



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:59 AM GMT

PDB ID : 3GR1
Title : Periplamic domain of the T3SS inner membrane protein PrgH from
S.typhimurium (fragment 170-392)
Authors : Yip, C.K.; Vockovic, M.; Yu, A.C.; Strynadka, N.C.J.
Deposited on : 2009-03-24
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

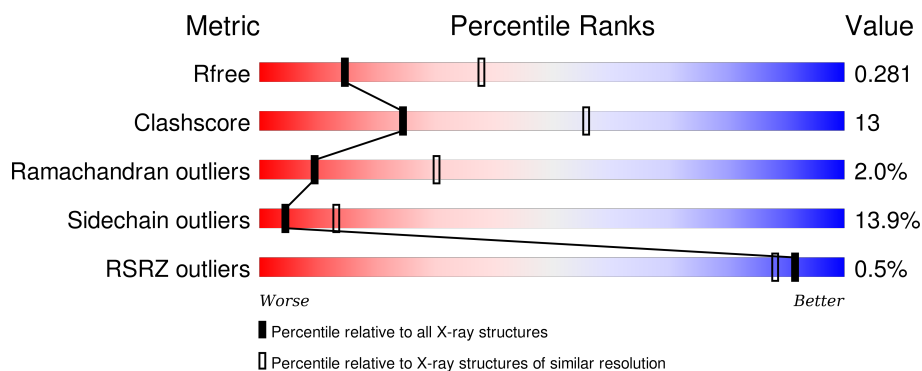
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. 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	227	<div> <div>63%</div> <div>19%</div> <div>5%</div> <div>14%</div> </div>
1	B	227	<div> <div>58%</div> <div>22%</div> <div>5%</div> <div>15%</div> </div>
1	C	227	<div> <div>63%</div> <div>16%</div> <div>5%</div> <div>16%</div> </div>
1	D	227	<div> <div>56%</div> <div>25%</div> <div>•</div> <div>15%</div> </div>
1	E	227	<div> <div>55%</div> <div>24%</div> <div>• •</div> <div>15%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	227	<div><div></div><div>57%</div><div>22%</div><div>•</div><div>17%</div></div>
1	G	227	<div><div></div><div>54%</div><div>24%</div><div>• •</div><div>17%</div></div>
1	H	227	<div>%<div><div></div><div>53%</div><div>25%</div><div>7%</div><div>16%</div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12613 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 prgH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	195	Total	C	N	O	S	0	0	0
			1602	1014	289	294	5			
1	B	193	Total	C	N	O	S	0	0	0
			1589	1006	287	292	4			
1	C	190	Total	C	N	O	S	0	0	0
			1570	995	284	287	4			
1	D	193	Total	C	N	O	S	0	0	0
			1589	1006	287	292	4			
1	E	192	Total	C	N	O	S	0	0	0
			1584	1003	286	291	4			
1	F	189	Total	C	N	O	S	0	0	0
			1554	986	281	283	4			
1	G	189	Total	C	N	O	S	0	0	0
			1554	986	281	283	4			
1	H	191	Total	C	N	O	S	0	0	0
			1571	996	285	285	5			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	166	GLY	-	EXPRESSION TAG	UNP P41783
A	167	SER	-	EXPRESSION TAG	UNP P41783
A	168	HIS	-	EXPRESSION TAG	UNP P41783
A	169	MET	-	EXPRESSION TAG	UNP P41783
B	166	GLY	-	EXPRESSION TAG	UNP P41783
B	167	SER	-	EXPRESSION TAG	UNP P41783
B	168	HIS	-	EXPRESSION TAG	UNP P41783
B	169	MET	-	EXPRESSION TAG	UNP P41783
C	166	GLY	-	EXPRESSION TAG	UNP P41783
C	167	SER	-	EXPRESSION TAG	UNP P41783
C	168	HIS	-	EXPRESSION TAG	UNP P41783
C	169	MET	-	EXPRESSION TAG	UNP P41783
D	166	GLY	-	EXPRESSION TAG	UNP P41783

