



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 27, 2024 – 11:44 AM EDT

PDB ID : 1NXZ  
Title : X-Ray Crystal Structure of Protein yggj\_haein of Haemophilus influenzae.  
Northeast Structural Genomics Consortium Target IR73.  
Authors : Forouhar, F.; Shen, J.; Xiao, R.; Acton, T.B.; Rost, B.; Montelione, G.T.;  
Tong, L.; Northeast Structural Genomics Consortium (NESG)  
Deposited on : 2003-02-11  
Resolution : 2.00 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

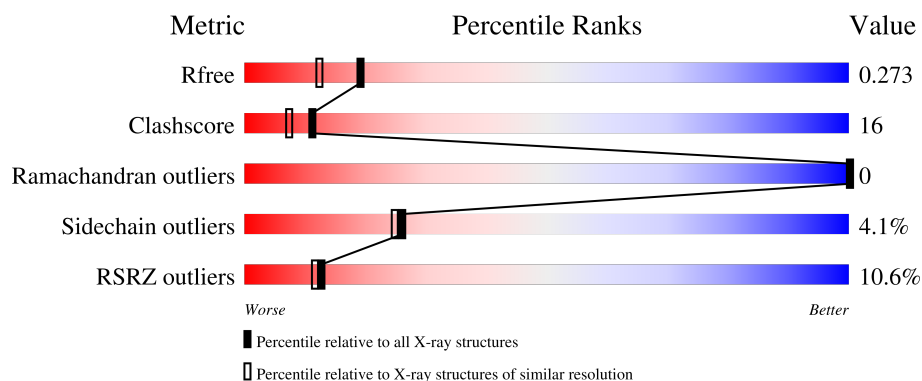
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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 of 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	246	<div> <div>6%</div> <div>71%</div> <div>27%</div> <div>.</div> </div>
1	B	246	<div> <div>15%</div> <div>66%</div> <div>32%</div> <div>.</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4155 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 Hypothetical protein HI0303.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	Se	0	0	0
			1920	1205	346	359	6	4			
1	B	245	Total	C	N	O	S	Se	0	0	0
			1915	1202	345	358	6	4			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	34	MSE	MET	modified residue	UNP P44627
A	92	MSE	MET	modified residue	UNP P44627
A	124	MSE	MET	modified residue	UNP P44627
A	154	MSE	MET	modified residue	UNP P44627
A	246	ALA	-	cloning artifact	UNP P44627
A	247	ALA	-	cloning artifact	UNP P44627
B	34	MSE	MET	modified residue	UNP P44627
B	92	MSE	MET	modified residue	UNP P44627
B	124	MSE	MET	modified residue	UNP P44627
B	154	MSE	MET	modified residue	UNP P44627
B	246	ALA	-	cloning artifact	UNP P44627
B	247	ALA	-	cloning artifact	UNP P44627

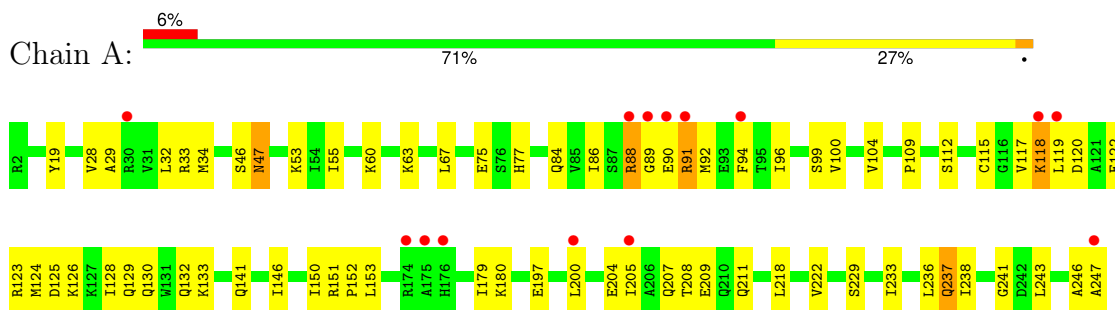
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	176	Total	O	0	0
			176	176		
2	B	144	Total	O	0	0
			144	144		

