Full wwPDB X-ray Structure Validation Report (i)

Dec 17, 2023 – 03:24 pm GMT

PDB ID	:	4BCE
Title	:	crystal structure of Ttb-gly N282T mutant
Authors	:	Teze, D.; Tran, V.; Tellier, C.; Dion, M.; Leroux, C.; Roncza, J.; Czjzek, M.
Deposited on	:	2012-10-02
Resolution	:	2.00 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

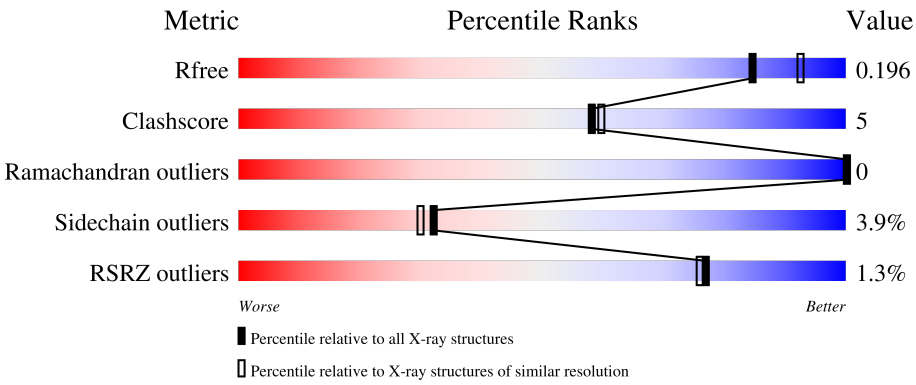
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	437	.% 84% 11% • •
1	B	437	% 85% 11% • •
1	C	437	2% 84% 12% • •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 10817 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 BETA-GLUCOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	424	3430	2209	617	599	5	0	3	0
1	B	425	3427	2207	615	600	5	0	1	0
1	C	424	3417	2202	610	600	5	0	2	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	432	HIS	-	expression tag	UNP Q53W75
A	433	HIS	-	expression tag	UNP Q53W75
A	434	HIS	-	expression tag	UNP Q53W75
A	435	HIS	-	expression tag	UNP Q53W75
A	436	HIS	-	expression tag	UNP Q53W75
A	437	HIS	-	expression tag	UNP Q53W75
A	282	THR	ASN	engineered mutation	UNP Q53W75
A	320	HIS	TYR	engineered mutation	UNP Q53W75
B	432	HIS	-	expression tag	UNP Q53W75
B	433	HIS	-	expression tag	UNP Q53W75
B	434	HIS	-	expression tag	UNP Q53W75
B	435	HIS	-	expression tag	UNP Q53W75
B	436	HIS	-	expression tag	UNP Q53W75
B	437	HIS	-	expression tag	UNP Q53W75
B	282	THR	ASN	engineered mutation	UNP Q53W75
B	320	HIS	TYR	engineered mutation	UNP Q53W75
C	432	HIS	-	expression tag	UNP Q53W75
C	433	HIS	-	expression tag	UNP Q53W75
C	434	HIS	-	expression tag	UNP Q53W75
C	435	HIS	-	expression tag	UNP Q53W75
C	436	HIS	-	expression tag	UNP Q53W75
C	437	HIS	-	expression tag	UNP Q53W75
C	282	THR	ASN	engineered mutation	UNP Q53W75

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Chain	Residue	Modelled	Actual	Comment	Reference
C	320	HIS	TYR	engineered mutation	UNP Q53W75

- Molecule 2 is water.

