



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:00 PM GMT

PDB ID : 1IAI  
Title : IDIOTYPE-ANTI-IDIOTYPE FAB COMPLEX  
Authors : Ban, N.; Escobar, C.; Garcia, R.; Hasel, K.; Day, J.; Greenwood, A.; McPherson, A.  
Deposited on : 1993-12-28  
Resolution : 2.90 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

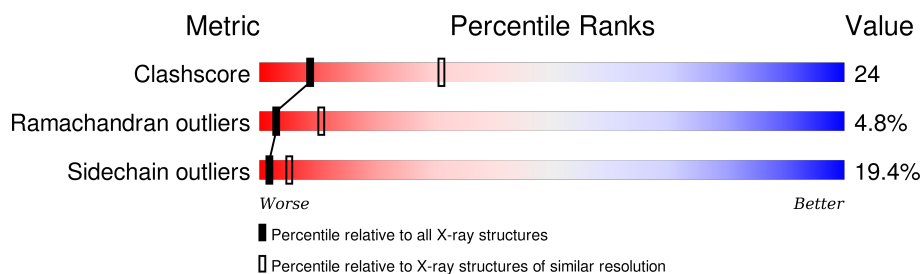
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	214	 50% 37% 11% •
2	H	219	 51% 39% 9% •
3	M	215	 56% 34% 9%
4	I	218	 43% 44% 11% •

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6672 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 IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS NEUTRALIZING ANTIBODY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	214	Total	C	N	O	S	0	0	0
			1675	1045	281	341	8			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	8	HIS	GLN	CONFLICT	GB 10121892
L	21	ILE	VAL	CONFLICT	GB 10121892
L	28	ASP	ASN	CONFLICT	GB 10121892
L	30	SER	GLY	CONFLICT	GB 10121892
L	32	ALA	ASN	CONFLICT	GB 10121892
L	46	LEU	ALA	CONFLICT	GB 10121892
L	54	GLN	ARG	CONFLICT	GB 10121892
L	56	THR	SER	CONFLICT	GB 10121892
L	68	ARG	GLY	CONFLICT	GB 10121892
L	73	PHE	LEU	CONFLICT	GB 10121892
L	76	ASN	SER	CONFLICT	GB 10121892
L	77	SER	ASN	CONFLICT	GB 10121892
L	80	ALA	SER	CONFLICT	GB 10121892
L	85	VAL	GLU	CONFLICT	GB 10121892
L	87	TYR	PHE	CONFLICT	GB 10121892
L	89	HIS	GLN	CONFLICT	GB 10121892
L	91	HIS	TYR	CONFLICT	GB 10121892
L	92	TYR	ASN	CONFLICT	GB 10121892
L	94	THR	TYR	CONFLICT	GB 10121892
L	96	PHE	LEU	CONFLICT	GB 10121892
L	100	SER	ALA	CONFLICT	GB 10121892
L	106	ILE	LEU	CONFLICT	GB 10121892

- Molecule 2 is a protein called IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS NEUTRALIZING ANTIBODY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	219	Total	C	N	O	S	0	0	0
			1666	1057	265	336	8			

- Molecule 3 is a protein called ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	215	Total	C	N	O	S	0	0	0
			1655	1029	273	345	8			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	3	GLN	VAL	CONFLICT	GB 1042224
M	10	PHE	ILE	CONFLICT	GB 1042224
M	12	ALA	SER	CONFLICT	GB 1042224
M	18	LYS	ARG	CONFLICT	GB 1042224
M	21	ILE	MET	CONFLICT	GB 1042224
M	25	VAL	ALA	CONFLICT	GB 1042224
M	26	SER	ASN	CONFLICT	GB 1042224
M	28	SER	-	INSERTION	GB 1042224
M	29	ILE	-	INSERTION	GB 1042224
M	31	SER	VAL	CONFLICT	GB 1042224
M	33	ASN	TYR	CONFLICT	GB 1042224
M	34	LEU	MET	CONFLICT	GB 1042224
M	42	GLU	GLY	CONFLICT	GB 1042224
M	47	PRO	ARG	CONFLICT	GB 1042224
M	51	GLY	ASP	CONFLICT	GB 1042224
M	54	ASN	LYS	CONFLICT	GB 1042224
M	61	VAL	ALA	CONFLICT	GB 1042224
M	93	ASN	SER	CONFLICT	GB 1042224
M	95	TYR	HIS	CONFLICT	GB 1042224
M	114	PRO	GLN	CONFLICT	GB 1042224

- Molecule 4 is a protein called ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	I	218	Total	C	N	O	S	0	0	0
			1676	1066	277	325	8			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	5	GLN	GLU	CONFLICT	GB 1042226

