Full wwPDB X-ray Structure Validation Report ⓘ

Jul 7, 2021 – 10:05 am BST

PDB ID	:	7BOB
Title	:	Exo-beta-1,4-mannosidase Op5Man5 from Opitutaceae bacterium strain TAV5
Authors	:	Kalyani, D.C.; Reichenbach, T.; Keskitalo, M.M.; Conrad, J.; Aspeborg, H.; Divne, C.
Deposited on	:	2021-01-24
Resolution	:	2.20 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 following versions of software and data (see references ⓘ) were used in the production of this report:

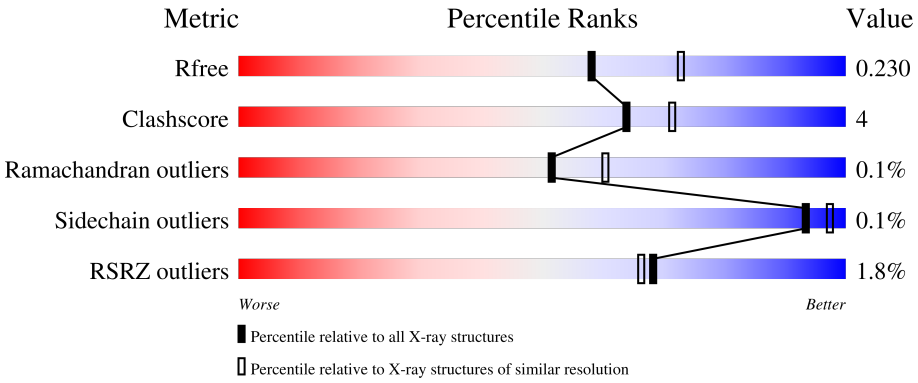
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.22
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.22

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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	601	2% 85% 8% 6%
1	B	601	2% 84% 9% 6%
1	C	601	. % 82% 11% 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 13498 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 Endo-beta-mannanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	564	Total	C	N	O	S	0	0	0
			4444	2833	785	803	23			
1	B	563	Total	C	N	O	S	0	0	0
			4440	2834	785	798	23			
1	C	560	Total	C	N	O	S	0	1	0
			4425	2824	782	796	23			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	595	ALA	-	expression tag	UNP W0J1H8
A	596	HIS	-	expression tag	UNP W0J1H8
A	597	HIS	-	expression tag	UNP W0J1H8
A	598	HIS	-	expression tag	UNP W0J1H8
A	599	HIS	-	expression tag	UNP W0J1H8
A	600	HIS	-	expression tag	UNP W0J1H8
A	601	HIS	-	expression tag	UNP W0J1H8
B	595	ALA	-	expression tag	UNP W0J1H8
B	596	HIS	-	expression tag	UNP W0J1H8
B	597	HIS	-	expression tag	UNP W0J1H8
B	598	HIS	-	expression tag	UNP W0J1H8
B	599	HIS	-	expression tag	UNP W0J1H8
B	600	HIS	-	expression tag	UNP W0J1H8
B	601	HIS	-	expression tag	UNP W0J1H8
C	595	ALA	-	expression tag	UNP W0J1H8
C	596	HIS	-	expression tag	UNP W0J1H8
C	597	HIS	-	expression tag	UNP W0J1H8
C	598	HIS	-	expression tag	UNP W0J1H8
C	599	HIS	-	expression tag	UNP W0J1H8
C	600	HIS	-	expression tag	UNP W0J1H8
C	601	HIS	-	expression tag	UNP W0J1H8

- Molecule 2 is water.