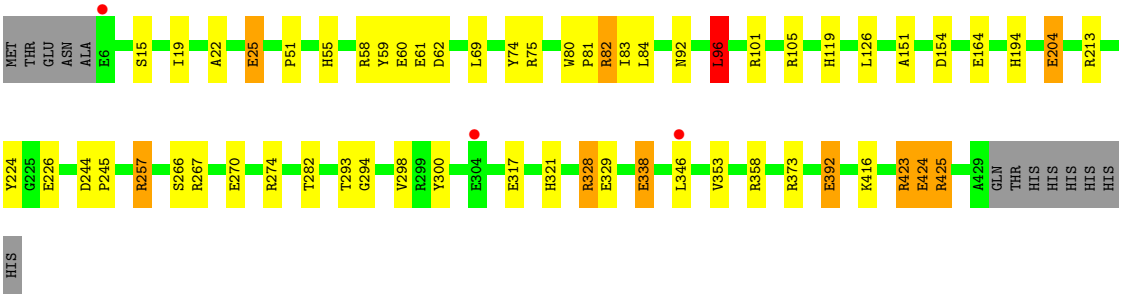
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	223	224	224	0	1
			Total	O		
2	B	187	187	187	0	0
			Total	O		
2	C	132	132	132	0	0

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.

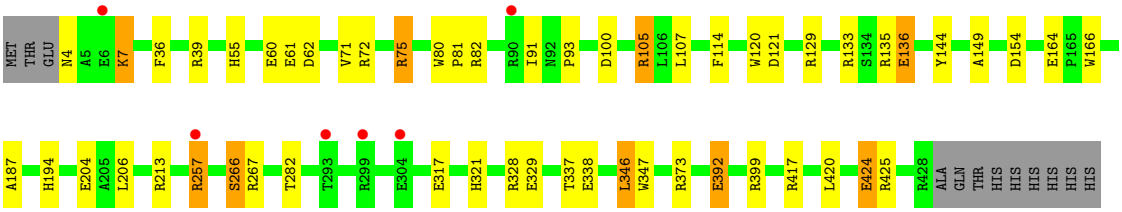
• Molecule 1: BETA-GLUCOSIDASE

Chain A:



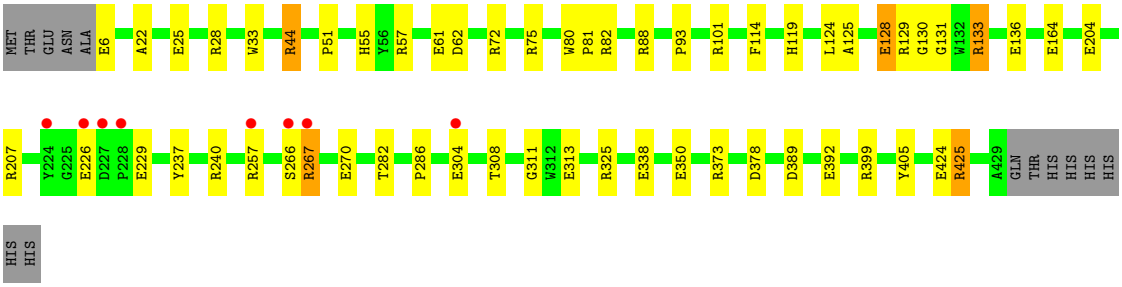
• Molecule 1: BETA-GLUCOSIDASE

Chain B:



• Molecule 1: BETA-GLUCOSIDASE

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	143.17Å 77.67Å 122.02Å 90.00° 100.08° 90.00°	Depositor
Resolution (Å)	39.97 – 2.00 39.97 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (39.97-2.00) 99.3 (39.97-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.50 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.156 , 0.190 0.173 , 0.196	Depositor DCC
R_{free} test set	4438 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	23.5	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 46.9	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	0.96	EDS
Total number of atoms	10817	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% 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 (i)

5.1 Standard geometry (i)

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	1.34	18/3542 (0.5%)	1.11	10/4831 (0.2%)
1	B	1.33	11/3539 (0.3%)	1.08	11/4828 (0.2%)
1	C	1.22	10/3529 (0.3%)	0.98	9/4815 (0.2%)
All	All	1.30	39/10610 (0.4%)	1.06	30/14474 (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	B	0	1

