



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 10:24 am BST

PDB ID : 6NMS  
Title : Blocking Fab 136 anti-SIRP-alpha antibody in complex with SIRP-alpha Variant 1  
Authors : Wibowo, A.S.; Carter, J.J.; Sim, J.  
Deposited on : 2019-01-11  
Resolution : 2.11 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](mailto: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.

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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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

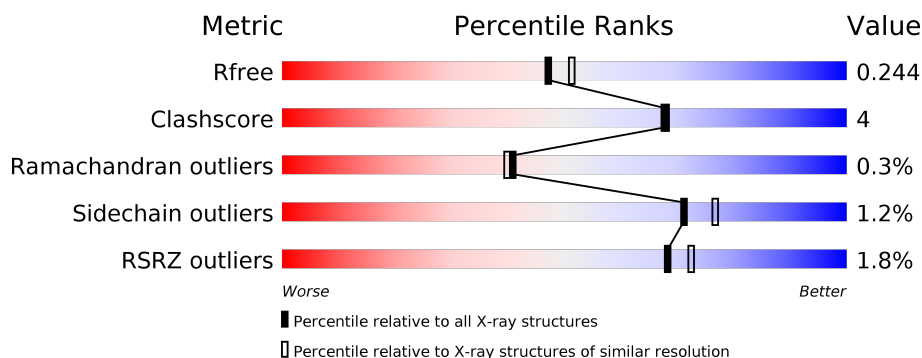
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.11 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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 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  $\leq 5\%$ . 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	215	<div> <div>91%</div> <div>8%</div> </div>
1	L	215	<div> <div>2%</div> <div>93%</div> <div>6%</div> </div>
2	B	228	<div> <div>2%</div> <div>82%</div> <div>11%</div> <div>5%</div> </div>
2	H	228	<div> <div>2%</div> <div>85%</div> <div>10%</div> <div>5%</div> </div>
3	C	127	<div> <div>2%</div> <div>79%</div> <div>13%</div> <div>8%</div> </div>
3	S	127	<div> <div>4%</div> <div>79%</div> <div>11%</div> <div>9%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8613 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 Fab 136 anti-SIRP-alpha antibody Variable Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	214	Total	C	N	O	S	0	0	0
			1643	1031	275	333	4			
1	A	214	Total	C	N	O	S	0	0	0
			1643	1030	274	335	4			

- Molecule 2 is a protein called Fab 136 anti-SIRP-alpha antibody Variable Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	217	Total	C	N	O	S	0	0	0
			1627	1026	274	321	6			
2	B	216	Total	C	N	O	S	0	0	0
			1617	1017	270	324	6			

- Molecule 3 is a protein called Tyrosine-protein phosphatase non-receptor type substrate 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	S	116	Total	C	N	O	S	0	0	0
			873	550	153	167	3			
3	C	117	Total	C	N	O	S	0	0	0
			871	547	153	168	3			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	80	ALA	ASN	conflict	UNP P78324
S	120	THR	-	expression tag	UNP P78324
S	121	ARG	-	expression tag	UNP P78324
S	122	HIS	-	expression tag	UNP P78324
S	123	HIS	-	expression tag	UNP P78324
S	124	HIS	-	expression tag	UNP P78324
S	125	HIS	-	expression tag	UNP P78324
S	126	HIS	-	expression tag	UNP P78324

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Chain	Residue	Modelled	Actual	Comment	Reference
S	127	HIS	-	expression tag	UNP P78324
C	80	ALA	ASN	conflict	UNP P78324
C	120	THR	-	expression tag	UNP P78324
C	121	ARG	-	expression tag	UNP P78324
C	122	HIS	-	expression tag	UNP P78324
C	123	HIS	-	expression tag	UNP P78324
C	124	HIS	-	expression tag	UNP P78324
C	125	HIS	-	expression tag	UNP P78324
C	126	HIS	-	expression tag	UNP P78324
C	127	HIS	-	expression tag	UNP P78324

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	L	103	Total O 103 103	0	0
4	H	50	Total O 50 50	0	0
4	S	21	Total O 21 21	0	0
4	A	97	Total O 97 97	0	0
4	B	44	Total O 44 44	0	0
4	C	24	Total O 24 24	0	0

### 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 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.

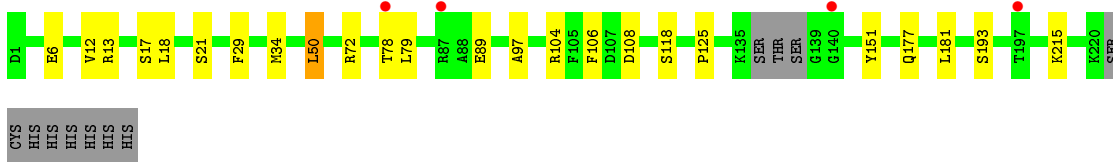
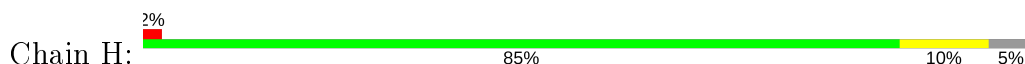
- Molecule 1: Fab 136 anti-SIRP-alpha antibody Variable Light Chain



