



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:11 PM GMT

PDB ID : 4KUC  
Title : Crystal structure of ricin-A chain in complex with the antibody 6C2  
Authors : Zhu, Y.; Li, X.; Teng, M.  
Deposited on : 2013-05-21  
Resolution : 2.79 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  
<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

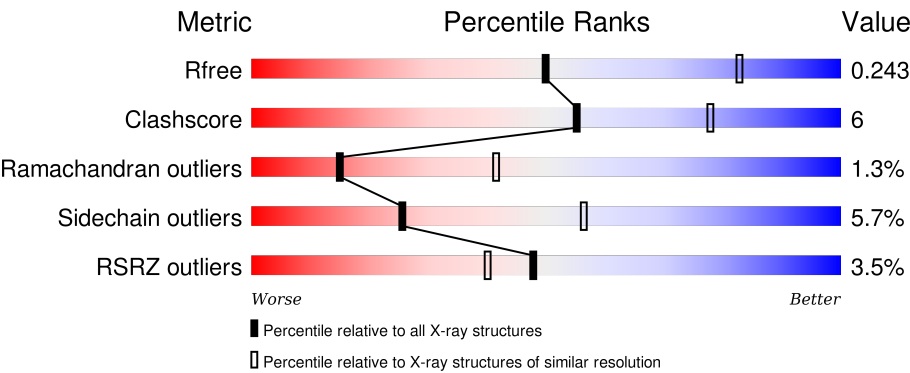
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.79 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.



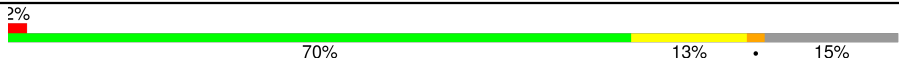
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	91344	3004 (2.80-2.76)
Clashscore	102246	3480 (2.80-2.76)
Ramachandran outliers	100387	3423 (2.80-2.76)
Sidechain outliers	100360	3425 (2.80-2.76)
RSRZ outliers	91569	3016 (2.80-2.76)

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 <=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	267	<div><div></div><div>83%13%•</div></div>
1	I	267	<div><div>%</div><div>84%12%•</div></div>
2	D	231	<div><div>4%</div><div>71%17%•10%</div></div>
2	E	231	<div><div>6%</div><div>37%10%•53%</div></div>
3	F	237	<div><div>5%</div><div>42%8%50%</div></div>

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Mol	Chain	Length	Quality of chain
3	H	237	 A horizontal bar chart showing the quality of chain H. The bar is divided into four segments: a small red segment at the beginning labeled '2%', a large green segment labeled '70%', a yellow segment labeled '13%', and a small grey segment at the end labeled '15%'. There is a small black dot on the yellow segment.

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8287 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 Ricin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	0	0
			1987	1259	353	370	5			
1	I	259	Total	C	N	O	S	0	0	0
			1989	1260	353	371	5			

- Molecule 2 is a protein called mAb6c2 fab-Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	208	Total	C	N	O	S	0	0	0
			1397	881	240	272	4			
2	E	109	Total	C	N	O	S	0	0	0
			732	463	130	137	2			

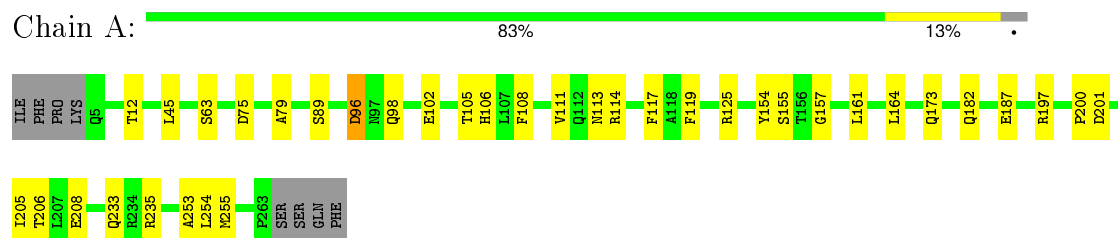
- Molecule 3 is a protein called mAb6c2 fab-Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	202	Total	C	N	O	S	0	0	0
			1361	879	224	254	4			
3	F	119	Total	C	N	O	S	0	0	0
			821	526	135	158	2			