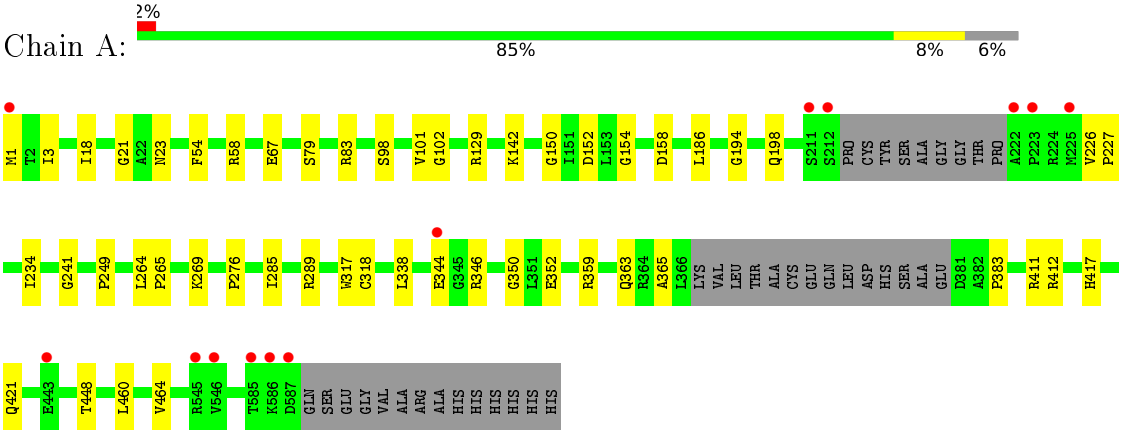
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	73	Total O 73 73	0	0
2	B	56	Total O 56 56	0	0
2	C	60	Total O 60 60	0	0

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.

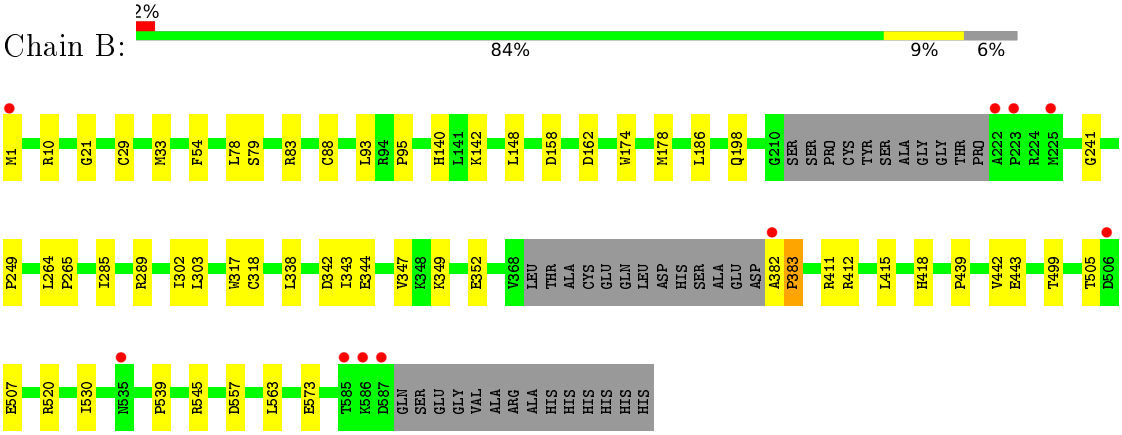
- Molecule 1: Endo-beta-mannanase

Chain A:



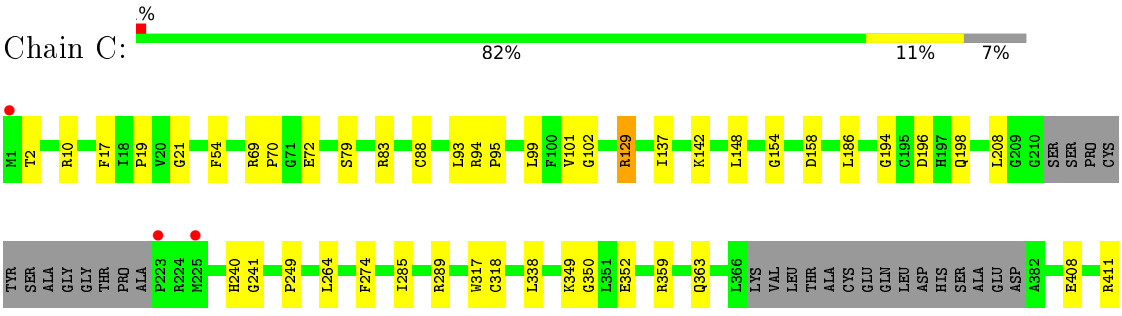
- Molecule 1: Endo-beta-mannanase

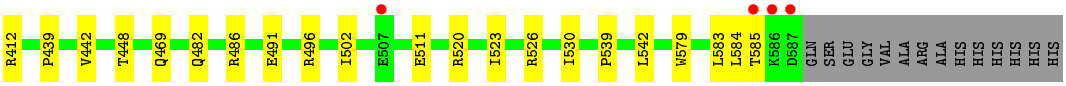
Chain B:



