Full wwPDB X-ray Structure Validation Report (i)

Nov 16, 2023 – 01:13 AM JST

PDB ID	:	6KY1
Title	:	Crystal structural of human glutathione-specific gamma-glutamylcyclotransferase 2 (ChaC2)mutant with Glutamate 83 replaced by Glutamine
Authors	:	Nguyen, T.K.Y.; Han, B.W.
Deposited on	:	2019-09-16
Resolution	:	2.04 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:

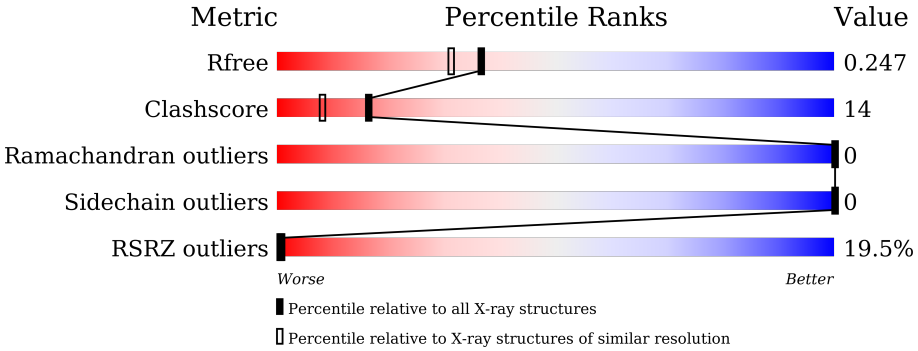
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.04 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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	182	11% 78% 21% •
1	B	182	12% 76% 23% •
1	C	182	32% 60% 24% 16%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4185 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 Glutathione-specific gamma-glutamylcyclotransferase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	180	1443	935	241	264	3	0	0	0
			Total	C	N	O	S			
1	B	180	1435	928	240	264	3	0	0	0
			Total	C	N	O	S			
1	C	152	1222	798	202	221	1	0	0	0

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LYS	-	expression tag	UNP Q8WUX2
A	-5	VAL	-	expression tag	UNP Q8WUX2
A	-4	PRO	-	expression tag	UNP Q8WUX2
A	-3	ARG	-	expression tag	UNP Q8WUX2
A	-2	GLY	-	expression tag	UNP Q8WUX2
A	-1	SER	-	expression tag	UNP Q8WUX2
A	0	HIS	-	expression tag	UNP Q8WUX2
A	82	GLY	ARG	engineered mutation	UNP Q8WUX2
A	83	GLN	GLU	engineered mutation	UNP Q8WUX2
B	-6	LYS	-	expression tag	UNP Q8WUX2
B	-5	VAL	-	expression tag	UNP Q8WUX2
B	-4	PRO	-	expression tag	UNP Q8WUX2
B	-3	ARG	-	expression tag	UNP Q8WUX2
B	-2	GLY	-	expression tag	UNP Q8WUX2
B	-1	SER	-	expression tag	UNP Q8WUX2
B	0	HIS	-	expression tag	UNP Q8WUX2
B	82	GLY	ARG	engineered mutation	UNP Q8WUX2
B	83	GLN	GLU	engineered mutation	UNP Q8WUX2
C	-6	LYS	-	expression tag	UNP Q8WUX2
C	-5	VAL	-	expression tag	UNP Q8WUX2
C	-4	PRO	-	expression tag	UNP Q8WUX2
C	-3	ARG	-	expression tag	UNP Q8WUX2
C	-2	GLY	-	expression tag	UNP Q8WUX2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	SER	-	expression tag	UNP Q8WUX2
C	0	HIS	-	expression tag	UNP Q8WUX2
C	82	GLY	ARG	engineered mutation	UNP Q8WUX2
C	83	GLN	GLU	engineered mutation	UNP Q8WUX2

- Molecule 2 is water.

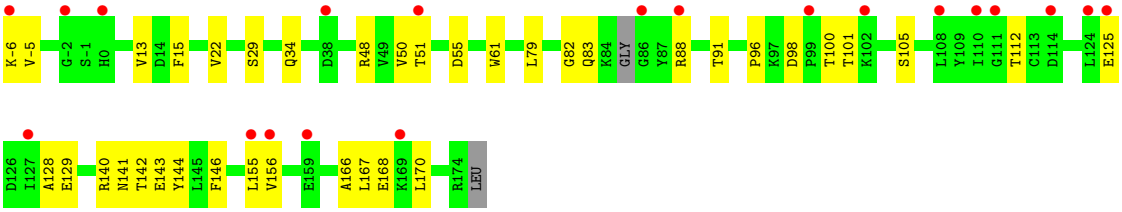
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	31	31	31	0	0
			Total	O		
2	B	38	38	38	0	0
			Total	O		
2	C	16	16	16	0	0

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.