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	424	GLU	CG-CD	11.73	1.69	1.51
1	A	424	GLU	CD-OE1	10.09	1.36	1.25
1	C	204	GLU	CG-CD	9.38	1.66	1.51
1	C	204	GLU	CD-OE1	9.32	1.35	1.25
1	B	424	GLU	CD-OE1	9.23	1.35	1.25
1	A	204	GLU	CD-OE1	8.63	1.35	1.25
1	B	424	GLU	CG-CD	8.53	1.64	1.51
1	C	424	GLU	CG-CD	8.29	1.64	1.51
1	A	204	GLU	CG-CD	8.28	1.64	1.51
1	B	204	GLU	CD-OE1	7.80	1.34	1.25
1	A	294	GLY	N-CA	7.34	1.57	1.46
1	A	270	GLU	CG-CD	6.99	1.62	1.51
1	A	204	GLU	CB-CG	6.93	1.65	1.52
1	B	204	GLU	CG-CD	6.91	1.62	1.51
1	C	204	GLU	CB-CG	6.79	1.65	1.52
1	B	392	GLU	CG-CD	6.65	1.61	1.51
1	C	136	GLU	CG-CD	6.59	1.61	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	392	GLU	CG-CD	6.37	1.61	1.51
1	A	338	GLU	CD-OE1	6.16	1.32	1.25
1	A	226	GLU	CG-CD	6.07	1.61	1.51
1	B	204	GLU	CB-CG	5.81	1.63	1.52
1	A	74	TYR	CE1-CZ	-5.72	1.31	1.38
1	B	136	GLU	CD-OE1	5.68	1.31	1.25
1	B	329	GLU	CB-CG	-5.68	1.41	1.52
1	A	328	ARG	CG-CD	5.64	1.66	1.51
1	A	204	GLU	CD-OE2	5.61	1.31	1.25
1	C	237	TYR	CE1-CZ	5.57	1.45	1.38
1	B	71	VAL	CB-CG1	-5.53	1.41	1.52
1	A	300	TYR	CG-CD2	5.42	1.46	1.39
1	B	120	TRP	CD2-CE2	5.37	1.47	1.41
1	C	204	GLU	CD-OE2	5.31	1.31	1.25
1	C	424	GLU	CD-OE1	5.27	1.31	1.25
1	C	125	ALA	CA-CB	5.26	1.63	1.52
1	A	213	ARG	CG-CD	-5.23	1.38	1.51
1	A	329	GLU	CG-CD	5.17	1.59	1.51
1	A	328	ARG	CZ-NH2	5.17	1.39	1.33
1	A	338	GLU	CG-CD	5.16	1.59	1.51
1	C	33	TRP	CE3-CZ3	5.04	1.47	1.38
1	B	166	TRP	CE3-CZ3	5.02	1.47	1.38

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	425	ARG	NE-CZ-NH2	-13.23	113.69	120.30
1	A	293	THR	C-N-CA	-10.81	99.60	122.30
1	B	75	ARG	NE-CZ-NH2	-8.63	115.98	120.30
1	A	373	ARG	NE-CZ-NH2	-7.90	116.35	120.30
1	C	207	ARG	NE-CZ-NH1	7.37	123.98	120.30
1	A	425	ARG	NE-CZ-NH1	7.25	123.92	120.30
1	C	28	ARG	NE-CZ-NH2	-7.23	116.68	120.30
1	B	72	ARG	NE-CZ-NH2	-6.87	116.87	120.30
1	C	28	ARG	NE-CZ-NH1	6.70	123.65	120.30
1	A	96	LEU	CB-CG-CD1	6.44	121.94	111.00
1	B	213	ARG	NE-CZ-NH2	-6.40	117.10	120.30
1	C	133	ARG	NE-CZ-NH2	-6.28	117.16	120.30
1	B	373	ARG	CG-CD-NE	-6.15	98.88	111.80
1	B	154	ASP	CB-CG-OD1	6.15	123.83	118.30
1	B	135	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	A	154	ASP	CB-CG-OD1	5.97	123.67	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	358	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	B	399	ARG	NE-CZ-NH2	-5.90	117.35	120.30
1	B	82	ARG	NE-CZ-NH2	-5.83	117.39	120.30
1	B	328	ARG	NE-CZ-NH1	-5.83	117.39	120.30
1	A	96	LEU	CB-CG-CD2	-5.80	101.14	111.00
1	C	88	ARG	NE-CZ-NH2	-5.77	117.41	120.30
1	B	121	ASP	CB-CG-OD1	5.76	123.48	118.30
1	C	373	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	C	378	ASP	CB-CG-OD1	5.65	123.39	118.30
1	C	240	ARG	NE-CZ-NH2	-5.45	117.58	120.30
1	C	57	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	A	424	GLU	CG-CD-OE1	5.16	128.62	118.30
1	B	417	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	A	293	THR	O-C-N	-5.09	114.54	123.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	4	ASN	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	3430	0	3321	44	0
1	B	3427	0	3316	25	0
1	C	3417	0	3302	29	0
2	A	224	0	0	6	0
2	B	187	0	0	4	0
2	C	132	0	0	6	0
All	All	10817	0	9939	97	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 5.