- Molecule 1: Endo-beta-mannanase

Chain C:




R412
P439
V442
T448
Q469
Q482
R486
E491
R496
I502
E507
E511
R520
I523
R526
I530
P539
L542
W579
L583
L584
T585
K586
D587
GLN
SER
GLU
GLY
VAL
ALA
ARG
ALA
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	102.14Å 162.45Å 168.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.87 – 2.20 49.14 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.87-2.20) 99.7 (49.14-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	1.95 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.15.2-3472	Depositor
R, R_{free}	0.201 , 0.227 0.202 , 0.230	Depositor DCC
R_{free} test set	2012 reflections (1.42%)	wwPDB-VP
Wilson B-factor (Å^2)	45.2	Xtriage
Anisotropy	0.702	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 41.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.005 for -h,l,k	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	13498	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% 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	0.47	0/4579	0.60	0/6250
1	B	0.41	0/4575	0.55	0/6244
1	C	0.43	0/4563	0.57	0/6227
All	All	0.44	0/13717	0.57	0/18721

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	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	129	ARG	Sidechain

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	4444	0	4300	31	0
1	B	4440	0	4308	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4425	0	4290	48	0
2	A	73	0	0	1	0
2	B	56	0	0	0	0
2	C	60	0	0	0	0
All	All	13498	0	12898	110	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 4.