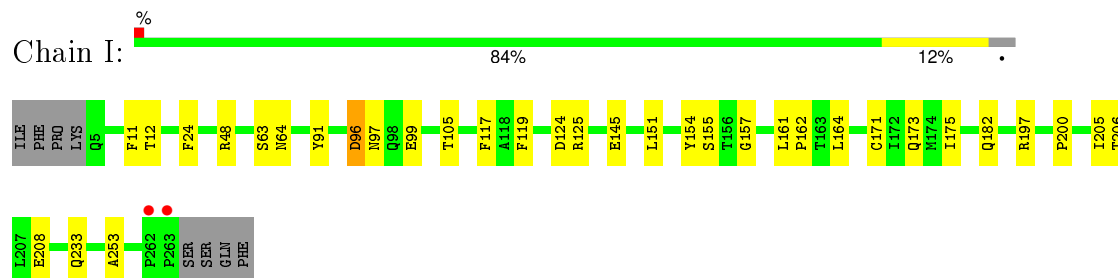
### 3 Residue-property plots [i](#)

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.

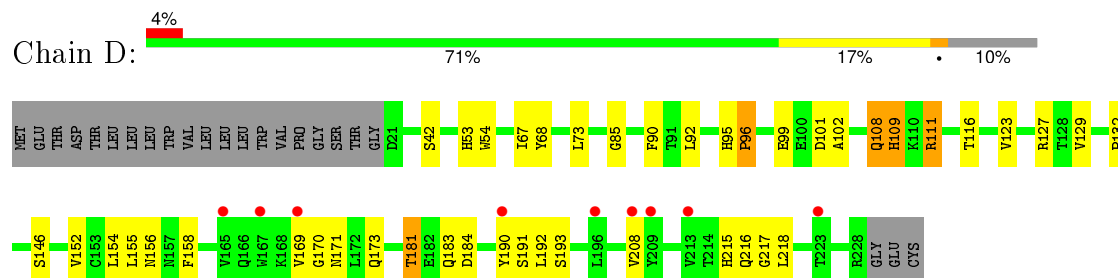
- Molecule 1: Ricin



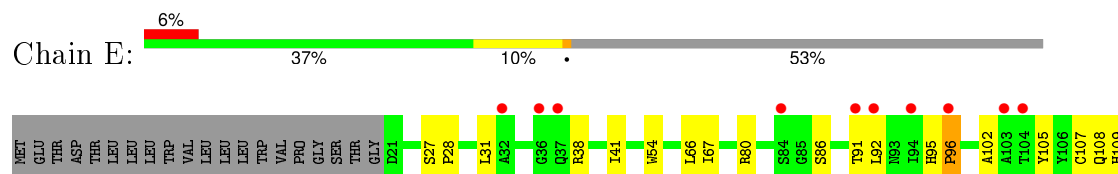
- Molecule 1: Ricin



- Molecule 2: mAb6c2 fab-Heavy chain

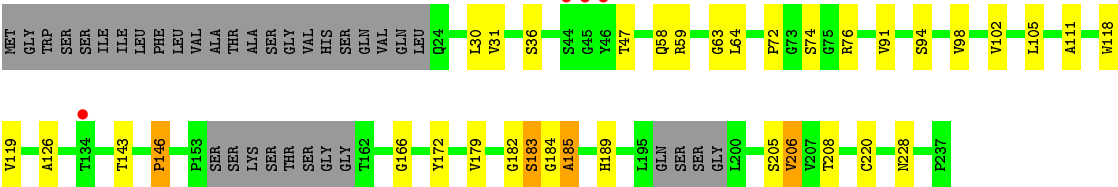


- Molecule 2: mAb6c2 fab-Heavy chain

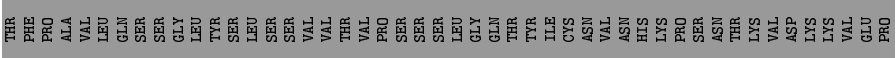
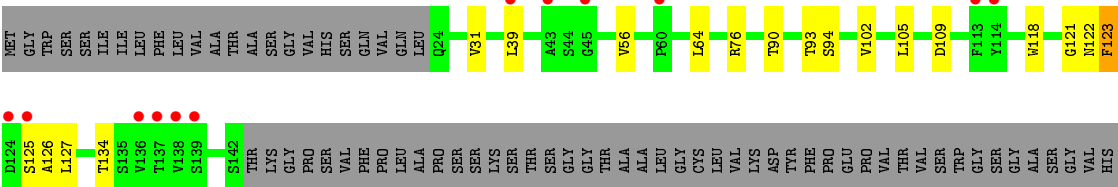
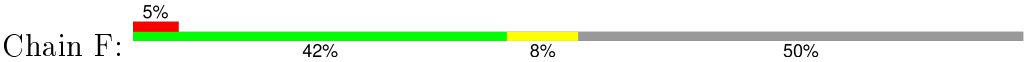




• Molecule 3: mAb6c2 fab-Light chain



• Molecule 3: mAb6c2 fab-Light chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.52Å 151.80Å 208.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.44 – 2.79 48.13 – 2.79	Depositor EDS
% Data completeness (in resolution range)	93.6 (36.44-2.79) 93.7 (48.13-2.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.83 (at 2.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.238 , 0.289 0.249 , 0.243	Depositor DCC
$R_{free}$ test set	2025 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	50.2	Xtriage
Anisotropy	1.043	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 50.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 40571 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	8287	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% 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 [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	0.46	0/2031	0.59	0/2769
1	I	0.45	0/2033	0.60	0/2772
2	D	0.50	0/1430	0.62	0/1967
2	E	0.35	0/749	0.52	0/1026
3	F	0.35	0/844	0.51	0/1161
3	H	0.54	0/1398	0.66	1/1929 (0.1%)
All	All	0.46	0/8485	0.60	1/11624 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	183	SER	N-CA-C	5.60	126.13	111.00

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	1987	0	1898	24	0
1	I	1989	0	1903	22	0
2	D	1397	0	1166	25	0
2	E	732	0	627	12	0
3	F	821	0	660	8	0
3	H	1361	0	1124	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8287	0	7378	99	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 6.