All (97) 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:129:ARG:NH1	2:C:2059:HOH:O	1.74	1.18
1:A:266:SER:O	1:A:267[B]:ARG:HB2	1.51	1.07
1:A:423:ARG:HH11	1:A:423:ARG:HG2	0.99	1.07
1:A:423:ARG:HG2	1:A:423:ARG:NH1	1.75	0.97
1:C:101[B]:ARG:HH11	1:C:101[B]:ARG:HG2	1.24	0.97
1:C:257:ARG:HD2	2:C:2096:HOH:O	1.67	0.92
1:B:129:ARG:NH1	1:B:136:GLU:OE1	2.05	0.90
1:C:101[B]:ARG:HH11	1:C:101[B]:ARG:CG	1.86	0.88
1:C:101[B]:ARG:CG	1:C:101[B]:ARG:NH1	2.42	0.79
1:A:224:TYR:OH	1:A:321:HIS:HD2	1.65	0.78
1:B:257:ARG:HH11	1:B:257:ARG:HG3	1.48	0.78
1:B:392:GLU:OE1	2:B:2185:HOH:O	2.06	0.73
1:C:101[B]:ARG:CZ	2:C:2051:HOH:O	2.37	0.73
1:A:266:SER:O	1:A:267[B]:ARG:CB	2.27	0.71
1:C:101[B]:ARG:HG2	1:C:101[B]:ARG:NH1	2.02	0.70
1:C:425:ARG:NH1	2:C:2116:HOH:O	2.17	0.70
1:B:133:ARG:HD2	1:B:187:ALA:HB1	1.72	0.70
1:B:55:HIS:HD2	1:B:62:ASP:OD2	1.76	0.68
1:B:164:GLU:OE2	1:B:282:THR:HG21	1.94	0.68
1:C:55:HIS:HD2	1:C:62:ASP:OD2	1.76	0.67
1:B:194:HIS:HE1	2:B:2076:HOH:O	1.79	0.64
1:A:266:SER:O	1:A:267[A]:ARG:HB2	2.01	0.61
1:A:392:GLU:OE1	2:A:2221:HOH:O	2.16	0.61
1:A:224:TYR:OH	1:A:321:HIS:CD2	2.52	0.59
1:A:59:TYR:OH	1:A:101[A]:ARG:NE	2.36	0.59
1:A:59:TYR:OH	1:A:101[B]:ARG:NE	2.36	0.59
1:C:80:TRP:HB3	1:C:81:PRO:HD3	1.86	0.57
1:A:164:GLU:OE2	1:A:282:THR:HG21	2.04	0.56
1:A:194:HIS:HE1	2:A:2092:HOH:O	1.89	0.56
1:C:164:GLU:OE2	1:C:282:THR:HG21	2.07	0.55
1:C:350:GLU:H	1:C:350:GLU:CD	2.11	0.55
1:C:44:ARG:NH2	1:C:399:ARG:HH12	2.05	0.53
1:A:101[A]:ARG:NH2	1:A:105:ARG:HD3	2.23	0.53
1:A:101[B]:ARG:NH2	1:A:105:ARG:HD3	2.23	0.53
1:C:22:ALA:HA	1:C:25:GLU:HG3	1.90	0.53
1:C:282:THR:HG23	1:C:338:GLU:HB2	1.89	0.53
1:A:55:HIS:HD2	1:A:62:ASP:OD2	1.93	0.52
1:A:59:TYR:OH	1:A:101[A]:ARG:HD3	2.10	0.51
1:A:60:GLU:CD	1:A:101[A]:ARG:HH21	2.14	0.51
1:A:60:GLU:CD	1:A:101[B]:ARG:HH21	2.14	0.51
1:A:59:TYR:OH	1:A:101[B]:ARG:HD3	2.10	0.50
1:A:22:ALA:HB1	1:A:25:GLU:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:GLU:HG2	1:B:105:ARG:HD2	1.94	0.49
1:B:7:LYS:O	2:B:2003:HOH:O	2.20	0.49
1:C:101[B]:ARG:NH1	1:C:101[B]:ARG:HG3	2.26	0.49
1:A:59:TYR:OH	1:A:101[A]:ARG:CD	2.61	0.48
1:A:59:TYR:OH	1:A:101[B]:ARG:CD	2.61	0.48
1:A:83:ILE:HG23	1:A:96:LEU:HD13	1.95	0.48
1:A:257[A]:ARG:HD3	1:A:257[A]:ARG:HA	1.59	0.48
1:C:124:LEU:O	1:C:128:GLU:HG2	2.13	0.48
1:C:389:ASP:OD2	1:C:405:TYR:HA	2.13	0.48
1:B:149:ALA:HB2	1:B:206:LEU:HD23	1.95	0.48