All (110) 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:C:289:ARG:NH2	1:C:349:LYS:HZ1	1.38	1.20
1:C:289:ARG:HH21	1:C:349:LYS:NZ	1.46	1.11
1:C:289:ARG:NH2	1:C:349:LYS:NZ	2.02	1.00
1:B:505:THR:HG23	1:B:507:GLU:H	1.36	0.88
1:C:2:THR:HG23	1:C:10:ARG:HB2	1.54	0.88
1:A:241:GLY:HA3	1:A:264:LEU:HD13	1.63	0.78
1:A:344:GLU:OE1	1:A:346:ARG:HD3	1.87	0.74
1:B:412:ARG:NH2	1:B:557:ASP:OD2	2.22	0.72
1:A:129:ARG:NH1	2:A:701:HOH:O	2.22	0.72
1:C:289:ARG:CZ	1:C:349:LYS:NZ	2.57	0.68
1:B:343:ILE:H	1:B:343:ILE:HD12	1.57	0.68
1:C:289:ARG:CZ	1:C:349:LYS:HZ2	2.07	0.67
1:C:289:ARG:HE	1:C:349:LYS:HE3	1.60	0.67
1:B:249:PRO:HB2	1:B:411:ARG:HG3	1.77	0.66
1:A:344:GLU:OE1	1:A:346:ARG:CG	2.44	0.66
1:C:17:PHE:CZ	1:C:94:ARG:HD2	2.30	0.66
1:C:241:GLY:HA3	1:C:264:LEU:HD13	1.80	0.63
1:A:1:MET:HE1	1:A:150:GLY:H	1.64	0.62
1:C:249:PRO:HB2	1:C:411:ARG:HG3	1.82	0.62
1:A:344:GLU:OE1	1:A:346:ARG:CD	2.48	0.62
1:C:70:PRO:HB3	1:C:129:ARG:HE	1.65	0.61
1:B:241:GLY:HA3	1:B:264:LEU:HD13	1.84	0.59
1:C:289:ARG:NE	1:C:349:LYS:HZ2	2.02	0.57
1:B:499:THR:O	1:B:520:ARG:NH1	2.38	0.56
1:C:289:ARG:HH21	1:C:349:LYS:HZ1	0.66	0.56
1:A:344:GLU:OE1	1:A:346:ARG:HG3	2.07	0.54
1:B:79:SER:O	1:B:83:ARG:HG3	2.08	0.54
1:A:249:PRO:HB2	1:A:411:ARG:HG3	1.89	0.54
1:A:23:ASN:OD1	1:A:58:ARG:HD3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:ARG:HH11	1:B:349:LYS:HD2	1.73	0.54
1:C:289:ARG:NH2	1:C:349:LYS:HZ2	1.97	0.54
1:C:408:GLU:OE1	1:C:411:ARG:NH1	2.41	0.53
1:A:412:ARG:HD3	1:A:448:THR:O	2.09	0.53
1:C:158:ASP:OD2	1:C:198:GLN:HB2	2.09	0.52
1:C:289:ARG:HE	1:C:349:LYS:CE	2.21	0.52
1:B:78:LEU:HD22	1:B:140:HIS:CD2	2.44	0.52
1:A:67:GLU:OE2	1:A:129:ARG:NH1	2.43	0.52
1:A:352:GLU:H	1:A:352:GLU:CD	2.14	0.51
1:A:142:LYS:HG3	1:A:186:LEU:HD21	1.92	0.51
1:C:469:GLN:HB3	1:C:585:THR:OG1	2.11	0.51
1:B:530:ILE:HD13	1:B:539:PRO:HG3	1.93	0.50
1:B:439:PRO:HA	1:B:442:VAL:O	2.13	0.49
1:B:382:ALA:N	1:B:383:PRO:HD3	2.28	0.49
1:C:496:ARG:HG3	1:C:520:ARG:HB3	1.95	0.49
1:A:350:GLY:N	1:A:352:GLU:OE2	2.43	0.49
1:B:21:GLY:HA2	1:B:54:PHE:CG	2.48	0.49
1:C:579:TRP:CZ2	1:C:583:LEU:HD11	2.48	0.49
1:C:289:ARG:NE	1:C:349:LYS:NZ	2.61	0.48
1:B:158:ASP:OD2	1:B:198:GLN:HB2	2.14	0.48
1:C:412:ARG:HD3	1:C:448:THR:O	2.13	0.48
1:B:418:HIS:NE2	1:B:573:GLU:OE2	2.35	0.48
1:B:174:TRP:O	1:B:178:MET:HG2	2.14	0.48
1:C:95:PRO:HG2	1:C:148:LEU:HD23	1.97	0.47
1:B:439:PRO:O	1:B:443:GLU:HG2	2.14	0.47
1:A:285:ILE:HA	1:A:338:LEU:HD22	1.96	0.47
1:C:285:ILE:HA	1:C:338:LEU:HD22	1.97	0.47
1:C:196:ASP:HB2	1:C:240:HIS:HB2	1.97	0.47
1:C:491:GLU:HG3	1:C:526:ARG:HG3	1.97	0.47
1:B:1:MET:HB3	1:B:10:ARG:O	2.15	0.47
1:A:21:GLY:HA2	1:A:54:PHE:CG	2.50	0.46
1:C:439:PRO:HA	1:C:442:VAL:O	2.15	0.46
1:C:530:ILE:HD13	1:C:539:PRO:HG3	1.98	0.46
1:B:142:LYS:HB2	1:B:186:LEU:HD21	1.97	0.45
1:A:158:ASP:OD2	1:A:198:GLN:HB2	2.16	0.45
1:A:154:GLY:O	1:A:194:GLY:HA3	2.17	0.45
1:A:289:ARG:NH1	1:C:526:ARG:HH22	2.15	0.45
1:C:350:GLY:N	1:C:352:GLU:OE1	2.49	0.45
1:C:482:GLN:O	1:C:486:ARG:HG3	2.17	0.45
1:A:359:ARG:O	1:A:363:GLN:HG3	2.17	0.44
1:C:154:GLY:O	1:C:194:GLY:HA3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:VAL:HG13	1:A:234:ILE:O	2.16	0.44
1:B:342:ASP:OD1	1:B:344:GLU:HG2	2.18	0.44
1:A:79:SER:O	1:A:83:ARG:HG3	2.18	0.44