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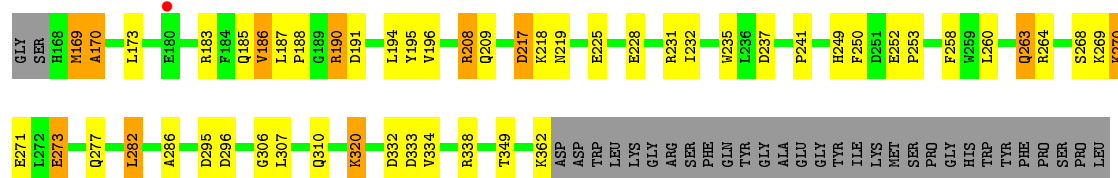
Chain	Residue	Modelled	Actual	Comment	Reference
D	167	SER	-	EXPRESSION TAG	UNP P41783
D	168	HIS	-	EXPRESSION TAG	UNP P41783
D	169	MET	-	EXPRESSION TAG	UNP P41783
E	166	GLY	-	EXPRESSION TAG	UNP P41783
E	167	SER	-	EXPRESSION TAG	UNP P41783
E	168	HIS	-	EXPRESSION TAG	UNP P41783
E	169	MET	-	EXPRESSION TAG	UNP P41783
F	166	GLY	-	EXPRESSION TAG	UNP P41783
F	167	SER	-	EXPRESSION TAG	UNP P41783
F	168	HIS	-	EXPRESSION TAG	UNP P41783
F	169	MET	-	EXPRESSION TAG	UNP P41783
G	166	GLY	-	EXPRESSION TAG	UNP P41783
G	167	SER	-	EXPRESSION TAG	UNP P41783
G	168	HIS	-	EXPRESSION TAG	UNP P41783
G	169	MET	-	EXPRESSION TAG	UNP P41783
H	166	GLY	-	EXPRESSION TAG	UNP P41783
H	167	SER	-	EXPRESSION TAG	UNP P41783
H	168	HIS	-	EXPRESSION TAG	UNP P41783
H	169	MET	-	EXPRESSION TAG	UNP P41783

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

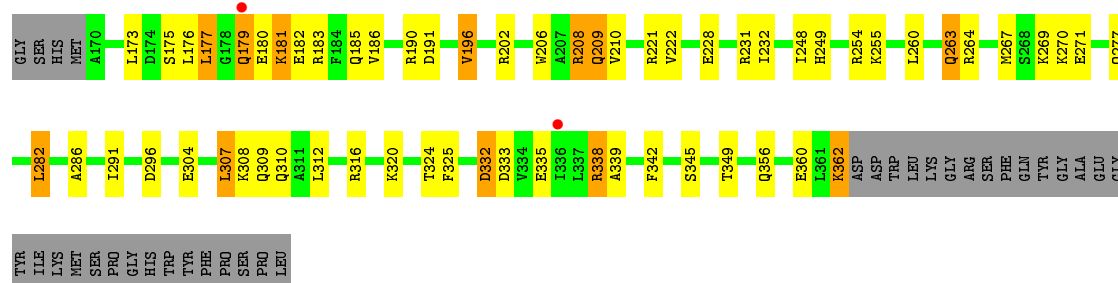
• Molecule 1: Protein prgH

Chain A: 



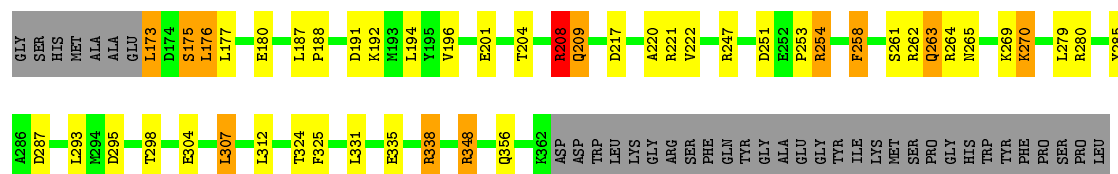
• Molecule 1: Protein prgH

Chain B: 



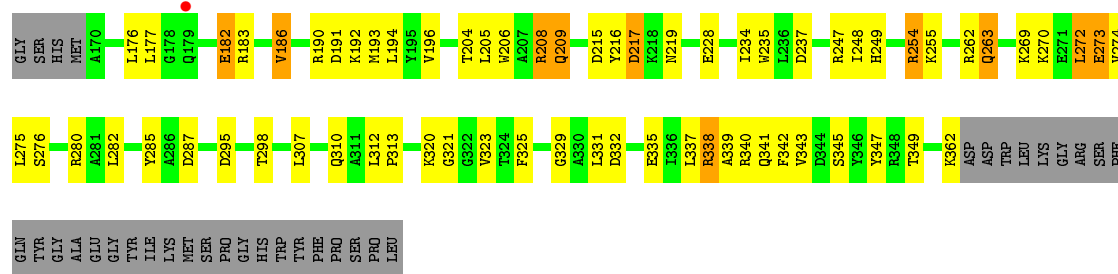
• Molecule 1: Protein prgH

Chain C: 



