
1:C:53:ILE:HD12	1:C:80:ILE:HD13	1.86	0.58
1:A:47:GLU:O	1:A:47:GLU:HG2	2.04	0.57
1:A:49:ASN:ND2	1:A:49:ASN:H	2.02	0.57
1:C:79:MSE:HG2	1:C:79:MSE:O	2.05	0.57
1:A:169:THR:HG22	1:B:174:ALA:HB1	1.87	0.56
1:B:155:LYS:HB3	2:B:189:HOH:O	2.05	0.56
1:C:63:VAL:HA	1:C:67:LEU:HB2	1.86	0.56
1:A:79:MSE:SE	1:A:81:GLU:HG3	2.55	0.56
1:C:129:ARG:HD2	1:C:167:PHE:CE1	2.41	0.56
1:C:58:PHE:CD2	1:C:63:VAL:HG11	2.40	0.56
1:A:98:GLN:HE22	1:A:105:ASP:N	2.03	0.56
1:C:114:THR:O	1:C:115:THR:O	2.23	0.56
1:A:113:SER:OG	1:A:118:GLN:HG3	2.07	0.55
1:B:100:ASN:HB2	2:B:230:HOH:O	2.07	0.55
1:A:73:LEU:HD12	1:A:78:PRO:HG3	1.88	0.55
1:A:99:ILE:HD12	1:A:107:PHE:CD2	2.42	0.55
1:C:111:SER:O	1:C:112:ILE:HD13	2.06	0.55
1:A:99:ILE:HD12	1:A:107:PHE:CE2	2.42	0.54
1:A:99:ILE:HD13	1:A:163:LEU:HD23	1.90	0.54
1:B:140:MSE:HG2	1:B:166:ILE:HD13	1.90	0.54
1:A:84:PHE:HD2	1:A:91:MSE:HE3	1.71	0.54
1:A:98:GLN:HE22	1:A:105:ASP:HA	1.73	0.54
1:C:83:ILE:HG13	1:C:92:GLY:C	2.27	0.54
1:C:64:ASN:N	1:C:64:ASN:HD22	2.07	0.53
1:A:175:VAL:H	1:B:169:THR:HG23	1.73	0.53
1:C:71:LYS:HZ1	1:C:146:ASN:HB3	1.74	0.53
1:C:47:GLU:O	1:C:49:ASN:OD1	2.27	0.53
1:C:90:GLU:OE2	1:C:92:GLY:O	2.26	0.53
1:A:80:ILE:CG2	1:A:93:LEU:HD11	2.39	0.53
1:A:154:LEU:O	1:A:157:ILE:HB	2.09	0.53
1:B:94:ASN:OD1	1:B:112:ILE:HD12	2.09	0.53
1:B:99:ILE:HD13	1:B:163:LEU:HD23	1.91	0.52
1:A:158:SER:HB3	2:A:216:HOH:O	2.09	0.52
1:A:175:VAL:H	1:B:169:THR:CG2	2.22	0.52
1:C:63:VAL:HG12	1:C:68:LYS:HD2	1.92	0.52
1:C:163:LEU:HA	1:C:166:ILE:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ILE:HD11	1:A:67:LEU:HD23	1.92	0.51
1:C:60:PHE:HE2	1:C:93:LEU:HB2	1.75	0.51
1:C:65:ARG:O	1:C:69:LYS:HD3	2.10	0.51
1:B:117:LYS:HD3	1:B:118:GLN:N	2.26	0.50
1:A:73:LEU:HD12	1:A:78:PRO:CG	2.42	0.50
1:C:62:ILE:HD11	1:C:109:PHE:HZ	1.77	0.50
1:A:56:GLU:HG2	1:A:57:VAL:N	2.27	0.50
1:C:52:ILE:HG13	1:C:56:GLU:OE2	2.11	0.50
1:C:70:ILE:O	1:C:70:ILE:HG22	2.12	0.50
1:C:53:ILE:O	1:C:68:LYS:HG2	2.11	0.50
1:C:100:ASN:O	1:C:103:VAL:O	2.30	0.50
1:C:82:LYS:HD3	1:C:90:GLU:CB	2.41	0.50
1:A:66:VAL:HG12	1:A:70:ILE:HD11	1.94	0.49
1:B:55:ASP:OD2	1:B:56:GLU:N	2.45	0.49
1:C:131:ILE:HD12	1:C:170:ILE:HG12	1.92	0.49
1:A:142:LEU:O	1:A:146:ASN:HB2	2.13	0.49
1:A:165:LYS:O	1:A:169:THR:HB	2.11	0.49
1:B:140:MSE:HA	1:B:140:MSE:HE2	1.94	0.49
1:B:165:LYS:O	1:B:169:THR:HB	2.13	0.49
1:C:73:LEU:HG	1:C:78:PRO:HG3	1.95	0.48
1:A:96:GLU:HG3	1:A:110:LYS:HD3	1.95	0.48
1:A:172:CYS:HA	1:B:172:CYS:HA	1.95	0.48