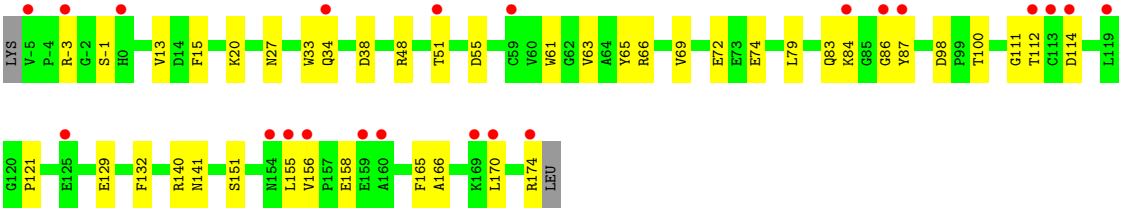
• Molecule 1: Glutathione-specific gamma-glutamylcyclotransferase 2

Chain A:



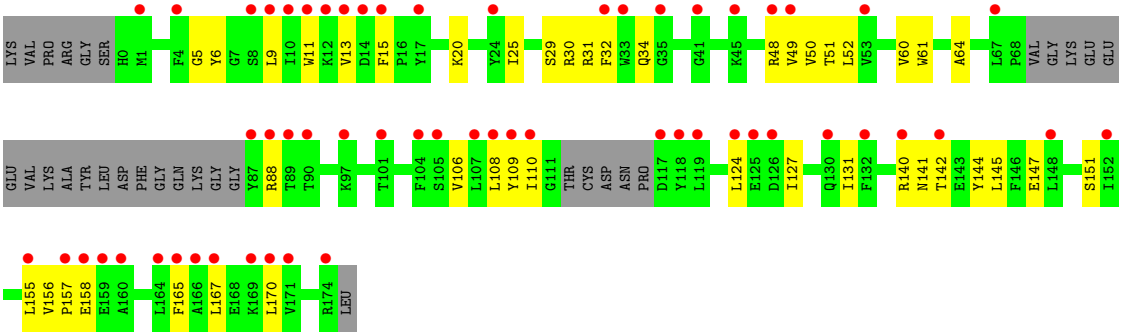
• Molecule 1: Glutathione-specific gamma-glutamylcyclotransferase 2

Chain B:



• Molecule 1: Glutathione-specific gamma-glutamylcyclotransferase 2

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	72.71Å 72.71Å 104.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	31.48 – 2.04 31.48 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.5 (31.48-2.04) 99.6 (31.48-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	3.54 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.225 , 0.256 0.219 , 0.247	Depositor DCC
R_{free} test set	2062 reflections (5.31%)	wwPDB-VP
Wilson B-factor (Å^2)	37.5	Xtriage
Anisotropy	0.818	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 47.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.034 for -h,-k,l 0.468 for h,-h-k,-l 0.034 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4185	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 5.17% 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	0.64	0/1486	0.76	0/2021
1	B	0.65	0/1479	0.80	0/2014
1	C	0.64	0/1259	0.72	0/1716
All	All	0.65	0/4224	0.76	0/5751