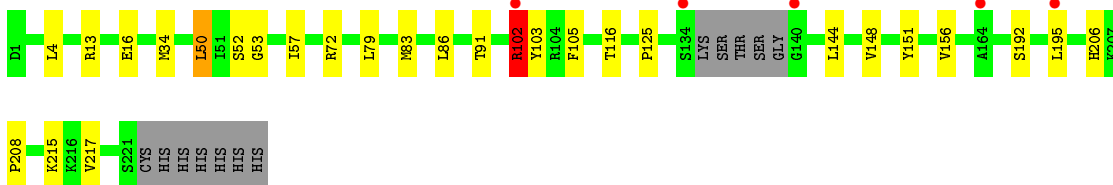
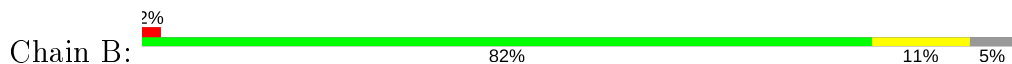
- Molecule 1: Fab 136 anti-SIRP-alpha antibody Variable Light Chain



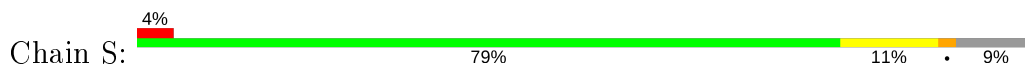
- Molecule 2: Fab 136 anti-SIRP-alpha antibody Variable Heavy Chain

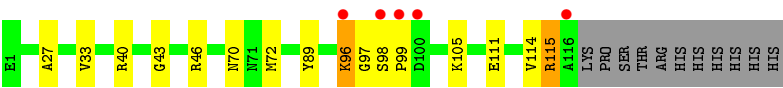


- Molecule 2: Fab 136 anti-SIRP-alpha antibody Variable Heavy Chain

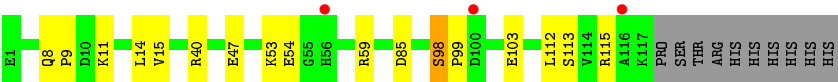
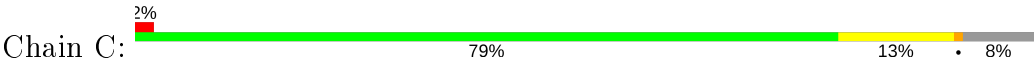


- Molecule 3: Tyrosine-protein phosphatase non-receptor type substrate 1





● Molecule 3: Tyrosine-protein phosphatase non-receptor type substrate 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.39 Å   75.19 Å   103.82 Å 90.00°   104.43°   90.00°	Depositor
Resolution (Å)	50.27 – 2.11 50.27 – 2.11	Depositor EDS
% Data completeness (in resolution range)	98.1 (50.27-2.11) 98.2 (50.27-2.11)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 2.10 Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, $R_{free}$	0.204   ,   0.244 0.204   ,   0.244	Depositor DCC
$R_{free}$ test set	3402 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.3	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 38.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8613	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.59% 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, 0.333 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	0.40	0/1680	0.62	1/2287 (0.0%)
1	L	0.39	0/1680	0.74	4/2286 (0.2%)
2	B	0.42	0/1654	0.66	2/2256 (0.1%)
2	H	0.42	0/1664	0.60	1/2264 (0.0%)
3	C	0.43	0/888	0.79	4/1207 (0.3%)
3	S	0.44	1/890 (0.1%)	0.72	3/1208 (0.2%)
All	All	0.41	1/8456 (0.0%)	0.68	15/11508 (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	L	0	1
3	C	0	1
3	S	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	S	97	GLY	C-N	-6.09	1.20	1.34