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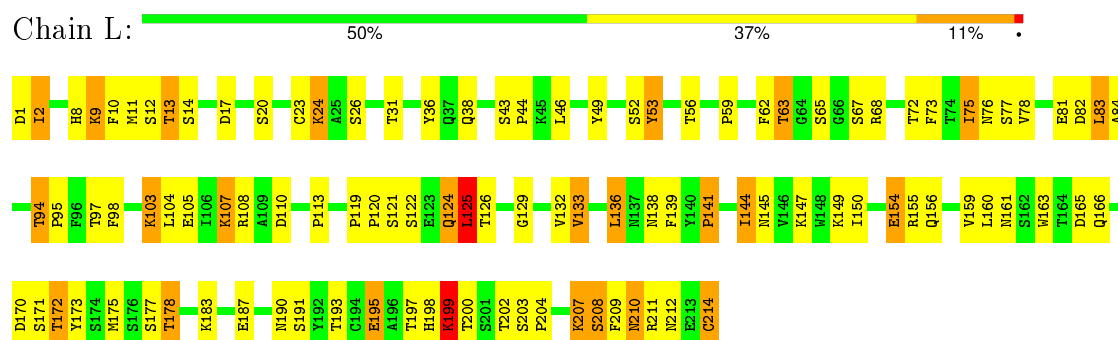
Chain	Residue	Modelled	Actual	Comment	Reference
I	20	LEU	VAL	CONFLICT	GB 1042226
I	28	THR	ALA	CONFLICT	GB 1042226
I	30	ASN	SER	CONFLICT	GB 1042226
I	31	ASN	TYR	CONFLICT	GB 1042226
I	35	SER	ASN	CONFLICT	GB 1042226
I	43	LYS	ARG	CONFLICT	GB 1042226
I	48	VAL	ILE	CONFLICT	GB 1042226
I	53	LEU	PHE	CONFLICT	GB 1042226
I	54	ASN	LYS	CONFLICT	GB 1042226
I	56	ASP	-	INSERTION	GB 1042226
I	58	PHE	ASN	CONFLICT	GB 1042226
I	59	ALA	TYR	CONFLICT	GB 1042226
I	69	LYS	ARG	CONFLICT	GB 1042226
I	71	ILE	THR	CONFLICT	GB 1042226
I	80	ARG	SER	CONFLICT	GB 1042226
I	81	LEU	VAL	CONFLICT	GB 1042226
I	87	SER	ASN	CONFLICT	GB 1042226
I	99	VAL	-	INSERTION	GB 1042226
I	100	LEU	THR	CONFLICT	GB 1042226
I	102	PRO	GLU	CONFLICT	GB 1042226
I	103	LEU	GLY	CONFLICT	GB 1042226
I	104	PHE	ILE	CONFLICT	GB 1042226
I	107	ALA	PRO	CONFLICT	GB 1042226
I	108	VAL	PHE	CONFLICT	GB 1042226
I	109	ASP	ALA	CONFLICT	GB 1042226
I	116	SER	LEU	CONFLICT	GB 1042226
I	121	SER	ALA	CONFLICT	GB 1042226
I	?	-	SER	DELETION	GB 1042226
I	196	ARG	-	INSERTION	GB 1042226

### 3 Residue-property plots

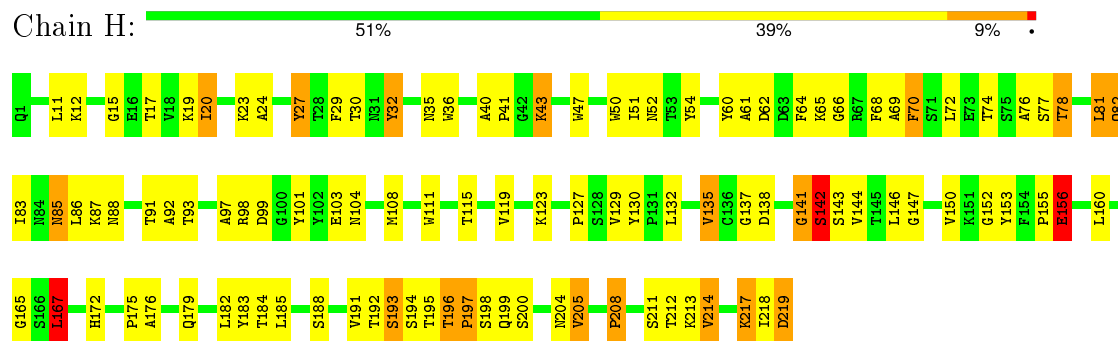
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

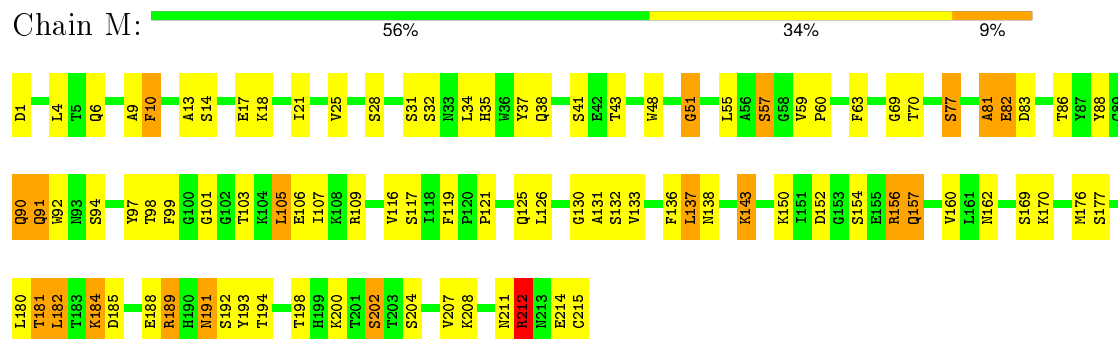
#### • Molecule 1: IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS NEUTRALIZING ANTIBODY



#### • Molecule 2: IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS NEUTRALIZING ANTIBODY

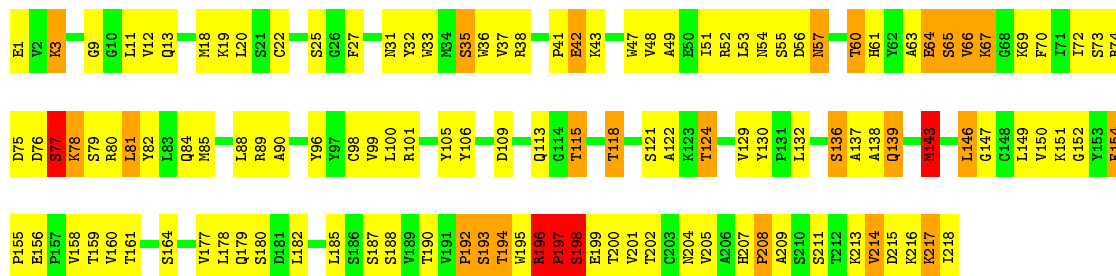


#### • Molecule 3: ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A)



● Molecule 4: ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A)

