



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:20 PM GMT

PDB ID : 4RGN  
Title : Structure of Staphylococcal Enterotoxin B bound to two neutralizing antibodies, 14G8 and 6D3  
Authors : Franklin, M.C.; Dutta, K.; Varshney, A.K.; Goger, M.J.; Fries, B.C.  
Deposited on : 2014-09-30  
Resolution : 2.70 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](mailto: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.

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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

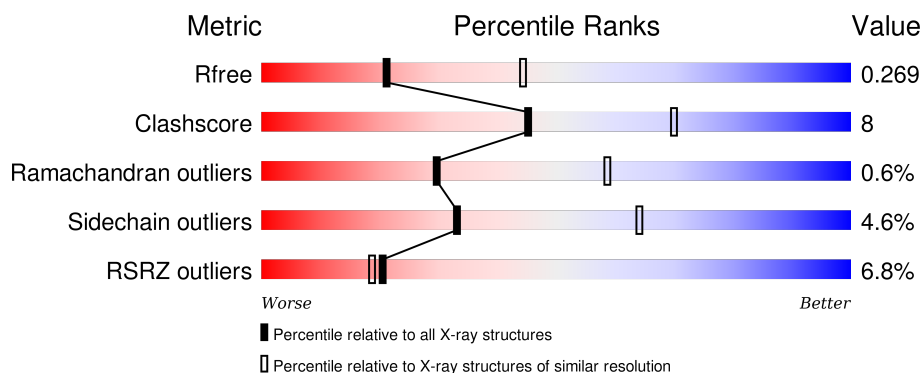
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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.





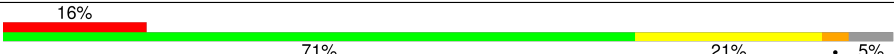
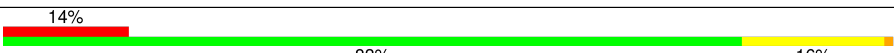
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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  $\geq 3$ , 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	245	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>13%</div> <div>13%</div> </div> </div>
1	S	245	<div> <div>4%</div> <div> <div></div> <div>74%</div> <div>15%</div> <div>10%</div> </div> </div>
2	B	222	<div> <div></div> <div> <div></div> <div>81%</div> <div>14%</div> <div>5%</div> </div> </div>
2	H	222	<div> <div></div> <div> <div></div> <div>79%</div> <div>15%</div> <div>5%</div> </div> </div>
3	C	214	<div> <div></div> <div> <div></div> <div>81%</div> <div>16%</div> <div>3%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	L	214	 79% 19% •
4	D	221	 13% 73% 19% • 5%
4	F	221	 16% 71% 21% • 5%
5	E	220	 15% 81% 18% •
5	G	220	 14% 83% 16% •

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16749 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 Enterotoxin type B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1789	1149	285	345	10			
1	S	220	Total	C	N	O	S	0	0	0
			1842	1181	297	354	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	EXPRESSION TAG	UNP P01552
A	-4	SER	-	EXPRESSION TAG	UNP P01552
A	-3	GLU	-	EXPRESSION TAG	UNP P01552
A	-2	PHE	-	EXPRESSION TAG	UNP P01552
A	-1	GLY	-	EXPRESSION TAG	UNP P01552
A	0	SER	-	EXPRESSION TAG	UNP P01552
S	-5	GLY	-	EXPRESSION TAG	UNP P01552
S	-4	SER	-	EXPRESSION TAG	UNP P01552
S	-3	GLU	-	EXPRESSION TAG	UNP P01552
S	-2	PHE	-	EXPRESSION TAG	UNP P01552
S	-1	GLY	-	EXPRESSION TAG	UNP P01552
S	0	SER	-	EXPRESSION TAG	UNP P01552

- Molecule 2 is a protein called 14G8 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1615	1031	265	313	6			
2	H	213	Total	C	N	O	S	0	0	0
			1615	1031	265	313	6			

- Molecule 3 is a protein called 14G8 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	213	Total	C	N	O	S	0	0	0
			1651	1025	282	338	6			
3	L	213	Total	C	N	O	S	0	0	0
			1651	1025	282	338	6			

- Molecule 4 is a protein called 6D3 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	210	Total	C	N	O	S	0	0	0
			1583	1008	254	314	7			
4	F	210	Total	C	N	O	S	0	0	0
			1583	1008	254	314	7			