All (99) 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)
3:H:183:SER:HB2	3:H:184:GLY:CA	1.58	1.31
3:H:183:SER:CB	3:H:184:GLY:HA2	1.62	1.28
3:H:184:GLY:HA3	3:H:185:ALA:HB2	1.46	0.94
1:A:98:GLN:HE22	3:H:119:VAL:HG13	1.32	0.94
3:H:183:SER:CB	3:H:184:GLY:CA	2.34	0.83
1:I:12:THR:HG22	1:I:63:SER:HB2	1.64	0.79
1:A:187:GLU:OE2	1:A:235:ARG:NH2	2.24	0.71
2:E:54:TRP:HB2	2:E:67:ILE:HB	1.73	0.70
3:H:183:SER:HB2	3:H:184:GLY:HA2	0.74	0.67
1:A:12:THR:HG22	1:A:63:SER:HB2	1.77	0.67
3:H:189:HIS:HB2	3:H:206:VAL:HG13	1.78	0.65
2:D:53:HIS:HB2	2:D:108:GLN:HB3	1.79	0.65
2:D:95:HIS:CG	2:D:96:PRO:HD3	2.32	0.64
3:F:126:ALA:HB3	3:F:127:LEU:HA	1.80	0.62
2:E:95:HIS:CG	2:E:96:PRO:HD3	2.37	0.59
1:A:96:ASP:N	1:A:96:ASP:OD1	2.24	0.59
1:I:105:THR:HG22	2:E:111:ARG:NH2	2.19	0.58
3:F:125:SER:OG	3:F:127:LEU:CB	2.52	0.57
1:I:105:THR:HG22	2:E:111:ARG:HH21	1.70	0.57
1:A:108:PHE:O	1:A:111:VAL:HG22	2.04	0.56
1:A:114:ARG:HH21	2:D:111:ARG:HH22	1.54	0.56
2:D:68:TYR:CE1	3:H:126:ALA:HB2	2.40	0.56
3:F:105:LEU:HD22	3:F:109:ASP:HB3	1.88	0.55
3:H:184:GLY:HA3	3:H:185:ALA:CB	2.17	0.55
1:A:98:GLN:NE2	3:H:119:VAL:HG13	2.14	0.54
2:D:170:GLY:HA2	2:D:208:VAL:HB	1.88	0.54
2:E:41:ILE:HD12	2:E:92:LEU:HD23	1.90	0.54
1:A:45:LEU:HD21	1:A:254:LEU:HD13	1.91	0.53
1:A:102:GLU:OE1	1:A:106:HIS:NE2	2.39	0.53
1:I:182:GLN:HG3	1:I:253:ALA:HB2	1.92	0.52
1:A:173:GLN:NE2	1:A:208:GLU:OE2	2.42	0.52
1:I:48:ARG:HH22	1:I:97:ASN:HD21	1.58	0.52
1:I:151:LEU:HD12	1:I:164:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:117:PHE:HB3	1:I:119:PHE:CE1	2.46	0.51
2:D:111:ARG:O	2:D:111:ARG:NH2	2.43	0.51
1:I:99:GLU:CD	3:F:76:ARG:HH21	2.14	0.51
2:D:102:ALA:HA	2:D:123:VAL:HG13	1.94	0.50
1:A:154:TYR:CE2	1:A:164:LEU:HD22	2.46	0.50
2:E:66:LEU:HD22	2:E:105:TYR:HE2	1.77	0.49
3:H:72:PRO:HB3	3:H:91:VAL:HG21	1.94	0.49
2:E:28:PRO:HG2	2:E:31:LEU:HB2	1.93	0.49
3:H:59:ARG:HG2	3:H:111:ALA:HB2	1.95	0.48
2:D:54:TRP:HB2	2:D:67:ILE:HB	1.94	0.48
1:A:75:ASP:O	1:A:79:ALA:N	2.42	0.48
2:E:107:CYS:O	2:E:118:GLY:N	2.46	0.48
2:D:68:TYR:CD1	3:H:126:ALA:HB2	2.49	0.48
2:D:132:PRO:HB3	2:D:158:PHE:HB3	1.95	0.48
1:A:197:ARG:HG3	1:A:197:ARG:O	2.13	0.48
3:H:182:GLY:N	3:H:183:SER:HA	2.28	0.48