Chain I:  43% 44% 11% •



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	187.58 Å   80.60 Å   75.20 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	40.00 – 2.90	Depositor
% Data completeness (in resolution range)	83.0 (40.00-2.90)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.210 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6672	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	6.0	wwPDB-VP



## 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	L	0.73	0/1715	0.95	3/2328 (0.1%)
2	H	0.72	0/1710	0.97	4/2335 (0.2%)
3	M	0.66	0/1696	0.92	3/2306 (0.1%)
4	I	0.78	0/1721	1.06	5/2347 (0.2%)
All	All	0.73	0/6842	0.98	15/9316 (0.2%)

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	2
3	M	0	1
All	All	0	3

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
4	I	76	ASP	N-CA-C	-10.30	83.20	111.00
4	I	77	SER	N-CA-C	-8.74	87.41	111.00
2	H	141	GLY	N-CA-C	-7.22	95.05	113.10
2	H	194	SER	N-CA-CB	-6.90	100.15	110.50
4	I	198	SER	N-CA-C	6.84	129.48	111.00
1	L	125	LEU	CA-CB-CG	6.56	130.39	115.30
3	M	51	GLY	N-CA-C	-6.44	97.00	113.10
3	M	202	SER	N-CA-C	5.88	126.88	111.00
2	H	195	THR	N-CA-C	5.84	126.77	111.00
4	I	197	PRO	N-CA-C	5.82	127.23	112.10
2	H	156	GLU	N-CA-C	5.32	125.36	111.00
1	L	75	ILE	N-CA-C	-5.31	96.66	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	156	GLU	N-CA-C	5.28	125.24	111.00
3	M	212	ARG	N-CA-C	5.26	125.20	111.00
1	L	199	LYS	N-CA-C	5.18	124.99	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	173	TYR	Sidechain
1	L	53	TYR	Sidechain
3	M	193	TYR	Sidechain

## 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	L	1675	0	1591	70	1
2	H	1666	0	1604	82	1
3	M	1655	0	1562	67	0
4	I	1676	0	1637	99	0
All	All	6672	0	6394	309	1

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 24.