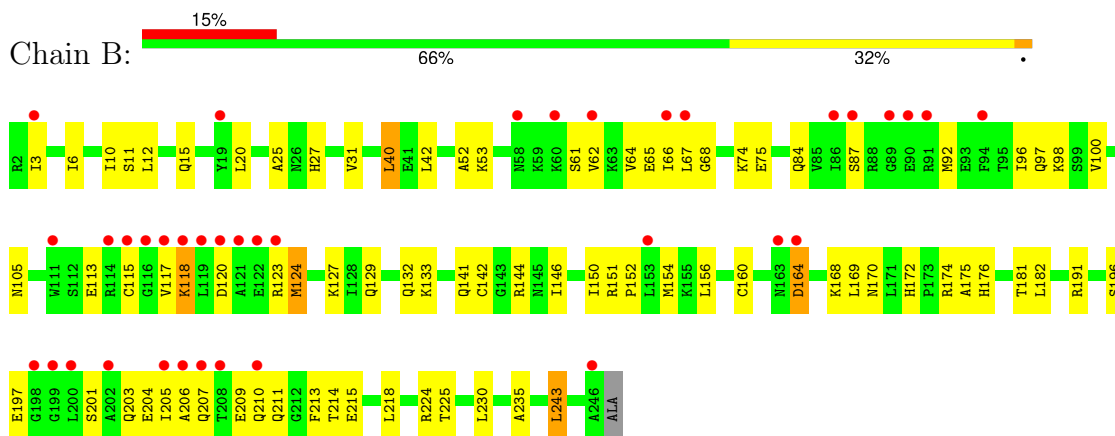
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Hypothetical protein HI0303



#### • Molecule 1: Hypothetical protein HI0303



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.30Å 73.52Å 109.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.52 – 2.00 29.52 – 2.00	Depositor EDS
% Data completeness (in resolution range)	85.0 (29.52-2.00) 94.3 (29.52-2.00)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.87 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.214 , 0.264 0.225 , 0.273	Depositor DCC
$R_{free}$ test set	3233 reflections (9.70%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.1	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 47.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4155	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.94% 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	0.32	0/1945	0.57	0/2617
1	B	0.29	0/1940	0.56	0/2610
All	All	0.31	0/3885	0.56	0/5227

There are no bond length outliers.

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	1920	0	1964	64	0
1	B	1915	0	1959	67	0
2	A	176	0	0	11	0
2	B	144	0	0	5	0
All	All	4155	0	3923	124	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 16.