1:A:69:LEU:HA	1:A:423:ARG:HD3	1.94	0.48
1:A:58:ARG:NH1	2:A:2048:HOH:O	2.47	0.47
1:B:257:ARG:HH11	1:B:257:ARG:CG	2.22	0.47
1:C:75:ARG:HA	1:C:114:PHE:O	2.15	0.47
1:C:308:THR:O	1:C:311:GLY:N	2.42	0.47
1:A:353:VAL:HB	1:A:416:LYS:HG2	1.97	0.46
1:A:151:ALA:HB1	1:C:93:PRO:HG3	1.98	0.45
1:A:423:ARG:O	1:A:423:ARG:HG3	2.16	0.45
1:B:317:GLU:HG3	1:B:321:HIS:CE1	2.50	0.45
1:A:119:HIS:HE1	2:A:2014:HOH:O	2.00	0.45
1:A:321:HIS:HE1	2:A:2184:HOH:O	1.99	0.45
1:C:80:TRP:N	1:C:81:PRO:HD2	2.31	0.45
1:B:91:ILE:O	1:B:93:PRO:HD3	2.17	0.44
1:B:75:ARG:HA	1:B:114:PHE:O	2.17	0.44
1:B:80:TRP:HB3	1:B:81:PRO:HD3	1.99	0.44
1:B:337:THR:O	1:B:338:GLU:HG3	2.19	0.43
1:A:22:ALA:CB	1:A:25:GLU:HG3	2.48	0.43
1:B:282:THR:HG21	2:B:2088:HOH:O	2.17	0.43
1:C:101[B]:ARG:NH2	2:C:2051:HOH:O	2.49	0.43
1:A:75:ARG:NH1	1:A:338:GLU:HG3	2.34	0.43
1:C:130:GLY:O	1:C:131:GLY:C	2.56	0.43
1:C:392[B]:GLU:HA	1:C:392[B]:GLU:OE1	2.19	0.43
1:C:119:HIS:HD2	2:C:2006:HOH:O	2.02	0.43
1:C:80:TRP:N	1:C:81:PRO:CD	2.82	0.42
1:B:75:ARG:NH1	1:B:338:GLU:HG3	2.33	0.42
1:A:22:ALA:HA	1:A:25:GLU:HG3	2.02	0.42
1:C:286:PRO:HD2	1:C:313:GLU:HB3	2.02	0.42
1:B:266:SER:O	1:B:267[B]:ARG:HB2	2.19	0.42
1:A:282:THR:HG21	2:A:2104:HOH:O	2.19	0.41
1:B:80:TRP:HA	1:B:144:TYR:CE1	2.55	0.41
1:B:266:SER:O	1:B:267[A]:ARG:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:LEU:HD23	1:A:126:LEU:HA	1.93	0.41
1:C:267:ARG:NH1	1:C:270:GLU:OE1	2.54	0.41
1:A:204:GLU:HB2	1:A:274:ARG:NH1	2.35	0.41
1:A:244:ASP:HB2	1:A:245:PRO:HD3	2.02	0.41
1:B:80:TRP:N	1:B:81:PRO:CD	2.83	0.41
1:A:80:TRP:HB3	1:A:81:PRO:HD3	2.02	0.41
1:A:423:ARG:NH1	1:A:423:ARG:CG	2.59	0.41
1:B:36:PHE:O	1:B:39:ARG:HB2	2.20	0.41
1:A:80:TRP:N	1:A:81:PRO:HD2	2.36	0.41
1:A:82:ARG:O	1:A:92:ASN:HB3	2.21	0.41
1:B:133:ARG:HH11	1:B:133:ARG:HD3	1.66	0.41
1:B:346:LEU:HD12	1:B:347:TRP:H	1.86	0.41
1:A:317:GLU:HG3	1:A:321:HIS:CE1	2.56	0.40
1:A:15:SER:O	1:A:19:ILE:HG12	2.22	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	425/437 (97%)	414 (97%)	11 (3%)	0	100	100
1	B	425/437 (97%)	410 (96%)	15 (4%)	0	100	100
1	C	424/437 (97%)	407 (96%)	17 (4%)	0	100	100
All	All	1274/1311 (97%)	1231 (97%)	43 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	336/345 (97%)	322 (96%)	14 (4%)	30	27
1	B	336/345 (97%)	325 (97%)	11 (3%)	38	37
1	C	335/345 (97%)	320 (96%)	15 (4%)	27	24
All	All	1007/1035 (97%)	967 (96%)	40 (4%)	32	29