1:A:108:THR:OG1	1:A:123:SER:HB3	2.13	0.48
1:C:49:ASN:HA	1:C:81:GLU:HA	1.95	0.48
1:C:65:ARG:CZ	1:C:135:ASN:OD1	2.61	0.48
1:C:66:VAL:HA	1:C:142:LEU:HD21	1.95	0.48
1:B:61:VAL:HG22	2:B:181:HOH:O	2.13	0.48
1:A:98:GLN:HE22	1:A:105:ASP:CA	2.27	0.47
1:A:166:ILE:O	1:A:170:ILE:HG13	2.14	0.47
1:C:92:GLY:HA3	1:C:113:SER:O	2.14	0.47
1:C:129:ARG:HD2	1:C:167:PHE:CZ	2.49	0.47
1:A:53:ILE:HD12	1:A:80:ILE:HD12	1.96	0.47
1:C:70:ILE:HD12	1:C:73:LEU:HD12	1.96	0.47
1:A:80:ILE:HG22	1:A:93:LEU:HD11	1.97	0.47
1:B:51:ASP:HB2	2:B:233:HOH:O	2.15	0.47
1:A:76:TYR:HB3	1:A:97:ILE:HG23	1.97	0.47
1:C:63:VAL:HG12	1:C:68:LYS:NZ	2.29	0.47
1:A:80:ILE:HD13	1:A:95:VAL:HG22	1.96	0.46
1:B:166:ILE:O	1:B:169:THR:HG22	2.15	0.46
1:C:53:ILE:HD12	1:C:80:ILE:CD1	2.45	0.46
1:C:70:ILE:CD1	1:C:73:LEU:HD12	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:LYS:HZ3	1:C:146:ASN:HB3	1.79	0.46
1:C:75:HIS:O	1:C:101:PRO:HB3	2.15	0.46
1:B:53:ILE:HG23	1:B:53:ILE:O	2.15	0.46
1:C:50:PRO:HG2	1:C:80:ILE:HG22	1.97	0.46
1:B:49:ASN:HB3	1:B:80:ILE:O	2.15	0.46
1:C:77:ASP:HB3	2:C:205:HOH:O	2.15	0.46
1:A:112:ILE:N	1:A:112:ILE:HD13	2.31	0.45
1:C:71:LYS:H	1:C:146:ASN:HD21	1.65	0.45
1:B:156:HIS:O	1:B:160:VAL:HG23	2.16	0.45
1:C:83:ILE:HG13	1:C:93:LEU:N	2.32	0.45
1:C:155:LYS:NZ	1:C:158:SER:HB3	2.31	0.45
1:A:158:SER:O	1:A:161:GLU:N	2.50	0.45
1:A:100:ASN:ND2	1:A:103:VAL:HG23	2.32	0.45
1:C:49:ASN:OD1	1:C:49:ASN:N	2.50	0.45
1:A:76:TYR:CZ	1:A:145:PHE:HA	2.52	0.44
1:B:50:PRO:HD2	1:B:80:ILE:O	2.17	0.44
1:B:47:GLU:N	2:B:218:HOH:O	2.50	0.44
1:A:49:ASN:HA	1:A:81:GLU:HA	1.99	0.44
1:C:51:ASP:OD1	1:C:51:ASP:N	2.50	0.44
1:C:75:HIS:O	1:C:75:HIS:ND1	2.51	0.44
1:C:149:ASP:O	1:C:153:LEU:HG	2.17	0.44
1:C:67:LEU:HD11	1:C:97:ILE:HD11	2.00	0.44
1:B:136:LYS:NZ	2:B:194:HOH:O	2.50	0.44
1:C:77:ASP:OD2	1:C:77:ASP:N	2.51	0.44
1:C:71:LYS:N	1:C:146:ASN:HD21	2.15	0.44
1:B:49:ASN:HA	1:B:81:GLU:HA	1.99	0.44
1:A:49:ASN:CB	1:A:81:GLU:HG2	2.47	0.43
1:C:155:LYS:HD2	1:C:155:LYS:HA	1.53	0.43
1:B:53:ILE:HD13	1:B:80:ILE:CD1	2.37	0.43
1:C:129:ARG:NH1	1:C:168:TYR:HA	2.33	0.43
1:C:148:TYR:CD2	1:C:153:LEU:HD21	2.53	0.43
1:C:66:VAL:HG12	1:C:67:LEU:N	2.33	0.43
1:A:76:TYR:OH	1:A:145:PHE:O	2.30	0.43
1:A:137:LEU:O	1:A:141:LEU:HG	2.19	0.43
1:C:63:VAL:CG1	1:C:68:LYS:HD2	2.49	0.43
1:B:47:GLU:HB2	2:B:218:HOH:O	2.18	0.43
1:B:60:PHE:O	1:B:63:VAL:HB	2.18	0.43
1:B:71:LYS:H	1:B:146:ASN:ND2	2.10	0.43
1:C:62:ILE:HD11	1:C:109:PHE:CZ	2.52	0.43