All (124) 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:28:VAL:HG13	1:A:34:MSE:HE3	1.40	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:120:ASP:HB3	1:B:123:ARG:HB2	1.57	0.86
1:B:124:MSE:HB3	2:B:311:HOH:O	1.77	0.84
1:A:88:ARG:HD3	1:A:88:ARG:H	1.46	0.80
1:B:52:ALA:HA	1:B:67:LEU:HD23	1.63	0.79
1:A:120:ASP:HB3	1:A:123:ARG:HB3	1.67	0.76
1:B:12:LEU:HD22	1:B:66:ILE:HD11	1.68	0.75
1:A:88:ARG:HH11	1:A:89:GLY:H	1.35	0.73
1:A:222:VAL:HG13	1:B:142:CYS:HA	1.70	0.72
1:A:237:GLN:HE21	1:A:237:GLN:HA	1.54	0.72
1:B:117:VAL:HG12	1:B:118:LYS:H	1.54	0.71
1:B:66:ILE:HG22	1:B:68:GLY:H	1.55	0.70
1:A:197:GLU:HG2	2:A:367:HOH:O	1.95	0.66
1:A:60:LYS:HA	2:A:302:HOH:O	1.96	0.65
1:A:118:LYS:HD2	1:A:118:LYS:H	1.60	0.64
1:B:12:LEU:HA	1:B:15:GLN:HG3	1.79	0.64
1:B:132:GLN:HE22	1:B:150:ILE:H	1.46	0.63
1:A:32:LEU:HD12	1:A:34:MSE:HE2	1.82	0.62
1:B:25:ALA:CB	1:B:62:VAL:HG12	2.31	0.61
1:A:91:ARG:HA	2:A:413:HOH:O	2.01	0.60
1:A:207:GLN:HE22	1:A:211:GLN:HE21	1.49	0.60
1:A:125:ASP:O	1:A:129:GLN:HG3	2.02	0.60
1:B:64:VAL:HG12	1:B:65:GLU:N	2.17	0.59
1:B:87:SER:HB3	1:B:196:SER:HB2	1.84	0.59
1:A:237:GLN:HE21	1:A:241:GLY:HA3	1.67	0.58
1:A:53:LYS:HG3	1:A:67:LEU:HD11	1.85	0.58
1:B:87:SER:HA	1:B:117:VAL:HG22	1.86	0.58
1:B:97:GLN:HE21	1:B:98:LYS:NZ	2.02	0.58
1:B:61:SER:HB2	2:B:287:HOH:O	2.03	0.58
1:B:123:ARG:HG3	2:B:372:HOH:O	2.03	0.58
1:B:53:LYS:O	1:B:64:VAL:HG13	2.04	0.57
1:B:92:MSE:O	1:B:96:ILE:HG12	2.04	0.57
1:A:229:SER:O	1:A:233:ILE:HG12	2.05	0.57
1:A:179:ILE:HG23	1:A:236:LEU:HD23	1.87	0.57
1:A:55:ILE:HD11	1:A:63:LYS:HD2	1.87	0.56
1:A:90:GLU:HG2	1:A:91:ARG:N	2.21	0.56
1:A:75:GLU:HG3	1:A:146:ILE:HD12	1.86	0.56
1:A:96:ILE:O	1:A:100:VAL:HG23	2.07	0.53
1:A:247:ALA:HB3	1:B:176:HIS:HA	1.89	0.53
1:A:132:GLN:HE22	1:A:150:ILE:H	1.56	0.53
1:A:246:ALA:HB2	1:B:181:THR:HG21	1.90	0.53
1:B:205:ILE:O	1:B:209:GLU:HG3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:GLN:NE2	1:A:211:GLN:HE21	2.07	0.52
1:B:96:ILE:O	1:B:100:VAL:HG23	2.09	0.52
1:A:46:SER:O	1:A:47:ASN:CB	2.58	0.52
1:B:172:HIS:ND1	1:B:174:ARG:HG2	2.24	0.52
1:B:151:ARG:HB3	1:B:152:PRO:HD2	1.92	0.51
1:A:19:TYR:OH	1:A:63:LYS:HE2	2.10	0.51
1:B:25:ALA:HB1	1:B:62:VAL:HG12	1.92	0.51
1:B:132:GLN:NE2	1:B:150:ILE:H	2.08	0.51