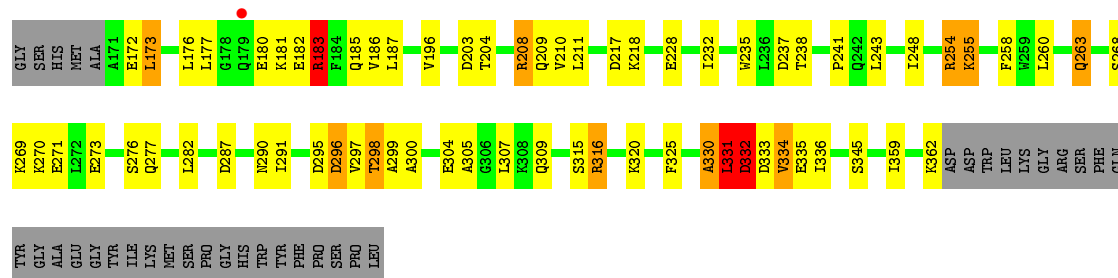
• Molecule 1: Protein prgH

Chain D: 



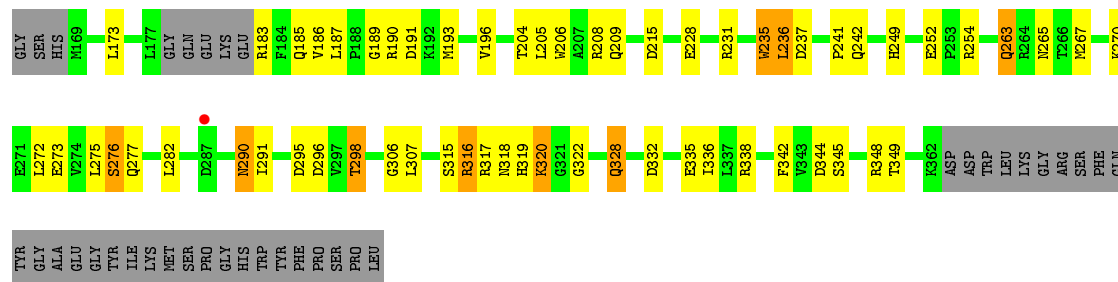
• Molecule 1: Protein prgH

Chain E:



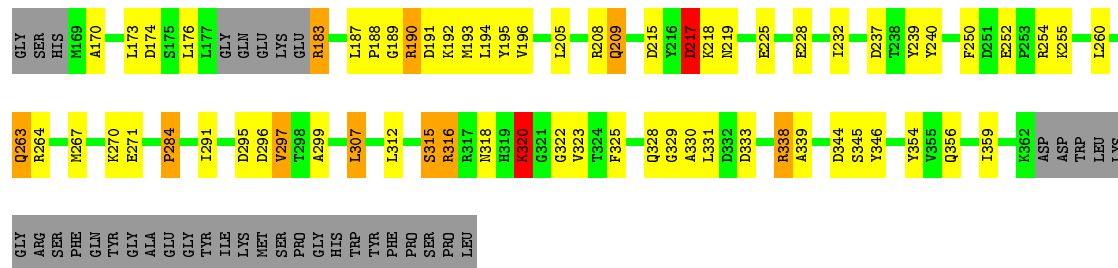
• Molecule 1: Protein prgH

Chain F:



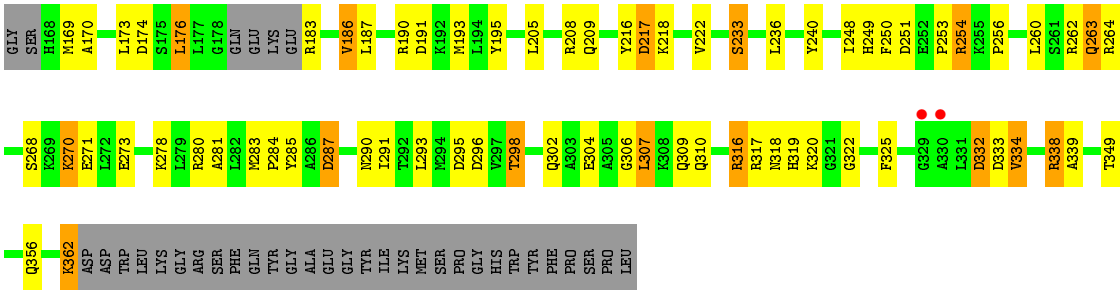
• Molecule 1: Protein prgH

Chain G:



• Molecule 1: Protein prgH





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	79.61Å 188.75Å 305.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	152.50 – 2.80 152.78 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.5 (152.50-2.80) 96.5 (152.78-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 2.82Å)	Xtriage
Refinement program	REFMAC5 5.2.0019	Depositor
R, R_{free}	0.247 , 0.295 0.237 , 0.281	Depositor DCC
R_{free} test set	2812 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	55.2	Xtriage
Anisotropy	0.429	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 55189 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12613	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 14.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.77	0/1634	0.81	1/2206 (0.0%)
1	B	0.77	0/1621	0.82	1/2189 (0.0%)
1	C	0.70	0/1602	0.82	2/2163 (0.1%)
1	D	0.68	0/1621	0.79	2/2189 (0.1%)
1	E	0.70	0/1616	0.81	2/2182 (0.1%)
1	F	0.70	0/1585	0.76	0/2141
1	G	0.70	1/1585 (0.1%)	0.76	0/2141
1	H	0.65	0/1603	0.76	1/2164 (0.0%)
All	All	0.71	1/12867 (0.0%)	0.79	9/17375 (0.1%)