All (309) 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:H:143:SER:HA	2:H:193:SER:HA	1.21	1.18
2:H:217:LYS:NZ	2:H:217:LYS:HB2	1.76	0.98
4:I:196:ARG:HB3	4:I:196:ARG:NH1	1.85	0.91
4:I:27:PHE:CZ	4:I:100:LEU:HD11	2.05	0.91
2:H:143:SER:CA	2:H:193:SER:HA	2.03	0.88
2:H:143:SER:HA	2:H:193:SER:CA	2.03	0.86
3:M:131:ALA:O	3:M:182:LEU:HD23	1.75	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:214:CYS:SG	2:H:135:VAL:HG22	2.17	0.84
4:I:195:TRP:C	4:I:197:PRO:HD2	1.98	0.83
2:H:60:TYR:HB2	2:H:65:LYS:HD3	1.61	0.83
1:L:120:PRO:HD3	1:L:132:VAL:HG22	1.61	0.83
4:I:196:ARG:HB3	4:I:196:ARG:HH11	1.45	0.82
2:H:60:TYR:CD2	2:H:65:LYS:HD3	2.13	0.82
4:I:13:GLN:OE1	4:I:121:SER:HA	1.79	0.82
2:H:217:LYS:HB2	2:H:217:LYS:HZ2	1.41	0.80
4:I:202:THR:HG21	4:I:214:VAL:HG13	1.64	0.79
2:H:60:TYR:HD2	2:H:65:LYS:HD3	1.47	0.78
2:H:97:ALA:HB1	2:H:108:MET:HB3	1.66	0.77
4:I:154:PHE:HB3	4:I:155:PRO:HD3	1.67	0.77
2:H:127:PRO:HB3	2:H:153:TYR:HB3	1.64	0.77
2:H:51:ILE:HB	2:H:70:PHE:CE2	2.22	0.75
1:L:138:ASN:HD22	1:L:172:THR:HG21	1.51	0.75
2:H:11:LEU:HD13	2:H:155:PRO:HG3	1.69	0.75
3:M:4:LEU:HD11	3:M:91:GLN:HB2	1.69	0.74
2:H:129:VAL:HG11	2:H:205:VAL:HG21	1.68	0.73
1:L:145:ASN:HB2	1:L:197:THR:HB	1.68	0.73
2:H:12:LYS:O	2:H:119:VAL:HA	1.89	0.73
2:H:69:ALA:HB3	2:H:82:GLN:HB3	1.70	0.72
1:L:161:ASN:HB3	1:L:175:MET:HE1	1.70	0.72
2:H:129:VAL:HG21	2:H:213:LYS:HB3	1.71	0.71
4:I:19:LYS:HE3	4:I:82:TYR:CD2	2.26	0.71
2:H:153:TYR:O	2:H:183:TYR:HB2	1.91	0.71
3:M:126:LEU:HD21	3:M:131:ALA:HB2	1.73	0.70
4:I:19:LYS:HE3	4:I:82:TYR:HD2	1.56	0.70
2:H:156:GLU:CD	2:H:156:GLU:H	1.95	0.70
2:H:93:THR:HA	2:H:115:THR:O	1.92	0.70
2:H:68:PHE:CE1	2:H:83:ILE:HG23	2.27	0.70
4:I:51:ILE:HG13	4:I:60:THR:HG23	1.72	0.70
3:M:90:GLN:NE2	3:M:98:THR:O	2.26	0.69
2:H:196:THR:N	2:H:197:PRO:HD2	2.07	0.68
1:L:59:PRO:HG2	1:L:62:PHE:HD2	1.58	0.68
2:H:205:VAL:HG23	2:H:213:LYS:O	1.92	0.68
2:H:101:TYR:OH	2:H:104:ASN:HA	1.94	0.68
1:L:11:MET:HB3	1:L:104:LEU:HD12	1.75	0.68
2:H:218:ILE:O	2:H:219:ASP:HB2	1.94	0.67
4:I:27:PHE:CD2	4:I:100:LEU:HD21	2.29	0.67
4:I:20:LEU:HD12	4:I:20:LEU:N	2.10	0.67
4:I:124:THR:HG21	4:I:209:ALA:CB	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:144:VAL:HG13	2:H:191:VAL:HG23	1.76	0.67
2:H:40:ALA:HB3	2:H:43:LYS:HB2	1.76	0.67
4:I:3:LYS:HD3	4:I:25:SER:HB3	1.77	0.67
3:M:90:GLN:HE21	3:M:90:GLN:HA	1.60	0.67
4:I:27:PHE:CE2	4:I:100:LEU:HD21	2.31	0.66
1:L:191:SER:HA	1:L:210:ASN:HB3	1.78	0.66
1:L:133:VAL:HG12	1:L:178:THR:HG23	1.78	0.65
3:M:189:ARG:O	3:M:189:ARG:HG2	1.97	0.64
3:M:126:LEU:CD2	3:M:131:ALA:HB2	2.26	0.64
3:M:162:ASN:HA	3:M:177:SER:O	1.97	0.64
4:I:196:ARG:HG2	4:I:196:ARG:O	1.96	0.64
4:I:56:ASP:O	4:I:57:ASN:HB2	1.98	0.63
4:I:161:THR:OG1	4:I:204:ASN:ND2	2.31	0.63
1:L:9:LYS:H	1:L:9:LYS:CD	2.11	0.63
1:L:198:HIS:CE1	1:L:200:THR:HG22	2.35	0.62
1:L:63:THR:HG21	1:L:76:ASN:HD21	1.64	0.62
4:I:65:SER:O	4:I:66:VAL:HG13	2.00	0.61
4:I:33:TRP:HB3	4:I:52:ARG:HG3	1.81	0.61
4:I:143:MET:HA	4:I:193:SER:HA	1.82	0.61
4:I:136:SER:O	4:I:139:GLN:HG3	2.00	0.61
2:H:20:ILE:HD12	2:H:81:LEU:HB3	1.82	0.61
3:M:60:PRO:HG2	3:M:63:PHE:HD2	1.67	0.60
1:L:63:THR:CG2	1:L:76:ASN:HD21	2.15	0.60
2:H:68:PHE:HE1	2:H:83:ILE:HG23	1.65	0.60
3:M:191:ASN:C	3:M:191:ASN:HD22	2.05	0.60
1:L:49:TYR:CE1	1:L:53:TYR:HB2	2.35	0.60
3:M:57:SER:H	3:M:59:VAL:HG23	1.66	0.60
1:L:24:LYS:O	1:L:24:LYS:HG3	2.01	0.60
4:I:3:LYS:HD3	4:I:25:SER:CB	2.30	0.59
3:M:60:PRO:HG2	3:M:63:PHE:CD2	2.38	0.59
4:I:195:TRP:O	4:I:197:PRO:HD2	2.01	0.59
3:M:81:ALA:HB1	3:M:169:SER:O	2.03	0.59
1:L:149:LYS:HA	1:L:154:GLU:HA	1.84	0.59
3:M:150:LYS:HA	3:M:154:SER:O	2.02	0.59
4:I:51:ILE:HB	4:I:72:ILE:HG21	1.85	0.59
3:M:191:ASN:HA	3:M:212:ARG:CG	2.32	0.59
4:I:160:VAL:HG22	4:I:205:VAL:HG22	1.83	0.59
4:I:53:LEU:HA	4:I:57:ASN:O	2.03	0.59
4:I:150:VAL:HB	4:I:185:LEU:HD23	1.86	0.58
2:H:142:SER:O	2:H:193:SER:HB3	2.04	0.57
4:I:42:GLU:HG2	4:I:43:LYS:HG2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:59:PRO:HG2	1:L:62:PHE:CD2	2.39	0.57
1:L:94:THR:HB	1:L:95:PRO:HD3	1.85	0.57
2:H:60:TYR:HD2	2:H:65:LYS:CD	2.18	0.57
2:H:129:VAL:CG1	2:H:205:VAL:HG21	2.35	0.57
4:I:60:THR:HG21	4:I:72:ILE:HB	1.87	0.57
1:L:136:LEU:N	1:L:136:LEU:HD22	2.20	0.57
3:M:191:ASN:HD21	3:M:211:ASN:HB3	1.68	0.57
3:M:156:ARG:HA	3:M:156:ARG:HE	1.70	0.56
1:L:2:ILE:HG12	1:L:26:SER:OG	2.05	0.56
4:I:3:LYS:HD2	4:I:3:LYS:N	2.20	0.56
3:M:21:ILE:HG21	3:M:103:THR:HG21	1.86	0.56
4:I:64:GLU:HG2	4:I:65:SER:N	2.20	0.56