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	18	ARG	NE-CZ-NH1	-14.90	112.85	120.30
3	C	14	LEU	CB-CG-CD1	-10.19	93.67	111.00
1	L	18	ARG	NE-CZ-NH2	9.06	124.83	120.30
1	L	18	ARG	CG-CD-NE	-8.71	93.50	111.80
3	C	14	LEU	CB-CG-CD2	8.59	125.59	111.00
3	C	115	ARG	CG-CD-NE	8.12	128.85	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	S	96	LYS	CD-CE-NZ	7.83	129.72	111.70
1	L	18	ARG	CD-NE-CZ	6.89	133.25	123.60
2	B	102	ARG	CG-CD-NE	6.54	125.54	111.80
1	A	155	LEU	CB-CG-CD1	6.50	122.05	111.00
3	S	97	GLY	C-N-CA	-6.05	106.57	121.70
3	S	96	LYS	N-CA-CB	5.33	120.19	110.60
2	H	78	THR	OG1-CB-CG2	5.15	121.84	110.00
2	B	50	LEU	CA-CB-CG	5.05	126.93	115.30
3	C	98	SER	C-N-CD	-5.00	109.59	120.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	98	SER	Peptide
1	L	18	ARG	Sidechain
3	S	98	SER	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	1643	0	1579	11	0
1	L	1643	0	1586	8	0
2	B	1617	0	1540	17	0
2	H	1627	0	1569	14	0
3	C	871	0	847	8	0
3	S	873	0	865	8	0
4	A	97	0	0	2	0
4	B	44	0	0	2	0
4	C	24	0	0	0	0
4	H	50	0	0	2	0
4	L	103	0	0	4	0
4	S	21	0	0	1	0
All	All	8613	0	7986	62	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 (62) 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)
2:B:102:ARG:NH2	3:C:8:GLN:O	1.95	0.99
2:B:102:ARG:O	2:B:102:ARG:NH1	2.00	0.94
2:B:13:ARG:HB2	2:B:16:GLU:OE1	1.75	0.85
1:A:155:LEU:HD13	1:A:156:GLN:N	2.01	0.76
2:H:17:SER:OG	4:H:301:HOH:O	2.03	0.75
2:B:144:LEU:HD13	2:B:217:VAL:HG21	1.69	0.74
2:H:108:ASP:OD1	4:H:302:HOH:O	2.05	0.74
1:L:32:TYR:OH	4:L:301:HOH:O	1.99	0.74
1:L:214:GLU:O	4:L:302:HOH:O	2.07	0.72
2:B:102:ARG:HE	3:C:9:PRO:HA	1.55	0.71
1:A:155:LEU:HD13	1:A:156:GLN:H	1.61	0.65
3:S:33:VAL:HG23	3:S:96:LYS:HE2	1.77	0.64
1:L:151:VAL:HG22	1:L:156:GLN:NE2	2.14	0.62
3:S:115:ARG:NH2	4:S:202:HOH:O	2.33	0.61
1:A:18:ARG:NH1	1:A:74:THR:HG21	2.17	0.59
1:A:30:TYR:OH	3:C:103:GLU:OE2	2.20	0.56
2:H:29:PHE:O	2:H:72:ARG:NH2	2.39	0.55
3:C:40:ARG:NH2	3:C:47:GLU:OE1	2.38	0.55
2:B:192:SER:HA	2:B:195:LEU:HD13	1.89	0.54
2:B:125:PRO:HB3	2:B:151:TYR:HB3	1.89	0.54
1:L:40:PRO:HG3	4:L:396:HOH:O	2.09	0.53
1:L:155:LEU:HD22	1:L:156:GLN:H	1.74	0.52
3:S:43:GLY:O	3:S:46:ARG:HG3	2.12	0.50
2:H:89:GLU:CD	2:H:89:GLU:H	2.16	0.49
2:B:52:SER:HB3	2:B:57:ILE:HB	1.95	0.49
1:A:148:GLN:HG3	1:A:155:LEU:HD21	1.95	0.49
4:B:329:HOH:O	3:C:11:LYS:HB2	2.13	0.48
2:B:4:LEU:O	4:B:301:HOH:O	2.20	0.48
2:B:91:THR:HG23	2:B:116:THR:HA	1.96	0.47
2:H:12:VAL:HG11	2:H:18:LEU:HG	1.97	0.46
2:B:83:MET:HB3	2:B:86:LEU:HD21	1.97	0.46
3:C:59:ARG:NH2	3:C:85:ASP:OD1	2.48	0.46
2:B:102:ARG:HA	2:B:102:ARG:HD2	1.59	0.46
3:S:40:ARG:HD3	3:S:89:TYR:CZ	2.50	0.46
2:H:34:MET:HB3	2:H:79:LEU:HD22	1.97	0.46
2:H:125:PRO:HB3	2:H:151:TYR:HB3	1.99	0.45
3:C:15:VAL:HG12	3:C:112:LEU:HD11	1.98	0.45
1:A:81:GLU:HG3	4:A:382:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S:27:ALA:O	3:S:72:MET:HB3	2.17	0.44
2:B:148:VAL:HG11	2:B:156:VAL:HG11	1.99	0.44
1:A:164:VAL:HG22	1:A:176:LEU:HD12	2.00	0.44
1:L:184:LYS:O	1:L:188:GLU:HG3	2.17	0.44
3:S:114:VAL:HG12	3:S:115:ARG:HG3	1.99	0.44
1:A:48:ILE:HD13	1:A:54:ARG:HA	2.00	0.44
2:B:34:MET:HB3	2:B:79:LEU:HD22	1.99	0.43
2:H:97:ALA:HB1	2:H:106:PHE:HB3	2.00	0.43
2:B:103:TYR:HB2	2:B:105:PHE:CE2	2.54	0.43
2:B:53:GLY:HA2	2:B:72:ARG:NH1	2.33	0.42
2:H:215:LYS:HE2	2:H:215:LYS:HB2	1.82	0.42
2:H:6:GLU:HA	2:H:21:SER:O	2.20	0.42
1:A:45:ARG:HD2	4:A:364:HOH:O	2.19	0.42
1:L:164:VAL:HG22	1:L:176:LEU:HD12	2.02	0.42
2:H:50:LEU:C	2:H:50:LEU:HD12	2.40	0.41
1:A:106:GLU:OE1	1:A:174:TYR:OH	2.32	0.41
3:C:53:LYS:HB3	3:C:54:GLU:HG2	2.02	0.41
2:H:13:ARG:HA	2:H:118:SER:O	2.21	0.41
1:L:200:GLN:OE1	4:L:303:HOH:O	2.22	0.41
3:S:105:LYS:HE2	3:S:105:LYS:HB3	1.80	0.41
2:H:104:ARG:NH2	3:S:111:GLU:OE2	2.50	0.41
1:A:126:LEU:O	1:A:184:LYS:HD2	2.21	0.41
2:H:177:GLN:HG2	2:H:181:LEU:O	2.21	0.40
2:B:206:HIS:CD2	2:B:208:PRO:HD2	2.56	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	212/215 (99%)	206 (97%)	6 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	212/215 (99%)	208 (98%)	4 (2%)	0	100	100
2	B	212/228 (93%)	205 (97%)	7 (3%)	0	100	100
2	H	213/228 (93%)	210 (99%)	3 (1%)	0	100	100
3	C	115/127 (91%)	111 (96%)	3 (3%)	1 (1%)	17	12
3	S	114/127 (90%)	110 (96%)	2 (2%)	2 (2%)	8	3
All	All	1078/1140 (95%)	1050 (97%)	25 (2%)	3 (0%)	41	40