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	D	0	1
1	E	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	330	ALA	CA-CB	5.22	1.63	1.52

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	ARG	NE-CZ-NH2	7.46	124.03	120.30
1	D	321	GLY	N-CA-C	-6.54	96.75	113.10
1	B	208	ARG	NE-CZ-NH2	6.46	123.53	120.30
1	D	208	ARG	NE-CZ-NH2	5.81	123.20	120.30
1	E	330	ALA	N-CA-C	-5.59	95.92	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	320	LYS	Peptide
1	E	331	LEU	Peptide

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	1602	0	1588	34	0
1	B	1589	0	1577	47	0
1	C	1570	0	1561	35	0
1	D	1589	0	1577	47	0
1	E	1584	0	1572	50	0
1	F	1554	0	1542	41	0
1	G	1554	0	1542	39	0
1	H	1571	0	1559	52	0
All	All	12613	0	12518	323	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 13.

The worst 5 of 323 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:A:277:GLN:HG2	1:B:191:ASP:HA	1.36	1.07
1:G:316:ARG:HD3	1:G:318:ASN:HD21	1.21	1.05
1:E:330:ALA:CA	1:E:331:LEU:HB2	1.89	1.02
1:E:330:ALA:HA	1:E:331:LEU:HB2	1.02	1.02
1:E:330:ALA:HA	1:E:331:LEU:CB	1.90	1.01

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	193/227 (85%)	182 (94%)	9 (5%)	2 (1%)	19	52
1	B	191/227 (84%)	178 (93%)	9 (5%)	4 (2%)	9	29
1	C	188/227 (83%)	170 (90%)	15 (8%)	3 (2%)	12	38
1	D	191/227 (84%)	166 (87%)	22 (12%)	3 (2%)	12	38
1	E	190/227 (84%)	170 (90%)	15 (8%)	5 (3%)	7	22
1	F	185/227 (82%)	157 (85%)	23 (12%)	5 (3%)	6	21
1	G	185/227 (82%)	155 (84%)	24 (13%)	6 (3%)	5	17
1	H	187/227 (82%)	164 (88%)	21 (11%)	2 (1%)	17	50
All	All	1510/1816 (83%)	1342 (89%)	138 (9%)	30 (2%)	9	30

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	175	SER
1	C	176	LEU
1	D	272	LEU
1	D	273	GLU
1	E	331	LEU

5.3.2 Protein sidechains

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	166/193 (86%)	145 (87%)	21 (13%)	5	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	165/193 (86%)	143 (87%)	22 (13%)	5	14
1	C	164/193 (85%)	145 (88%)	19 (12%)	7	20
1	D	165/193 (86%)	146 (88%)	19 (12%)	7	21
1	E	165/193 (86%)	134 (81%)	31 (19%)	2	6
1	F	161/193 (83%)	142 (88%)	19 (12%)	6	19
1	G	161/193 (83%)	135 (84%)	26 (16%)	3	9
1	H	163/193 (84%)	138 (85%)	25 (15%)	3	10
All	All	1310/1544 (85%)	1128 (86%)	182 (14%)	4	13

5 of 182 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	173	LEU
1	E	307	LEU
1	H	263	GLN
1	E	177	LEU
1	E	218	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	249	HIS
1	E	185	GLN
1	H	263	GLN
1	D	341	GLN
1	E	263	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 [i](#)

There are no carbohydrates 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	195/227 (85%)	-0.13	1 (0%) 91 88	17, 40, 62, 73	0
1	B	193/227 (85%)	-0.12	2 (1%) 84 77	18, 40, 64, 70	0
1	C	190/227 (83%)	-0.05	0 100 100	20, 45, 69, 78	0
1	D	193/227 (85%)	0.02	1 (0%) 91 88	25, 49, 74, 83	0
1	E	192/227 (84%)	-0.05	1 (0%) 91 88	23, 47, 74, 89	0
1	F	189/227 (83%)	-0.00	1 (0%) 91 88	20, 47, 81, 94	0
1	G	189/227 (83%)	0.08	0 100 100	31, 53, 76, 80	0
1	H	191/227 (84%)	0.01	2 (1%) 84 77	32, 51, 76, 83	0
All	All	1532/1816 (84%)	-0.03	8 (0%) 91 88	17, 47, 74, 94	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	336	ILE	2.8
1	H	330	ALA	2.8
1	F	287	ASP	2.7
1	A	180	GLU	2.4
1	E	179	GLN	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 carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.