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1443	0	1410	36	0
1	B	1435	0	1392	43	0
1	C	1222	0	1188	38	0
2	A	31	0	0	0	0
2	B	38	0	0	1	0
2	C	16	0	0	0	0
All	All	4185	0	3990	116	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 (116) 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:20:LYS:HE3	1:B:63:VAL:HG11	1.30	1.08
1:B:20:LYS:CE	1:B:63:VAL:HG11	1.86	1.05
1:A:34:GLN:HB2	1:A:51:THR:OG1	1.53	1.05
1:C:48:ARG:H	1:C:141:ASN:HD21	1.11	0.99
1:B:48:ARG:H	1:B:141:ASN:HD21	1.13	0.97
1:C:48:ARG:HD2	1:C:127:ILE:HG23	1.51	0.92
1:A:88:ARG:CZ	1:A:112:THR:HG22	2.00	0.91
1:A:48:ARG:H	1:A:141:ASN:HD21	1.18	0.89
1:B:-3:ARG:HD2	1:B:69:VAL:HG21	1.59	0.84
1:C:32:PHE:O	1:C:48:ARG:HD3	1.77	0.84
1:B:-3:ARG:HH21	1:B:66:ARG:CZ	1.91	0.83
1:A:128:ALA:HB2	1:A:170:LEU:HD23	1.60	0.82
1:A:91:THR:CG2	1:A:105:SER:OG	2.28	0.81
1:A:34:GLN:HB2	1:A:51:THR:HG1	1.43	0.81
1:C:124:LEU:HG	1:C:170:LEU:HD12	1.62	0.79
1:B:129:GLU:OE1	1:B:174:ARG:NH1	2.16	0.78
1:C:30:ARG:HH11	1:C:60:VAL:HG13	1.52	0.75
1:A:34:GLN:CB	1:A:51:THR:OG1	2.36	0.72
1:A:88:ARG:NE	1:A:112:THR:HG22	2.05	0.71
1:B:34:GLN:HB2	1:B:51:THR:OG1	1.92	0.70
1:C:49:VAL:HG23	1:C:144:TYR:CZ	2.27	0.70
1:A:96:PRO:CB	1:A:101:THR:HG23	2.24	0.68
1:B:132:PHE:O	1:B:140:ARG:NH2	2.27	0.68
1:C:52:LEU:HD12	1:C:110:ILE:HD11	1.77	0.67
1:C:48:ARG:H	1:C:141:ASN:ND2	1.90	0.67
1:A:82:GLY:HA2	1:B:74:GLU:OE2	1.94	0.67
1:C:158:GLU:HA	1:C:165:PHE:CE2	2.29	0.66
1:C:30:ARG:NH1	1:C:60:VAL:HG13	2.10	0.66
1:B:86:GLY:O	1:B:112:THR:CB	2.45	0.65
1:B:20:LYS:HE3	1:B:63:VAL:CG1	2.19	0.65
1:A:167:LEU:O	1:A:170:LEU:HB3	1.97	0.65
1:B:87:TYR:HD1	1:B:111:GLY:HA2	1.63	0.64
1:A:48:ARG:H	1:A:141:ASN:ND2	1.93	0.63
1:C:34:GLN:HB2	1:C:51:THR:HB	1.80	0.63
1:A:29:SER:OG	1:A:55:ASP:OD2	2.11	0.63
1:B:83:GLN:HB3	1:B:87:TYR:CD2	2.34	0.62
1:B:166:ALA:O	1:B:170:LEU:HD13	1.99	0.62
1:A:142:THR:OG1	1:A:146:PHE:CE2	2.53	0.62
1:A:98:ASP:OD2	1:A:100:THR:HB	2.00	0.61
1:B:-3:ARG:HH21	1:B:66:ARG:NH1	1.98	0.61
1:C:9:LEU:HD12	1:C:13:VAL:HG22	1.83	0.60
1:B:98:ASP:CG	1:B:100:THR:HG22	2.21	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:GLY:CA	1:C:9:LEU:HD23	2.32	0.60
1:B:151:SER:O	1:B:155:LEU:HG	2.02	0.59
1:C:30:ARG:NH1	1:C:61:TRP:O	2.34	0.59
1:C:131:ILE:CD1	1:C:167:LEU:HD21	2.33	0.58
1:C:48:ARG:N	1:C:141:ASN:HD21	1.91	0.58
1:A:79:LEU:O	1:A:83:GLN:HG2	2.03	0.58
1:B:20:LYS:HE2	1:B:63:VAL:HG11	1.81	0.58
1:C:151:SER:O	1:C:155:LEU:HD13	2.04	0.58
1:C:109:TYR:O	1:C:110:ILE:HD13	2.04	0.58
1:A:128:ALA:HB2	1:A:170:LEU:CD2	2.32	0.57
1:B:38:ASP:OD1	2:B:201:HOH:O	2.17	0.57
1:B:86:GLY:O	1:B:112:THR:OG1	2.18	0.57
1:B:48:ARG:H	1:B:141:ASN:ND2	1.93	0.56
1:C:6:TYR:HB2	1:C:30:ARG:HD3	1.86	0.56
1:A:140:ARG:HB3	1:A:142:THR:HG22	1.87	0.56
1:C:88:ARG:N	1:C:110:ILE:O	2.37	0.56
1:B:83:GLN:HB3	1:B:87:TYR:HD2	1.71	0.56
1:B:79:LEU:O	1:B:83:GLN:HG2	2.06	0.56