1:C:10:ARG:HG2	1:C:10:ARG:HH11	1.83	0.43
1:B:285:ILE:HA	1:B:338:LEU:HD22	2.00	0.43
1:C:17:PHE:CE2	1:C:19:PRO:HG3	2.52	0.43
1:A:98:SER:HA	1:A:152:ASP:HB3	2.00	0.43
1:A:317:TRP:HA	1:A:318:CYS:HA	1.82	0.43
1:C:21:GLY:HA2	1:C:54:PHE:CG	2.54	0.43
1:C:99:LEU:HD22	1:C:137:ILE:HG21	2.00	0.43
1:C:142:LYS:HG3	1:C:186:LEU:HD21	2.01	0.42
1:C:359:ARG:NH1	1:C:363:GLN:OE1	2.52	0.42
1:A:265:PRO:O	1:A:269:LYS:HG3	2.20	0.42
1:B:264:LEU:HB3	1:B:265:PRO:HD3	2.01	0.42
1:B:29:CYS:SG	1:B:33:MET:HA	2.59	0.42
1:B:302:ILE:HG13	1:B:303:LEU:N	2.34	0.42
1:B:95:PRO:HG2	1:B:148:LEU:HD23	2.01	0.42
1:C:208:LEU:HB3	1:C:274:PHE:CD1	2.55	0.42
1:A:101:VAL:HA	1:A:102:GLY:HA3	1.73	0.42
1:C:584:LEU:HD23	1:C:584:LEU:HA	1.80	0.42
1:B:415:LEU:HD22	1:B:563:LEU:HG	2.01	0.41
1:C:289:ARG:HE	1:C:349:LYS:NZ	2.18	0.41
1:A:18:ILE:HG12	1:A:365:ALA:HB2	2.01	0.41
1:B:545:ARG:HE	1:B:545:ARG:HB3	1.62	0.41
1:C:88:CYS:HB3	1:C:93:LEU:O	2.20	0.41
1:C:317:TRP:HA	1:C:318:CYS:HA	1.82	0.41
1:B:186:LEU:HD23	1:B:186:LEU:HA	1.91	0.41
1:C:101:VAL:HA	1:C:102:GLY:HA3	1.76	0.41
1:B:88:CYS:HB3	1:B:93:LEU:O	2.20	0.41
1:B:289:ARG:NH1	1:B:349:LYS:HD2	2.36	0.41
1:C:69:ARG:NH2	1:C:72:GLU:OE1	2.46	0.41
1:B:317:TRP:HA	1:B:318:CYS:HA	1.66	0.41
1:A:417:HIS:O	1:A:421:GLN:HG3	2.21	0.41
1:A:460:LEU:O	1:A:464:VAL:HG23	2.21	0.41
1:B:347:VAL:HG11	1:B:352:GLU:HA	2.02	0.41
1:C:523:ILE:HD13	1:C:542:LEU:HD11	2.01	0.40
1:C:502:ILE:HG12	1:C:511:GLU:HG3	2.03	0.40
1:C:79:SER:O	1:C:83:ARG:HG3	2.22	0.40
1:A:3:ILE:HG21	1:A:276:PRO:HG3	2.04	0.40
1:A:226:VAL:HG13	1:A:227:PRO:HD2	2.03	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	558/601 (93%)	540 (97%)	17 (3%)	1 (0%)	47 55
1	B	557/601 (93%)	537 (96%)	19 (3%)	1 (0%)	47 55
1	C	555/601 (92%)	538 (97%)	17 (3%)	0	100 100
All	All	1670/1803 (93%)	1615 (97%)	53 (3%)	2 (0%)	51 60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	383	PRO
1	A	383	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	463/492 (94%)	463 (100%)	0	100 100
1	B	462/492 (94%)	461 (100%)	1 (0%)	93 97
1	C	461/492 (94%)	461 (100%)	0	100 100
All	All	1386/1476 (94%)	1385 (100%)	1 (0%)	93 97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	162	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	570	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 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	564/601 (93%)	-0.10	13 (2%)	60	58	42, 52, 73, 102	0
1	B	563/601 (93%)	-0.09	10 (1%)	68	66	43, 58, 82, 110	0
1	C	560/601 (93%)	-0.15	7 (1%)	77	75	43, 53, 75, 99	0
All	All	1687/1803 (93%)	-0.11	30 (1%)	68	66	42, 54, 78, 110	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	7.7
1	C	586	LYS	6.9
1	B	222	ALA	6.7
1	B	586	LYS	5.6
1	A	1	MET	5.5
1	B	223	PRO	5.0
1	A	222	ALA	4.9
1	B	585	THR	4.8
1	C	223	PRO	4.7
1	C	587	ASP	4.7
1	A	225	MET	4.7
1	A	211	SER	4.7
1	C	585	THR	4.6
1	B	382	ALA	4.0
1	A	586	LYS	3.9
1	B	587	ASP	3.8
1	A	212	SER	3.3
1	A	587	ASP	3.1
1	A	585	THR	3.0
1	C	1	MET	2.9
1	B	535	ASN	2.9
1	A	223	PRO	2.8
1	B	225	MET	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	545	ARG	2.6
1	C	507	GLU	2.5
1	C	225	MET	2.4
1	A	344	GLU	2.2
1	A	443	GLU	2.2
1	B	506	ASP	2.2
1	A	546	VAL	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.