1:I:96:ASP:N	1:I:96:ASP:OD1	2.45	0.48
1:I:200:PRO:HG2	1:I:205:ILE:HD11	1.96	0.47
2:E:102:ALA:HA	2:E:123:VAL:HG13	1.96	0.47
1:A:102:GLU:OE2	3:H:76:ARG:NH1	2.47	0.47
3:H:146:PRO:HB3	3:H:172:TYR:HB3	1.96	0.47
1:I:197:ARG:O	1:I:197:ARG:HG3	2.14	0.47
2:D:99:GLU:C	2:D:101:ASP:H	2.19	0.46
1:I:64:ASN:HB2	1:I:145:GLU:CD	2.37	0.45
1:I:99:GLU:OE2	3:F:76:ARG:NH2	2.45	0.45
1:A:200:PRO:HG2	1:A:205:ILE:HD11	1.98	0.45
1:A:182:GLN:HG3	1:A:253:ALA:HB2	1.99	0.45
3:F:39:LEU:HD22	3:F:134:THR:HG21	1.98	0.44
2:D:216:GLN:O	2:D:218:LEU:N	2.50	0.44
2:D:155:LEU:HB2	2:D:192:LEU:HB3	2.00	0.44
1:I:11:PHE:HB2	1:I:24:PHE:CD1	2.53	0.44
2:E:27:SER:HA	2:E:28:PRO:HA	1.77	0.44
1:I:173:GLN:NE2	1:I:208:GLU:OE2	2.49	0.44
1:A:12:THR:HA	1:A:63:SER:O	2.18	0.43
2:D:85:GLY:HA3	2:D:90:PHE:HA	2.00	0.43
2:E:108:GLN:HG2	2:E:116:THR:O	2.18	0.43
2:D:67:ILE:CD1	2:D:92:LEU:HD13	2.49	0.43
1:I:161:LEU:HB3	1:I:162:PRO:HD3	2.00	0.43
2:D:67:ILE:HD12	2:D:92:LEU:HD13	2.00	0.43
2:D:181:THR:OG1	2:D:191:SER:HB2	2.18	0.43
2:D:215:HIS:CG	2:D:216:GLN:N	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:171:CYS:O	1:I:175:ILE:HG12	2.19	0.43
1:A:206:THR:HG21	1:A:233:GLN:N	2.34	0.43
1:I:91:TYR:OH	1:I:155:SER:HA	2.19	0.43
2:D:108:GLN:NE2	2:D:109:HIS:O	2.51	0.42
2:D:111:ARG:HD2	2:D:111:ARG:HA	1.65	0.42
3:F:56:VAL:HG11	3:F:64:LEU:HG	2.01	0.42
1:A:201:ASP:CG	1:A:235:ARG:HG2	2.39	0.42
2:D:129:VAL:HG21	2:D:216:GLN:OE1	2.18	0.42
3:H:31:VAL:HG11	3:H:105:LEU:HD12	2.01	0.42
1:A:89:SER:HA	1:A:113:ASN:O	2.20	0.42
1:A:105:THR:HG22	2:D:111:ARG:NH2	2.34	0.42
2:D:192:LEU:HD23	2:D:193:SER:N	2.35	0.42
3:H:58:GLN:HG3	3:H:63:GLY:O	2.20	0.41
1:I:154:TYR:CE1	1:I:164:LEU:HD22	2.55	0.41
3:H:166:GLY:HA2	3:H:205:SER:O	2.20	0.41
1:A:255:MET:HE3	1:A:255:MET:HB2	1.87	0.41
2:D:183:GLN:HB2	2:D:190:TYR:CE1	2.55	0.41
2:D:156:ASN:OD1	3:H:206:VAL:HG21	2.21	0.41
1:I:48:ARG:HH22	1:I:97:ASN:ND2	2.18	0.41
1:A:117:PHE:HB3	1:A:119:PHE:CE1	2.55	0.41
1:A:161:LEU:HD12	1:A:161:LEU:HA	1.91	0.41
2:E:107:CYS:SG	2:E:118:GLY:HA3	2.61	0.41
3:F:121:GLY:O	3:F:123:PHE:N	2.41	0.40
1:I:161:LEU:HD12	1:I:161:LEU:HA	1.87	0.40
1:I:206:THR:HG21	1:I:233:GLN:HB2	2.03	0.40