1:B:86:GLY:O	1:B:112:THR:HB	2.06	0.56
1:A:96:PRO:HB2	1:A:101:THR:HG23	1.87	0.55
1:A:166:ALA:O	1:A:170:LEU:HB2	2.07	0.55
1:B:61:TRP:CE3	1:B:156:VAL:HG11	2.42	0.54
1:A:61:TRP:CE3	1:A:156:VAL:HG11	2.42	0.54
1:C:50:VAL:HG22	1:C:144:TYR:OH	2.08	0.53
1:B:87:TYR:CD1	1:B:111:GLY:HA2	2.43	0.53
1:C:5:GLY:HA3	1:C:9:LEU:HD23	1.90	0.53
1:A:48:ARG:N	1:A:141:ASN:HD21	1.98	0.52
1:C:32:PHE:HB3	1:C:48:ARG:HG2	1.91	0.52
1:B:155:LEU:O	1:B:156:VAL:HG13	2.10	0.52
1:C:156:VAL:HB	1:C:157:PRO:HD2	1.90	0.52
1:B:158:GLU:HA	1:B:165:PHE:CE2	2.45	0.52
1:B:48:ARG:N	1:B:141:ASN:HD21	1.95	0.51
1:B:20:LYS:HG2	1:B:63:VAL:CG1	2.41	0.51
1:B:-3:ARG:CD	1:B:69:VAL:HG21	2.37	0.51
1:A:142:THR:HG23	1:A:143:GLU:N	2.25	0.50
1:C:32:PHE:O	1:C:48:ARG:CD	2.56	0.49
1:B:112:THR:HG22	1:B:114:ASP:H	1.78	0.49
1:A:50:VAL:HG22	1:A:144:TYR:OH	2.12	0.49
1:B:98:ASP:OD2	1:B:100:THR:HG22	2.12	0.49
1:C:20:LYS:HA	1:C:64:ALA:O	2.13	0.49
1:C:106:VAL:HG23	1:C:108:LEU:CD1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:THR:OG1	1:A:146:PHE:HE2	1.94	0.48
1:C:25:ILE:HD13	1:C:108:LEU:HD21	1.96	0.47
1:B:158:GLU:O	1:B:165:PHE:CD2	2.67	0.47
1:C:131:ILE:HD12	1:C:167:LEU:HD21	1.97	0.47
1:B:-1:SER:O	1:B:66:ARG:NH2	2.48	0.47
1:B:20:LYS:CG	1:B:63:VAL:CG1	2.93	0.47
1:C:109:TYR:O	1:C:109:TYR:CD2	2.68	0.47
1:A:-6:LYS:HG2	1:A:-5:VAL:H	1.80	0.46
1:C:61:TRP:CE3	1:C:156:VAL:HG11	2.50	0.46
1:B:84:LYS:H	1:B:87:TYR:HE2	1.64	0.46
1:A:91:THR:HG22	1:A:105:SER:OG	2.15	0.45
1:C:9:LEU:HD11	1:C:15:PHE:CZ	2.51	0.45
1:A:22:VAL:HG13	1:A:155:LEU:HD23	1.98	0.45
1:C:140:ARG:HB3	1:C:142:THR:HG22	1.99	0.44
1:B:69:VAL:HA	1:B:72:GLU:OE2	2.16	0.44
1:A:142:THR:CG2	1:A:143:GLU:N	2.81	0.43
1:C:124:LEU:HD11	1:C:167:LEU:HB2	2.00	0.43
1:A:91:THR:HG21	1:A:105:SER:OG	2.16	0.43
1:A:125:GLU:O	1:A:129:GLU:HG3	2.19	0.43
1:B:20:LYS:HE3	1:B:65:TYR:CZ	2.54	0.43
1:C:52:LEU:CD1	1:C:110:ILE:HD11	2.48	0.43
1:C:11:TRP:HB3	1:C:147:GLU:OE2	2.19	0.42
1:C:145:LEU:HD13	1:C:167:LEU:HD23	2.01	0.42
1:B:33:TRP:CZ3	1:B:121:PRO:HG3	2.55	0.42
1:C:29:SER:OG	1:C:31:ARG:CZ	2.68	0.42
1:A:96:PRO:HG2	1:A:101:THR:HG23	2.02	0.42
1:B:13:VAL:HG13	1:B:15:PHE:CE2	2.55	0.42
1:A:96:PRO:CG	1:A:101:THR:HG23	2.49	0.41
1:B:20:LYS:NZ	1:B:65:TYR:OH	2.45	0.41
1:A:13:VAL:HG13	1:A:15:PHE:CE2	2.56	0.41
1:A:168:GLU:C	1:A:170:LEU:N	2.73	0.41
1:B:27:ASN:HA	1:B:55:ASP:O	2.21	0.40
1:A:98:ASP:HB3	1:A:101:THR:HG22	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	176/182 (97%)	168 (96%)	8 (4%)	0	100	100
1	B	178/182 (98%)	176 (99%)	2 (1%)	0	100	100
1	C	146/182 (80%)	140 (96%)	6 (4%)	0	100	100
All	All	500/546 (92%)	484 (97%)	16 (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	153/154 (99%)	153 (100%)	0	100	100
1	B	151/154 (98%)	151 (100%)	0	100	100
1	C	128/154 (83%)	128 (100%)	0	100	100
All	All	432/462 (94%)	432 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	39	HIS
1	A	141	ASN