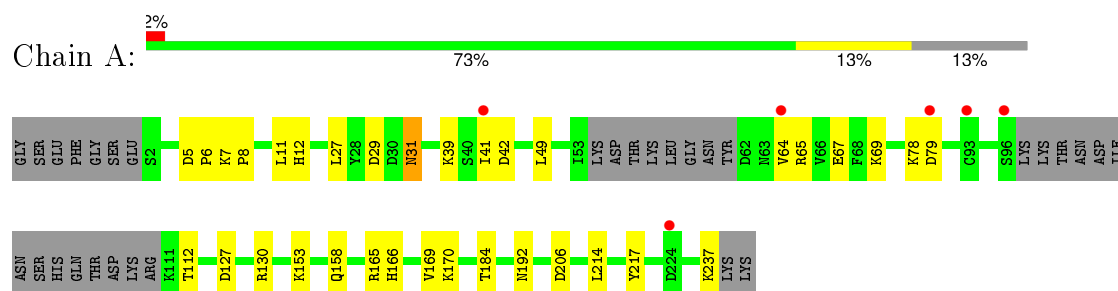
- Molecule 5 is a protein called 6D3 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	220	Total	C	N	O	S	0	0	0
			1710	1069	280	353	8			
5	G	220	Total	C	N	O	S	0	0	0
			1710	1069	280	353	8			

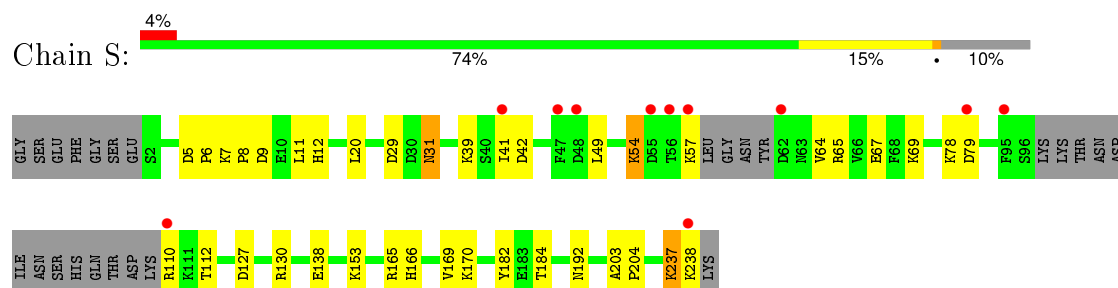
### 3 Residue-property plots [i](#)

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.

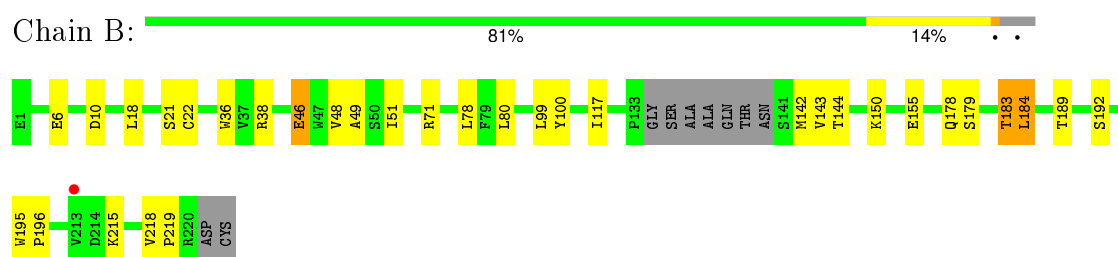
- Molecule 1: Enterotoxin type B



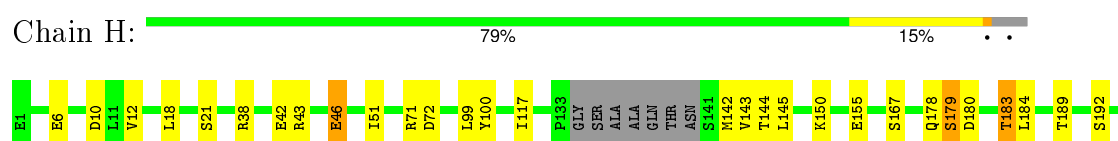
- Molecule 1: Enterotoxin type B

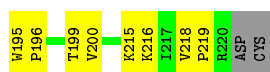


- Molecule 2: 14G8 heavy chain



- Molecule 2: 14G8 heavy chain





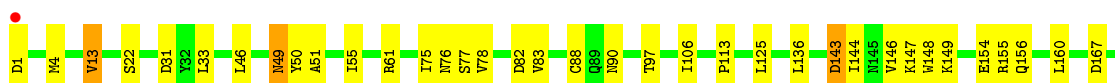
• Molecule 3: 14G8 light chain

Chain C: 81% 16%



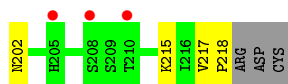
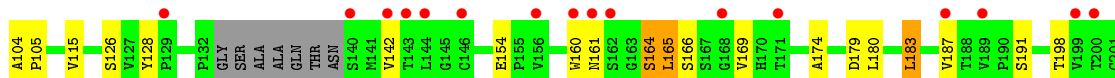
• Molecule 3: 14G8 light chain