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	257/267 (96%)	248 (96%)	8 (3%)	1 (0%)	39 73

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	257/267 (96%)	247 (96%)	9 (4%)	1 (0%)	39	73
2	D	206/231 (89%)	183 (89%)	18 (9%)	5 (2%)	7	23
2	E	107/231 (46%)	96 (90%)	9 (8%)	2 (2%)	10	30
3	F	117/237 (49%)	101 (86%)	14 (12%)	2 (2%)	11	33
3	H	196/237 (83%)	176 (90%)	16 (8%)	4 (2%)	9	28
All	All	1140/1470 (78%)	1051 (92%)	74 (6%)	15 (1%)	15	41

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	96	PRO
2	D	146	SER
2	D	173	GLN
3	H	228	ASN
3	F	122	ASN
2	D	217	GLY
3	H	143	THR
3	H	185	ALA
1	I	157	GLY
2	E	80	ARG
2	E	96	PRO
2	D	171	ASN
3	F	123	PHE
1	A	157	GLY
3	H	146	PRO

### 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	200/226 (88%)	197 (98%)	3 (2%)	72	92
1	I	201/226 (89%)	198 (98%)	3 (2%)	72	92
2	D	118/201 (59%)	106 (90%)	12 (10%)	9	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	59/201 (29%)	53 (90%)	6 (10%)	9	24
3	F	67/201 (33%)	61 (91%)	6 (9%)	12	31
3	H	114/201 (57%)	101 (89%)	13 (11%)	7	20
All	All	759/1256 (60%)	716 (94%)	43 (6%)	25	56

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	ASP
1	A	125	ARG
1	A	155	SER
2	D	42	SER
2	D	73	LEU
2	D	108	GLN
2	D	109	HIS
2	D	111	ARG
2	D	116	THR
2	D	127	ARG
2	D	152	VAL
2	D	154	LEU
2	D	169	VAL
2	D	181	THR
2	D	184	ASP
3	H	30	LEU
3	H	36	SER
3	H	47	THR
3	H	64	LEU
3	H	74	SER
3	H	94	SER
3	H	98	VAL
3	H	102	VAL
3	H	118	TRP
3	H	179	VAL
3	H	206	VAL
3	H	208	THR
3	H	220	CYS
1	I	96	ASP
1	I	124	ASP
1	I	125	ARG
2	E	38	ARG
2	E	86	SER

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Mol	Chain	Res	Type
2	E	91	THR
2	E	109	HIS
2	E	110	LYS
2	E	116	THR
3	F	31	VAL
3	F	90	THR
3	F	93	THR
3	F	94	SER
3	F	102	VAL
3	F	118	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	GLN
1	A	231	GLN
3	H	189	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 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 ⓘ

There are no chain breaks in this entry.

## 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	259/267 (97%)	0.02	0 100 100	27, 42, 57, 69	2 (0%)
1	I	259/267 (97%)	0.03	2 (0%) 87 83	30, 45, 60, 87	1 (0%)
2	D	208/231 (90%)	0.05	9 (4%) 39 31	34, 51, 84, 96	0
2	E	109/231 (47%)	0.64	14 (12%) 5 3	46, 75, 114, 147	0
3	F	119/237 (50%)	0.57	12 (10%) 9 5	47, 72, 96, 107	0
3	H	202/237 (85%)	-0.02	4 (1%) 68 62	29, 46, 63, 76	0
All	All	1156/1470 (78%)	0.14	41 (3%) 48 40	27, 48, 89, 147	3 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	124	ASP	5.7
3	F	125	SER	5.4
1	I	263	PRO	5.1
3	F	139	SER	4.4
3	F	114	TYR	3.8
2	D	167	TRP	3.7
1	I	262	PRO	3.7
3	F	136	VAL	3.6
2	E	91	THR	3.4
2	E	36	GLY	3.4
2	E	127	ARG	3.2
2	E	92	LEU	3.2
3	F	113	PHE	3.1
3	H	45	GLY	3.1
2	E	124	GLU	3.0
2	D	165	VAL	3.0
3	F	138	VAL	3.0
2	E	103	ALA	3.0
3	F	39	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
2	D	196	LEU	2.9
2	E	84	SER	2.8
3	H	44	SER	2.8
2	D	169	VAL	2.7
2	D	223	THR	2.7
2	E	128	THR	2.6
2	D	213	VAL	2.4
2	D	209	TYR	2.4
3	F	45	GLY	2.4
2	E	37	GLN	2.4
2	E	104	THR	2.4
2	D	208	VAL	2.3
3	F	137	THR	2.3
2	D	190	TYR	2.3
3	H	46	TYR	2.2
2	E	125	ILE	2.2
3	F	60	PRO	2.2
2	E	32	ALA	2.2
3	F	43	ALA	2.1
2	E	94	ILE	2.1
2	E	96	PRO	2.1
3	H	134	THR	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 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.