3:M:188:GLU:OE2	3:M:214:GLU:HB2	2.05	0.56
3:M:150:LYS:HB2	3:M:194:THR:HB	1.87	0.56
2:H:27:TYR:HD2	2:H:32:TYR:CE1	2.24	0.55
4:I:194:THR:OG1	4:I:196:ARG:NH1	2.40	0.55
4:I:178:LEU:HD12	4:I:182:LEU:O	2.06	0.55
2:H:87:LYS:HD2	2:H:88:ASN:H	1.70	0.55
2:H:86:LEU:HD13	2:H:119:VAL:HG12	1.88	0.55
4:I:100:LEU:HD12	4:I:101:ARG:N	2.23	0.54
4:I:64:GLU:CG	4:I:65:SER:N	2.70	0.54
1:L:84:ALA:O	1:L:103:LYS:HA	2.08	0.54
4:I:196:ARG:CG	4:I:196:ARG:O	2.56	0.54
2:H:24:ALA:HB1	2:H:27:TYR:CE1	2.43	0.54
2:H:52:ASN:OD1	2:H:54:TYR:HB3	2.07	0.54
2:H:142:SER:O	2:H:193:SER:CB	2.55	0.54
4:I:202:THR:HG23	4:I:215:ASP:O	2.08	0.54
3:M:143:LYS:HE3	3:M:143:LYS:H	1.73	0.54
2:H:60:TYR:HB2	2:H:65:LYS:CD	2.36	0.53
2:H:98:ARG:O	2:H:108:MET:HA	2.07	0.53
4:I:18:MET:HB3	4:I:85:MET:HG3	1.89	0.53
1:L:190:ASN:OD1	1:L:210:ASN:HB2	2.08	0.53
2:H:47:TRP:HZ2	2:H:50:TRP:HB2	1.72	0.53
4:I:27:PHE:HE1	4:I:32:TYR:CD2	2.27	0.53
1:L:38:GLN:O	1:L:84:ALA:HB1	2.08	0.53
1:L:122:SER:O	1:L:125:LEU:HD13	2.08	0.52
4:I:216:LYS:C	4:I:217:LYS:HG2	2.29	0.52
3:M:191:ASN:HA	3:M:212:ARG:HG2	1.91	0.52
1:L:113:PRO:HB3	1:L:139:PHE:HB3	1.91	0.52
1:L:12:SER:HA	1:L:105:GLU:O	2.10	0.52
1:L:72:THR:HG22	1:L:73:PHE:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:60:TYR:CB	2:H:65:LYS:HD3	2.37	0.52
1:L:8:HIS:HA	1:L:9:LYS:HE3	1.92	0.52
2:H:15:GLY:O	2:H:85:ASN:HA	2.10	0.52
2:H:204:ASN:HA	2:H:214:VAL:HG12	1.92	0.52
3:M:132:SER:OG	3:M:181:THR:HG23	2.10	0.51
2:H:129:VAL:HG11	2:H:205:VAL:CG2	2.38	0.51
1:L:138:ASN:HD22	1:L:172:THR:CG2	2.19	0.51
2:H:204:ASN:OD1	2:H:214:VAL:HG12	2.09	0.51
1:L:161:ASN:HB3	1:L:175:MET:CE	2.40	0.51
3:M:9:ALA:HB3	3:M:10:PHE:CD1	2.45	0.51
4:I:100:LEU:HD12	4:I:101:ARG:H	1.74	0.51
1:L:190:ASN:O	1:L:210:ASN:HA	2.10	0.51
2:H:172:HIS:HB2	2:H:188:SER:OG	2.11	0.51
1:L:67:SER:OG	1:L:68:ARG:N	2.44	0.51
1:L:144:ILE:HD12	1:L:198:HIS:HB2	1.91	0.51
1:L:147:LYS:O	1:L:195:GLU:HB2	2.11	0.51
2:H:153:TYR:CZ	2:H:183:TYR:HB3	2.46	0.51
4:I:18:MET:HG3	4:I:20:LEU:HD11	1.92	0.51
2:H:29:PHE:CD2	2:H:77:SER:HA	2.46	0.51
3:M:90:GLN:HG2	3:M:99:PHE:CD2	2.46	0.50
4:I:160:VAL:HG11	4:I:187:SER:HB2	1.93	0.50
2:H:87:LYS:HG3	2:H:88:ASN:OD1	2.11	0.50
3:M:38:GLN:NE2	3:M:48:TRP:CH2	2.79	0.50
2:H:36:TRP:NE1	2:H:70:PHE:CE1	2.77	0.50
4:I:197:PRO:O	4:I:201:VAL:HG21	2.12	0.50
2:H:91:THR:O	2:H:92:ALA:HB2	2.11	0.50
2:H:141:GLY:O	2:H:142:SER:O	2.30	0.50
4:I:9:GLY:HA3	4:I:115:THR:HB	1.94	0.50
3:M:18:LYS:HA	3:M:77:SER:O	2.12	0.50
2:H:146:LEU:HD13	2:H:217:LYS:NZ	2.26	0.50
2:H:64:PHE:O	2:H:68:PHE:HB2	2.12	0.49
3:M:191:ASN:HD21	3:M:211:ASN:CB	2.26	0.49
3:M:10:PHE:N	3:M:10:PHE:CD1	2.79	0.49
1:L:120:PRO:CD	1:L:132:VAL:HG22	2.39	0.49
4:I:22:CYS:O	4:I:80:ARG:HA	2.12	0.49
4:I:56:ASP:O	4:I:57:ASN:CB	2.59	0.49
4:I:96:TYR:CD1	4:I:96:TYR:N	2.81	0.48
3:M:34:LEU:O	3:M:51:GLY:O	2.31	0.48
4:I:63:ALA:O	4:I:67:LYS:HB2	2.13	0.48
2:H:27:TYR:CD2	2:H:32:TYR:CE1	3.02	0.48
4:I:9:GLY:H	4:I:115:THR:HG21	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:130:TYR:HE2	4:I:151:LYS:HG3	1.78	0.48
1:L:198:HIS:CE1	1:L:200:THR:H	2.32	0.48
4:I:207:HIS:CE1	4:I:209:ALA:HB3	2.49	0.47
4:I:31:ASN:HA	4:I:53:LEU:O	2.13	0.47
1:L:163:TRP:O	2:H:175:PRO:HD2	2.14	0.47
2:H:217:LYS:HB2	2:H:217:LYS:HZ3	1.74	0.47
3:M:160:VAL:HG22	3:M:162:ASN:OD1	2.14	0.47
3:M:133:VAL:N	3:M:180:LEU:O	2.47	0.47
4:I:122:ALA:HB3	4:I:154:PHE:CE2	2.49	0.47
4:I:27:PHE:CE2	4:I:100:LEU:HD11	2.49	0.47
2:H:135:VAL:HB	2:H:219:ASP:HB3	1.95	0.47
3:M:57:SER:C	3:M:59:VAL:H	2.17	0.47
1:L:14:SER:O	1:L:17:ASP:HB2	2.15	0.47
4:I:89:ARG:CG	4:I:90:ALA:H	2.27	0.47
1:L:9:LYS:HD2	1:L:10:PHE:H	1.79	0.47
2:H:165:GLY:HA2	2:H:167:LEU:HD12	1.96	0.47
4:I:33:TRP:CZ3	4:I:35:SER:HB2	2.49	0.47
2:H:54:TYR:HE2	4:I:1:GLU:OE2	1.98	0.47
1:L:170:ASP:OD1	1:L:172:THR:HB	2.14	0.47
3:M:6:GLN:OE1	3:M:88:TYR:HA	2.15	0.47
4:I:96:TYR:HD1	4:I:96:TYR:N	2.13	0.46
3:M:156:ARG:NH2	3:M:157:GLN:OE1	2.48	0.46
1:L:110:ASP:OD1	1:L:141:PRO:HD3	2.15	0.46
3:M:90:GLN:HG2	3:M:99:PHE:CE2	2.51	0.46
3:M:32:SER:HB2	4:I:105:TYR:O	2.15	0.46
2:H:153:TYR:CE1	2:H:183:TYR:HB3	2.50	0.46
3:M:121:PRO:HG3	3:M:131:ALA:HB1	1.97	0.45
4:I:164:SER:HA	4:I:204:ASN:HD21	1.81	0.45
1:L:159:VAL:HG12	1:L:160:LEU:N	2.31	0.45
3:M:13:ALA:HB1	3:M:17:GLU:HG2	1.97	0.45
4:I:11:LEU:HA	4:I:118:THR:O	2.16	0.45
1:L:119:PRO:HB3	1:L:209:PHE:CE2	2.51	0.45
4:I:85:MET:HB2	4:I:88:LEU:HD21	1.98	0.45
1:L:83:LEU:HD21	1:L:166:GLN:HB2	1.97	0.45
1:L:121:SER:OG	2:H:130:TYR:HB3	2.16	0.45