Chain L: 79% 19%



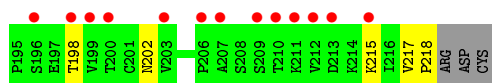
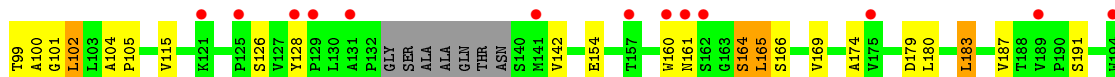
• Molecule 4: 6D3 heavy chain

Chain D: 13% 73% 19% 5%

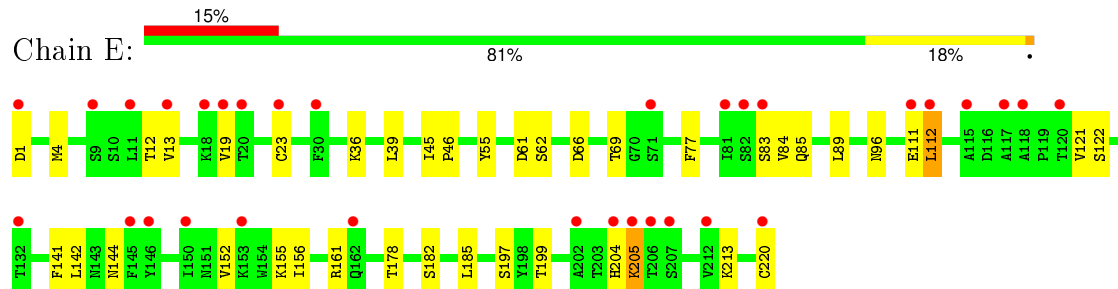


• Molecule 4: 6D3 heavy chain

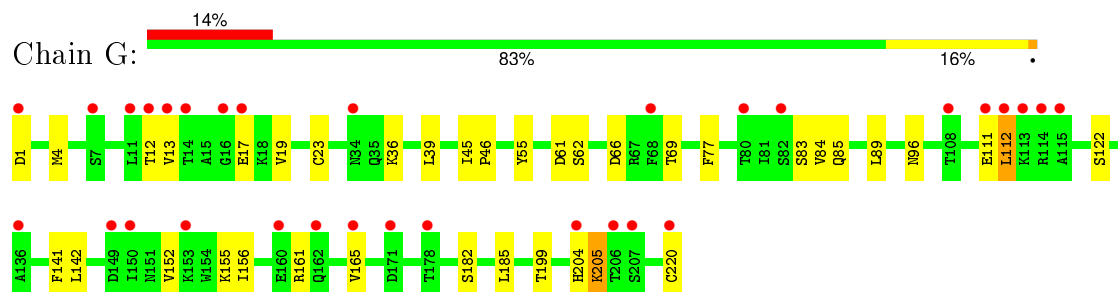
Chain F: 16% 71% 21% 5%



- Molecule 5: 6D3 light chain



- Molecule 5: 6D3 light chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	301.33Å 109.82Å 82.78Å 90.00° 94.53° 90.00°	Depositor
Resolution (Å)	45.71 – 2.70 41.26 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.7 (45.71-2.70) 97.7 (41.26-2.70)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.52 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.240 , 0.278 0.236 , 0.269	Depositor DCC
$R_{free}$ test set	3614 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	48.5	Xtriage
Anisotropy	0.404	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 33.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 72447 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	16749	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.44% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.79	0/1830	0.76	0/2462
1	S	0.74	0/1883	0.73	0/2530
2	B	0.85	1/1657 (0.1%)	0.82	0/2264
2	H	0.86	1/1657 (0.1%)	0.83	0/2264
3	C	0.85	0/1690	0.79	0/2296
3	L	0.87	0/1690	0.80	0/2296
4	D	0.52	0/1626	0.61	0/2228
4	F	0.48	0/1626	0.61	0/2228
5	E	0.50	0/1749	0.61	0/2380
5	G	0.49	0/1749	0.60	0/2380
All	All	0.71	2/17157 (0.0%)	0.72	0/23328

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	155	GLU	CD-OE1	6.74	1.33	1.25
2	B	155	GLU	CD-OE1	6.68	1.33	1.25

There are no bond angle outliers.