1:C:111:SER:C	1:C:112:ILE:HD13	2.39	0.43
1:C:114:THR:OG1	1:C:115:THR:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:PRO:HB2	1:B:51:ASP:H	1.57	0.42
1:C:64:ASN:HD22	1:C:64:ASN:H	1.66	0.42
1:C:98:GLN:NE2	1:C:105:ASP:H	2.14	0.42
1:A:53:ILE:HG22	2:A:210:HOH:O	2.18	0.42
1:C:104:LYS:O	1:C:105:ASP:HB2	2.18	0.42
1:B:47:GLU:OE1	1:B:84:PHE:HE1	2.02	0.42
1:C:71:LYS:HG3	1:C:146:ASN:CG	2.39	0.42
1:C:83:ILE:O	1:C:90:GLU:HA	2.20	0.42
1:C:67:LEU:HD12	1:C:73:LEU:CD1	2.49	0.42
1:A:139:ASN:O	1:A:142:LEU:N	2.53	0.42
1:C:82:LYS:HD3	1:C:90:GLU:HG3	2.02	0.42
1:A:164:LYS:O	1:A:167:PHE:HB3	2.20	0.42
1:B:56:GLU:OE1	1:B:82:LYS:NZ	2.50	0.42
1:B:91:MSE:HB2	1:B:91:MSE:HE3	1.62	0.42
1:B:148:TYR:CE2	1:B:153:LEU:HD21	2.54	0.42
1:C:77:ASP:N	1:C:78:PRO:HD3	2.35	0.42
1:C:64:ASN:ND2	1:C:68:LYS:HZ2	2.18	0.42
1:A:66:VAL:HG12	1:A:70:ILE:CD1	2.49	0.41
1:B:48:VAL:HG12	2:B:231:HOH:O	2.19	0.41
1:A:50:PRO:HD2	1:A:81:GLU:HA	2.01	0.41
1:A:61:VAL:O	1:A:65:ARG:HB2	2.19	0.41
1:C:71:LYS:H	1:C:146:ASN:ND2	2.17	0.41
1:B:91:MSE:HE2	1:B:91:MSE:O	2.20	0.41
1:B:114:THR:O	1:B:115:THR:C	2.59	0.41
1:C:117:LYS:HD2	1:C:118:GLN:N	2.29	0.41
1:A:110:LYS:HE3	1:A:110:LYS:HB2	1.14	0.41
1:A:131:ILE:HD11	1:B:176:TYR:OH	2.20	0.41
1:B:61:VAL:H	1:B:61:VAL:HG13	1.67	0.41
1:A:67:LEU:HD11	1:A:97:ILE:HD11	2.01	0.41
1:B:83:ILE:O	1:B:91:MSE:HG3	2.20	0.41
1:C:149:ASP:HA	1:C:150:PRO:HD2	1.92	0.41
1:B:58:PHE:HB2	1:B:63:VAL:HG11	2.02	0.41
1:A:83:ILE:HB	1:A:92:GLY:CA	2.51	0.40
1:C:149:ASP:H	1:C:153:LEU:HD23	1.86	0.40
1:C:74:LYS:HD3	1:C:74:LYS:HA	1.70	0.40
1:C:115:THR:HB	1:C:116:ASN:H	1.45	0.40
1:B:146:ASN:HD22	1:B:146:ASN:HA	1.65	0.40
1:A:74:LYS:HA	1:A:74:LYS:HD3	1.85	0.40
1:C:73:LEU:CD2	1:C:78:PRO:HG2	2.51	0.40
1:C:64:ASN:N	1:C:64:ASN:ND2	2.70	0.40
1:C:165:LYS:O	1:C:169:THR:HB	2.21	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	121/176 (69%)	102 (84%)	16 (13%)	3 (2%)	5	4
1	B	121/176 (69%)	110 (91%)	6 (5%)	5 (4%)	3	1
1	C	121/176 (69%)	107 (88%)	7 (6%)	7 (6%)	1	0
All	All	363/528 (69%)	319 (88%)	29 (8%)	15 (4%)	3	1

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	51	ASP
1	B	115	THR
1	C	50	PRO
1	C	53	ILE
1	C	115	THR
1	C	144	VAL
1	C	152	ASP
1	A	53	ILE
1	A	56	GLU
1	B	50	PRO
1	C	51	ASP
1	B	91	MSE
1	B	55	ASP
1	C	72	ASP
1	A	50	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	121/164 (74%)	98 (81%)	23 (19%)	1	1
1	B	121/164 (74%)	104 (86%)	17 (14%)	3	3