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	GLU
1	A	51	PRO
1	A	61	GLU
1	A	82	ARG
1	A	84	LEU
1	A	96	LEU
1	A	257[A]	ARG
1	A	257[B]	ARG
1	A	298	VAL
1	A	328	ARG
1	A	346	LEU
1	A	423	ARG
1	A	424	GLU
1	A	425	ARG
1	B	7	LYS
1	B	61	GLU
1	B	100	ASP
1	B	105	ARG
1	B	107	LEU
1	B	257	ARG
1	B	266	SER
1	B	346	LEU
1	B	420	LEU
1	B	424	GLU
1	B	425	ARG
1	C	6	GLU

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Mol	Chain	Res	Type
1	C	44	ARG
1	C	51	PRO
1	C	61	GLU
1	C	72	ARG
1	C	82	ARG
1	C	128	GLU
1	C	133	ARG
1	C	226	GLU
1	C	229	GLU
1	C	266	SER
1	C	267	ARG
1	C	304	GLU
1	C	325	ARG
1	C	425	ARG

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	55	HIS
1	A	119	HIS
1	A	194	HIS
1	A	321	HIS
1	B	4	ASN
1	B	55	HIS
1	B	119	HIS
1	B	194	HIS
1	B	320	HIS
1	B	321	HIS
1	C	55	HIS
1	C	119	HIS
1	C	194	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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	424/437 (97%)	-0.56	3 (0%)	87	87	14, 27, 46, 67	0
1	B	425/437 (97%)	-0.47	6 (1%)	75	74	14, 29, 51, 72	0
1	C	424/437 (97%)	-0.04	8 (1%)	66	65	23, 38, 67, 84	0
All	All	1273/1311 (97%)	-0.36	17 (1%)	77	76	14, 31, 58, 84	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	267	ARG	3.7
1	B	90	ARG	3.1
1	C	226	GLU	3.1
1	B	293	THR	3.0
1	A	304	GLU	2.9
1	C	304	GLU	2.6
1	C	224	TYR	2.5
1	B	6	GLU	2.5
1	B	257	ARG	2.5
1	B	299	ARG	2.5
1	C	257	ARG	2.4
1	C	228	PRO	2.4
1	B	304	GLU	2.2
1	C	227	ASP	2.2
1	A	346	LEU	2.1
1	A	6	GLU	2.0
1	C	266	SER	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 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.