1:L:198:HIS:HE1	1:L:200:THR:HG22	1.80	0.45
1:L:124:GLN:HG3	1:L:129:GLY:O	2.17	0.45
2:H:23:LYS:HE2	2:H:76:ALA:O	2.17	0.45
2:H:146:LEU:HD13	2:H:217:LYS:HZ1	1.81	0.45
2:H:11:LEU:HB2	2:H:155:PRO:HG2	1.99	0.45
3:M:152:ASP:HA	3:M:192:SER:OG	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:34:LEU:HD22	3:M:90:GLN:O	2.17	0.45
2:H:19:LYS:HA	2:H:81:LEU:O	2.16	0.45
4:I:18:MET:CB	4:I:88:LEU:HD11	2.47	0.44
3:M:132:SER:HA	3:M:180:LEU:O	2.18	0.44
4:I:129:VAL:HB	4:I:213:LYS:HD2	2.00	0.44
1:L:193:THR:HA	1:L:208:SER:OG	2.18	0.44
3:M:1:ASP:OD2	3:M:98:THR:HG21	2.18	0.44
3:M:143:LYS:CE	3:M:143:LYS:H	2.30	0.44
4:I:60:THR:O	4:I:61:HIS:CG	2.70	0.44
3:M:57:SER:C	3:M:59:VAL:N	2.70	0.44
3:M:86:THR:HA	3:M:103:THR:O	2.17	0.44
1:L:175:MET:HB2	1:L:175:MET:HE3	1.95	0.44
3:M:212:ARG:HD3	3:M:214:GLU:OE1	2.17	0.44
1:L:136:LEU:CD2	1:L:136:LEU:N	2.81	0.44
4:I:3:LYS:HB2	4:I:25:SER:HB3	2.00	0.44
3:M:157:GLN:O	3:M:160:VAL:HG12	2.18	0.44
4:I:89:ARG:CG	4:I:90:ALA:N	2.81	0.44
3:M:125:GLN:HG2	3:M:130:GLY:O	2.17	0.44
4:I:69:LYS:C	4:I:70:PHE:HD1	2.20	0.44
2:H:17:THR:HA	2:H:83:ILE:O	2.18	0.43
3:M:9:ALA:HB3	3:M:10:PHE:HD1	1.83	0.43
3:M:105:LEU:HD12	3:M:105:LEU:HA	1.80	0.43
4:I:32:TYR:C	4:I:32:TYR:CD1	2.91	0.43
4:I:35:SER:HG	4:I:47:TRP:HE1	1.65	0.43
4:I:73:SER:HB3	4:I:82:TYR:HB2	2.00	0.43
4:I:36:TRP:O	4:I:48:VAL:HG22	2.18	0.43
1:L:9:LYS:H	1:L:9:LYS:HE3	1.83	0.43
1:L:203:SER:HA	1:L:204:PRO:HD2	1.51	0.43
4:I:195:TRP:C	4:I:197:PRO:CD	2.81	0.43
4:I:36:TRP:NE1	4:I:81:LEU:HD13	2.33	0.43
2:H:32:TYR:CD1	2:H:32:TYR:N	2.86	0.43
4:I:54:ASN:O	4:I:55:SER:C	2.57	0.43
1:L:49:TYR:C	1:L:49:TYR:CD1	2.92	0.43
2:H:41:PRO:C	2:H:43:LYS:H	2.22	0.43
1:L:155:ARG:HA	1:L:155:ARG:HD3	1.92	0.43
3:M:208:LYS:HA	3:M:208:LYS:HD3	1.75	0.43
1:L:36:TYR:CE2	1:L:46:LEU:HD13	2.54	0.43
3:M:191:ASN:C	3:M:191:ASN:ND2	2.70	0.43
3:M:214:GLU:HG2	3:M:214:GLU:H	1.62	0.43
4:I:179:GLN:OE1	4:I:182:LEU:O	2.37	0.43
3:M:92:TRP:HA	3:M:97:TYR:CD1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:55:LEU:HD21	3:M:63:PHE:O	2.19	0.42
4:I:70:PHE:N	4:I:70:PHE:CD1	2.87	0.42
1:L:125:LEU:HD22	1:L:126:THR:N	2.33	0.42
4:I:196:ARG:CZ	4:I:196:ARG:HB3	2.47	0.42
1:L:2:ILE:HD13	1:L:2:ILE:O	2.19	0.42
3:M:119:PHE:CZ	4:I:146:LEU:HA	2.53	0.42
2:H:86:LEU:HB3	2:H:119:VAL:HG11	2.02	0.42
1:L:107:LYS:HD3	1:L:108:ARG:N	2.34	0.42
1:L:108:ARG:HD2	1:L:171:SER:HB2	2.01	0.42
3:M:184:LYS:O	3:M:188:GLU:HB2	2.19	0.42
1:L:83:LEU:O	1:L:84:ALA:HB2	2.20	0.42
2:H:132:LEU:HB2	2:H:147:GLY:O	2.20	0.42
2:H:60:TYR:CG	2:H:65:LYS:HD3	2.54	0.42
4:I:3:LYS:CD	4:I:3:LYS:N	2.83	0.42
3:M:81:ALA:O	3:M:83:ASP:N	2.53	0.42
2:H:23:LYS:HB2	2:H:78:THR:HG23	2.01	0.42
4:I:77:SER:O	4:I:78:LYS:CE	2.68	0.42
1:L:9:LYS:H	1:L:9:LYS:CE	2.32	0.41
4:I:35:SER:HB3	4:I:99:VAL:HG13	2.01	0.41
4:I:143:MET:HG3	4:I:190:THR:HG23	2.02	0.41
2:H:27:TYR:HE2	2:H:32:TYR:CD1	2.37	0.41
1:L:165:ASP:O	1:L:166:GLN:C	2.58	0.41
4:I:154:PHE:HB3	4:I:155:PRO:CD	2.45	0.41
2:H:51:ILE:HG21	2:H:70:PHE:CZ	2.55	0.41
2:H:61:ALA:HB3	2:H:64:PHE:HD1	1.85	0.41
4:I:48:VAL:HG23	4:I:49:ALA:N	2.35	0.41
4:I:132:LEU:HB2	4:I:147:GLY:H	1.85	0.41
2:H:97:ALA:CB	2:H:108:MET:HB3	2.46	0.41
1:L:94:THR:HG22	1:L:95:PRO:N	2.36	0.41
4:I:217:LYS:HB3	4:I:217:LYS:HE3	1.91	0.41
4:I:154:PHE:CB	4:I:155:PRO:HD3	2.46	0.41
3:M:37:TYR:HE1	3:M:90:GLN:HB2	1.85	0.41
3:M:191:ASN:ND2	3:M:212:ARG:HG3	2.35	0.41
3:M:119:PHE:CE1	4:I:146:LEU:HA	2.56	0.41
3:M:137:LEU:N	3:M:137:LEU:HD22	2.35	0.41
1:L:161:ASN:HD22	1:L:177:SER:HA	1.86	0.41
2:H:101:TYR:CZ	2:H:104:ASN:HA	2.55	0.41
4:I:18:MET:HB3	4:I:88:LEU:HD11	2.03	0.41
1:L:49:TYR:HE1	2:H:103:GLU:HG3	1.85	0.41
4:I:130:TYR:HB2	4:I:149:LEU:HB3	2.03	0.41
1:L:207:LYS:HA	1:L:207:LYS:HD2	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:176:ALA:HA	2:H:184:THR:O	2.20	0.41
1:L:136:LEU:HD23	1:L:175:MET:HG3	2.02	0.41
4:I:36:TRP:CD1	4:I:72:ILE:CD1	3.04	0.40
3:M:4:LEU:HD23	3:M:25:VAL:HG22	2.03	0.40
3:M:90:GLN:NE2	3:M:90:GLN:HA	2.33	0.40
1:L:44:PRO:HG2	2:H:111:TRP:CE3	2.56	0.40
1:L:13:THR:CG2	1:L:78:VAL:HG11	2.51	0.40
4:I:60:THR:CG2	4:I:72:ILE:HB	2.49	0.40
4:I:54:ASN:O	4:I:57:ASN:HB3	2.21	0.40
1:L:125:LEU:HD23	1:L:183:LYS:HD3	2.03	0.40
3:M:116:VAL:HA	3:M:136:PHE:O	2.22	0.40
4:I:100:LEU:O	4:I:109:ASP:HA	2.21	0.40
4:I:143:MET:HG3	4:I:190:THR:CG2	2.52	0.40
3:M:57:SER:O	3:M:59:VAL:HG23	2.22	0.40
4:I:218:ILE:HG13	4:I:218:ILE:OXT	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:31:THR:OG1	2:H:199:GLN:OE1[4_665]	2.11	0.09