1	C	121/164 (74%)	90 (74%)	31 (26%)	0	0
All	All	363/492 (74%)	292 (80%)	71 (20%)	1	1

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	51	ASP
1	A	52	ILE
1	A	54	LYS
1	A	57	VAL
1	A	61	VAL
1	A	65	ARG
1	A	67	LEU
1	A	73	LEU
1	A	80	ILE
1	A	90	GLU
1	A	91	MSE
1	A	104	LYS
1	A	110	LYS
1	A	113	SER
1	A	116	ASN
1	A	117	LYS
1	A	127	GLU
1	A	159	THR
1	A	162	SER
1	A	164	LYS
1	A	166	ILE
1	A	169	THR
1	B	47	GLU
1	B	48	VAL
1	B	49	ASN
1	B	52	ILE
1	B	53	ILE
1	B	54	LYS
1	B	59	ASP
1	B	65	ARG

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Mol	Chain	Res	Type
1	B	67	LEU
1	B	74	LYS
1	B	90	GLU
1	B	91	MSE
1	B	112	ILE
1	B	123	SER
1	B	154	LEU
1	B	155	LYS
1	B	169	THR
1	C	49	ASN
1	C	52	ILE
1	C	53	ILE
1	C	54	LYS
1	C	58	PHE
1	C	61	VAL
1	C	64	ASN
1	C	65	ARG
1	C	67	LEU
1	C	73	LEU
1	C	77	ASP
1	C	83	ILE
1	C	91	MSE
1	C	96	GLU
1	C	97	ILE
1	C	102	GLU
1	C	103	VAL
1	C	104	LYS
1	C	107	PHE
1	C	110	LYS
1	C	113	SER
1	C	116	ASN
1	C	117	LYS
1	C	118	GLN
1	C	123	SER
1	C	154	LEU
1	C	155	LYS
1	C	157	ILE
1	C	158	SER
1	C	162	SER
1	C	169	THR

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	49	ASN
1	A	64	ASN
1	A	98	GLN
1	A	139	ASN
1	A	146	ASN
1	B	98	GLN
1	B	116	ASN
1	B	139	ASN
1	B	146	ASN
1	C	64	ASN
1	C	98	GLN
1	C	139	ASN
1	C	146	ASN

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 monosaccharides 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	122/176 (69%)	0.90	14 (11%) 4 7	23, 47, 91, 115	0
1	B	122/176 (69%)	0.40	7 (5%) 23 30	14, 35, 76, 89	0
1	C	122/176 (69%)	1.09	20 (16%) 1 2	22, 55, 83, 112	0
All	All	366/528 (69%)	0.80	41 (11%) 5 7	14, 46, 84, 115	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	55	ASP	8.7
1	B	48	VAL	6.8
1	C	48	VAL	6.7
1	A	48	VAL	6.5
1	A	52	ILE	5.9
1	C	84	PHE	4.9
1	B	47	GLU	4.8
1	C	59	ASP	4.8
1	A	57	VAL	4.6
1	A	84	PHE	4.6
1	C	90	GLU	4.6
1	C	149	ASP	4.3
1	C	47	GLU	4.3
1	A	49	ASN	4.3
1	A	53	ILE	4.3
1	A	47	GLU	4.1
1	C	103	VAL	4.1
1	C	57	VAL	4.0
1	C	83	ILE	3.7
1	A	59	ASP	3.6
1	A	60	PHE	3.6
1	B	55	ASP	3.3
1	A	114	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	115	THR	3.1
1	C	73	LEU	3.1
1	C	82	LYS	3.0
1	C	52	ILE	2.8
1	B	49	ASN	2.7
1	B	52	ILE	2.7
1	C	148	TYR	2.7
1	C	65	ARG	2.7
1	B	90	GLU	2.5
1	C	142	LEU	2.4
1	A	92	GLY	2.4
1	C	152	ASP	2.3
1	C	55	ASP	2.3
1	B	54	LYS	2.2
1	C	114	THR	2.2
1	A	90	GLU	2.2
1	A	50	PRO	2.1
1	C	147	SER	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 monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.