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	1789	0	1724	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S	1842	0	1787	22	0
2	B	1615	0	1589	20	0
2	H	1615	0	1589	21	0
3	C	1651	0	1566	32	0
3	L	1651	0	1566	34	0
4	D	1583	0	1547	34	0
4	F	1583	0	1547	36	0
5	E	1710	0	1635	23	0
5	G	1710	0	1635	23	0
All	All	16749	0	16185	257	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 8.

The worst 5 of 257 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)
4:D:169:VAL:HG22	4:D:187:VAL:HG22	1.34	1.07
4:F:169:VAL:HG22	4:F:187:VAL:HG22	1.38	1.01
3:L:148:TRP:H	3:L:156:GLN:HE22	1.05	0.95
3:C:148:TRP:H	3:C:156:GLN:HE22	1.07	0.93
4:D:161:ASN:HB2	4:D:164:SER:OG	1.73	0.88

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	208/245 (85%)	199 (96%)	8 (4%)	1 (0%)	34 63
1	S	214/245 (87%)	203 (95%)	10 (5%)	1 (0%)	34 63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	209/222 (94%)	199 (95%)	10 (5%)	0	100	100
2	H	209/222 (94%)	198 (95%)	10 (5%)	1 (0%)	34	63
3	C	211/214 (99%)	202 (96%)	7 (3%)	2 (1%)	21	49
3	L	211/214 (99%)	204 (97%)	5 (2%)	2 (1%)	21	49
4	D	206/221 (93%)	190 (92%)	15 (7%)	1 (0%)	34	63
4	F	206/221 (93%)	189 (92%)	15 (7%)	2 (1%)	19	45
5	E	218/220 (99%)	204 (94%)	13 (6%)	1 (0%)	34	63
5	G	218/220 (99%)	204 (94%)	13 (6%)	1 (0%)	34	63
All	All	2110/2244 (94%)	1992 (94%)	106 (5%)	12 (1%)	30	59

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	165	LEU
4	F	102	LEU
4	F	165	LEU
1	A	192	ASN
3	C	212	ASN

### 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	201/229 (88%)	197 (98%)	4 (2%)	63	87
1	S	207/229 (90%)	198 (96%)	9 (4%)	35	66
2	B	182/188 (97%)	175 (96%)	7 (4%)	40	71
2	H	182/188 (97%)	175 (96%)	7 (4%)	40	71
3	C	190/191 (100%)	181 (95%)	9 (5%)	32	63
3	L	190/191 (100%)	182 (96%)	8 (4%)	36	68
4	D	182/190 (96%)	171 (94%)	11 (6%)	24	50
4	F	182/190 (96%)	170 (93%)	12 (7%)	21	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	198/198 (100%)	187 (94%)	11 (6%)	26	54
5	G	198/198 (100%)	188 (95%)	10 (5%)	29	59
All	All	1912/1992 (96%)	1824 (95%)	88 (5%)	33	64

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	197	SER
1	S	110	ARG
5	G	69	THR
5	E	205	LYS
1	S	29	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	144	ASN
1	S	31	ASN
3	L	189	HIS
5	E	34	ASN
4	F	5	GLN

### 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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	214/245 (87%)	0.33	6 (2%) 56 57	29, 46, 74, 82	0
1	S	220/245 (89%)	0.34	11 (5%) 32 31	29, 48, 81, 102	0
2	B	213/222 (95%)	0.01	1 (0%) 91 93	22, 34, 46, 56	0
2	H	213/222 (95%)	0.02	0 100 100	23, 34, 46, 53	0
3	C	213/214 (99%)	0.09	1 (0%) 91 93	24, 37, 60, 88	0
3	L	213/214 (99%)	0.13	1 (0%) 91 93	24, 37, 55, 80	0
4	D	210/221 (95%)	0.88	28 (13%) 4 3	46, 88, 135, 155	1 (0%)
4	F	210/221 (95%)	0.97	36 (17%) 2 1	49, 89, 142, 162	1 (0%)
5	E	220/220 (100%)	0.89	32 (14%) 3 2	45, 84, 150, 197	0
5	G	220/220 (100%)	0.82	31 (14%) 4 3	47, 87, 160, 199	0
All	All	2146/2244 (95%)	0.45	147 (6%) 20 19	22, 50, 130, 199	2 (0%)

The worst 5 of 147 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	210	THR	9.1
4	F	212	VAL	6.7
5	E	206	THR	6.3
5	G	115	ALA	6.2
4	F	207	ALA	5.7

### 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 [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.