## 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	L	212/214 (99%)	180 (85%)	27 (13%)	5 (2%)	7	29
2	H	217/219 (99%)	182 (84%)	24 (11%)	11 (5%)	2	9
3	M	213/215 (99%)	186 (87%)	19 (9%)	8 (4%)	4	16
4	I	216/218 (99%)	173 (80%)	26 (12%)	17 (8%)	1	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	858/866 (99%)	721 (84%)	96 (11%)	41 (5%)	3	10

All (41) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	199	LYS
2	H	142	SER
2	H	193	SER
3	M	41	SER
3	M	82	GLU
4	I	154	PHE
4	I	193	SER
4	I	197	PRO
1	L	52	SER
2	H	135	VAL
2	H	167	LEU
3	M	69	GLY
3	M	101	GLY
3	M	200	LYS
4	I	57	ASN
4	I	138	ALA
4	I	152	GLY
4	I	198	SER
1	L	94	THR
2	H	197	PRO
4	I	66	VAL
4	I	67	LYS
4	I	194	THR
4	I	196	ARG
2	H	43	LYS
2	H	192	THR
3	M	57	SER
3	M	81	ALA
4	I	65	SER
4	I	137	ALA
4	I	143	MET
4	I	192	PRO
2	H	152	GLY
2	H	208	PRO
3	M	77	SER
4	I	180	SER
4	I	208	PRO