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Mol	Chain	Res	Type
1	A	154	ASN
1	B	141	ASN
1	C	141	ASN

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	180/182 (98%)	1.07	20 (11%)	5	5	36, 50, 74, 86	0
1	B	180/182 (98%)	1.06	22 (12%)	4	3	33, 49, 74, 92	0
1	C	152/182 (83%)	2.09	58 (38%)	0	0	56, 74, 101, 109	0
All	All	512/546 (93%)	1.37	100 (19%)	1	0	33, 56, 90, 109	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	11	TRP	15.9
1	C	15	PHE	14.0
1	C	109	TYR	9.6
1	C	108	LEU	7.7
1	C	160	ALA	7.3
1	C	45	LYS	6.2
1	C	87	TYR	5.9
1	C	14	ASP	5.9
1	C	165	PHE	5.9
1	C	164	LEU	5.8
1	C	53	VAL	5.2
1	A	169	LYS	5.1
1	A	159	GLU	5.1
1	A	88	ARG	4.9
1	C	159	GLU	4.8
1	B	0	HIS	4.8
1	C	155	LEU	4.7
1	C	110	ILE	4.6
1	C	167	LEU	4.5
1	A	125	GLU	4.5
1	C	124	LEU	4.3
1	C	148	LEU	4.3
1	C	32	PHE	4.2

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Mol	Chain	Res	Type	RSRZ
1	C	126	ASP	4.1
1	B	159	GLU	4.0
1	C	88	ARG	3.8
1	A	99	PRO	3.8
1	A	-6	LYS	3.8
1	C	13	VAL	3.7
1	C	125	GLU	3.7
1	C	107	LEU	3.7
1	C	169	LYS	3.7
1	A	86	GLY	3.6
1	C	118	TYR	3.6
1	B	114	ASP	3.6
1	C	174	ARG	3.5
1	B	87	TYR	3.5
1	C	142	THR	3.4
1	A	124	LEU	3.4
1	B	84	LYS	3.3
1	C	9	LEU	3.3
1	C	67	LEU	3.3
1	C	12	LYS	3.2
1	C	166	ALA	3.2
1	C	140	ARG	3.2
1	C	152	ILE	3.2
1	C	170	LEU	3.0
1	C	101	THR	2.9
1	C	158	GLU	2.9
1	C	117	ASP	2.9
1	B	160	ALA	2.9
1	A	102	LYS	2.9
1	A	-2	GLY	2.8
1	C	132	PHE	2.8
1	A	114	ASP	2.7
1	B	155	LEU	2.7
1	A	38	ASP	2.7
1	C	49	VAL	2.7
1	B	86	GLY	2.6
1	C	33	TRP	2.6
1	C	105	SER	2.6
1	C	48	ARG	2.6
1	C	171	VAL	2.6
1	B	113	CYS	2.6
1	C	10	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	119	LEU	2.5
1	A	155	LEU	2.4
1	C	104	PHE	2.4
1	B	174	ARG	2.4
1	B	125	GLU	2.4
1	C	130	GLN	2.4
1	B	-5	VAL	2.4
1	B	154	ASN	2.3
1	B	156	VAL	2.3
1	C	41	GLY	2.3
1	B	-3	ARG	2.3
1	B	112	THR	2.3
1	C	17	TYR	2.3
1	C	119	LEU	2.2
1	B	51	THR	2.2
1	C	1	MET	2.2
1	A	0	HIS	2.2
1	B	169	LYS	2.2
1	A	110	ILE	2.2
1	C	89	THR	2.2
1	A	108	LEU	2.2
1	C	157	PRO	2.2
1	A	111	GLY	2.1
1	A	127	ILE	2.1
1	C	90	THR	2.1
1	B	59	CYS	2.1
1	C	35	GLY	2.1
1	A	51	THR	2.0
1	C	97	LYS	2.0
1	C	24	TYR	2.0
1	B	34	GLN	2.0
1	B	170	LEU	2.0
1	A	156	VAL	2.0
1	C	4	PHE	2.0
1	C	8	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.