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	S	99	PRO
3	C	99	PRO
3	S	115	ARG

### 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	183/186 (98%)	180 (98%)	3 (2%)	62	68
1	L	183/186 (98%)	182 (100%)	1 (0%)	88	92
2	B	179/195 (92%)	176 (98%)	3 (2%)	60	66
2	H	179/195 (92%)	177 (99%)	2 (1%)	73	79
3	C	90/106 (85%)	89 (99%)	1 (1%)	73	79
3	S	92/106 (87%)	91 (99%)	1 (1%)	73	79
All	All	906/974 (93%)	895 (99%)	11 (1%)	71	77

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	94	ARG
2	H	50	LEU
2	H	193	SER

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Mol	Chain	Res	Type
3	S	70	ASN
1	A	94	ARG
1	A	155	LEU
1	A	191	LYS
2	B	50	LEU
2	B	102	ARG
2	B	215	LYS
3	C	113	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	148	GLN
3	S	70	ASN

### 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 carbohydrates 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 ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	S	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S	97:GLY	C	98:SER	N	1.20

## 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<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	214/215 (99%)	0.10	1 (0%) 91 92	33, 47, 69, 88	0
1	L	214/215 (99%)	0.02	2 (0%) 84 86	37, 50, 67, 85	0
2	B	216/228 (94%)	0.16	5 (2%) 60 65	41, 59, 90, 103	0
2	H	217/228 (95%)	0.12	4 (1%) 68 72	42, 57, 81, 91	0
3	C	117/127 (92%)	0.18	3 (2%) 56 61	38, 59, 87, 97	0
3	S	116/127 (91%)	0.19	5 (4%) 35 41	42, 58, 82, 101	0
All	All	1094/1140 (95%)	0.12	20 (1%) 68 72	33, 55, 80, 103	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	116	ALA	4.9
3	S	116	ALA	3.9
3	S	100	ASP	3.7
3	S	98	SER	3.2
1	L	57	GLY	3.1
1	A	155	LEU	2.9
3	C	100	ASP	2.9
3	S	99	PRO	2.8
3	C	56	HIS	2.7
2	B	134	SER	2.7
2	H	140	GLY	2.6
3	S	96	LYS	2.5
2	B	195	LEU	2.5
2	H	87	ARG	2.5
2	B	102	ARG	2.5
2	H	78	THR	2.4
2	B	140	GLY	2.3
1	L	58	ILE	2.3
2	B	164	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
2	H	197	THR	2.2

## 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.