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Mol	Chain	Res	Type
1	L	82	ASP
1	L	211	ARG
2	H	137	GLY
2	H	66	GLY

### 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	L	192/192 (100%)	153 (80%)	39 (20%)	1	4
2	H	186/186 (100%)	152 (82%)	34 (18%)	2	6
3	M	190/190 (100%)	155 (82%)	35 (18%)	2	6
4	I	189/189 (100%)	150 (79%)	39 (21%)	1	4
All	All	757/757 (100%)	610 (81%)	147 (19%)	2	5

All (147) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	1	ASP
1	L	2	ILE
1	L	9	LYS
1	L	13	THR
1	L	20	SER
1	L	23	CYS
1	L	24	LYS
1	L	43	SER
1	L	56	THR
1	L	63	THR
1	L	65	SER
1	L	75	ILE
1	L	77	SER
1	L	81	GLU
1	L	83	LEU
1	L	97	THR
1	L	98	PHE

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Mol	Chain	Res	Type
1	L	103	LYS
1	L	107	LYS
1	L	124	GLN
1	L	125	LEU
1	L	133	VAL
1	L	136	LEU
1	L	141	PRO
1	L	144	ILE
1	L	150	ILE
1	L	154	GLU
1	L	156	GLN
1	L	172	THR
1	L	178	THR
1	L	187	GLU
1	L	195	GLU
1	L	199	LYS
1	L	202	THR
1	L	207	LYS
1	L	208	SER
1	L	210	ASN
1	L	212	ASN
1	L	214	CYS
2	H	20	ILE
2	H	27	TYR
2	H	30	THR
2	H	32	TYR
2	H	35	ASN
2	H	62	ASP
2	H	70	PHE
2	H	72	LEU
2	H	74	THR
2	H	78	THR
2	H	81	LEU
2	H	82	GLN
2	H	85	ASN
2	H	99	ASP
2	H	123	LYS
2	H	138	ASP
2	H	142	SER
2	H	150	VAL
2	H	156	GLU
2	H	160	LEU

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Mol	Chain	Res	Type
2	H	167	LEU
2	H	179	GLN
2	H	182	LEU
2	H	185	LEU
2	H	196	THR
2	H	198	SER
2	H	200	SER
2	H	205	VAL
2	H	208	PRO
2	H	211	SER
2	H	212	THR
2	H	214	VAL
2	H	217	LYS
2	H	219	ASP
3	M	10	PHE
3	M	14	SER
3	M	28	SER
3	M	31	SER
3	M	35	HIS
3	M	43	THR
3	M	70	THR
3	M	82	GLU
3	M	90	GLN
3	M	91	GLN
3	M	94	SER
3	M	105	LEU
3	M	106	GLU
3	M	107	ILE
3	M	109	ARG
3	M	117	SER
3	M	137	LEU
3	M	138	ASN
3	M	143	LYS
3	M	156	ARG
3	M	157	GLN
3	M	170	LYS
3	M	176	MET
3	M	181	THR
3	M	182	LEU
3	M	184	LYS
3	M	185	ASP
3	M	189	ARG

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Mol	Chain	Res	Type
3	M	191	ASN
3	M	198	THR
3	M	202	SER
3	M	204	SER
3	M	207	VAL
3	M	212	ARG
3	M	215	CYS
4	I	3	LYS
4	I	12	VAL
4	I	35	SER
4	I	37	VAL
4	I	38	ARG
4	I	41	PRO
4	I	42	GLU
4	I	60	THR
4	I	64	GLU
4	I	74	ARG
4	I	75	ASP
4	I	77	SER
4	I	78	LYS
4	I	79	SER
4	I	81	LEU
4	I	84	GLN
4	I	98	CYS
4	I	106	TYR
4	I	113	GLN
4	I	115	THR
4	I	118	THR
4	I	124	THR
4	I	136	SER
4	I	139	GLN
4	I	143	MET
4	I	146	LEU
4	I	158	VAL
4	I	159	THR
4	I	177	VAL
4	I	188	SER
4	I	192	PRO
4	I	196	ARG
4	I	198	SER
4	I	199	GLU
4	I	200	THR

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Mol	Chain	Res	Type
4	I	208	PRO
4	I	211	SER
4	I	214	VAL
4	I	217	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	76	ASN
1	L	138	ASN
1	L	161	ASN
1	L	212	ASN
2	H	31	ASN
2	H	82	GLN
2	H	172	HIS
3	M	33	ASN
3	M	38	GLN
3	M	90	GLN
3	M	93	ASN
3	M	190	HIS
3	M	191	ASN
3	M	213	ASN
4	I	5	GLN
4	I	39	GLN
4	I	139	GLN
4	I	172	HIS
4	I	204	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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.