1:A:86:ILE:HD12	1:A:117:VAL:HG11	1.93	0.50
1:A:237:GLN:NE2	1:A:241:GLY:HA3	2.26	0.50
1:A:112:SER:HB3	1:A:115:CYS:HB3	1.95	0.49
1:B:169:LEU:HD23	1:B:214:THR:HB	1.93	0.49
1:A:122:GLU:O	1:A:126:LYS:HG2	2.12	0.49
1:A:119:LEU:O	1:A:119:LEU:HG	2.13	0.48
1:B:164:ASP:HB2	1:B:191:ARG:HE	1.77	0.48
1:A:132:GLN:NE2	1:A:150:ILE:H	2.10	0.48
1:A:130:GLN:HG2	2:A:382:HOH:O	2.14	0.48
1:B:115:CYS:SG	1:B:117:VAL:HG23	2.54	0.47
1:A:119:LEU:HB2	2:A:380:HOH:O	2.15	0.47
1:A:222:VAL:CG1	1:B:142:CYS:HA	2.42	0.47
1:B:62:VAL:HG13	1:B:62:VAL:O	2.15	0.47
1:B:225:THR:HG22	2:B:313:HOH:O	2.15	0.47
1:B:230:LEU:C	1:B:230:LEU:HD23	2.35	0.47
1:B:98:LYS:HD2	1:B:98:LYS:N	2.30	0.46
1:B:120:ASP:HB3	1:B:123:ARG:CB	2.38	0.46
1:B:160:CYS:HB3	1:B:211:GLN:HG3	1.97	0.46
1:B:170:ASN:HD22	1:B:213:PHE:HB3	1.80	0.46
1:A:88:ARG:HD3	1:A:88:ARG:N	2.22	0.46
1:A:204:GLU:O	1:A:208:THR:HG23	2.16	0.46
1:B:129:GLN:O	1:B:133:LYS:HD3	2.16	0.46
1:A:200:LEU:N	1:A:200:LEU:HD12	2.31	0.45
1:B:201:SER:O	1:B:205:ILE:HG13	2.16	0.45
2:A:312:HOH:O	1:B:224:ARG:HD3	2.16	0.45
1:A:118:LYS:HG2	1:A:123:ARG:HH21	1.82	0.44
1:A:151:ARG:HB3	1:A:152:PRO:HD2	2.00	0.44
1:B:156:LEU:HD13	1:B:204:GLU:HG2	1.99	0.44
1:B:203:GLN:O	1:B:206:ALA:HB3	2.18	0.44
1:A:118:LYS:HD2	1:A:118:LYS:N	2.31	0.43
1:A:207:GLN:HE21	1:A:211:GLN:HG2	1.83	0.43
1:A:237:GLN:HA	1:A:237:GLN:NE2	2.29	0.43
1:B:27:HIS:O	1:B:31:VAL:HB	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:ASN:HD22	1:A:47:ASN:HA	1.59	0.43
1:B:10:ILE:HG12	1:B:11:SER:H	1.84	0.43
1:B:124:MSE:HE3	1:B:124:MSE:HA	2.00	0.43
1:A:124:MSE:HG2	1:A:153:LEU:HD22	2.00	0.43
1:B:6:ILE:HB	1:B:42:LEU:HD23	2.00	0.43
1:A:120:ASP:OD1	1:A:122:GLU:HG2	2.18	0.43
1:A:128:ILE:HD13	1:A:152:PRO:HA	1.99	0.43
1:B:15:GLN:HB2	1:B:66:ILE:HD12	2.00	0.43
1:A:29:ALA:O	1:A:33:ARG:HA	2.19	0.43
1:B:168:LYS:HB3	1:B:213:PHE:CE1	2.53	0.43
1:B:170:ASN:O	1:B:215:GLU:HA	2.19	0.43
1:A:92:MSE:O	1:A:96:ILE:HG12	2.19	0.42
1:B:3:ILE:HD11	1:B:40:LEU:C	2.39	0.42
1:B:84:GLN:HG2	1:B:92:MSE:SE	2.70	0.42
1:A:205:ILE:O	1:A:209:GLU:HG3	2.19	0.42
1:B:64:VAL:HG12	1:B:65:GLU:H	1.81	0.42
1:B:75:GLU:HG3	1:B:146:ILE:HD12	2.01	0.42
1:A:118:LYS:NZ	1:A:118:LYS:HB3	2.34	0.42
1:A:243:LEU:HG	1:B:218:LEU:HD12	2.01	0.42
1:B:243:LEU:HD23	1:B:243:LEU:HA	1.82	0.42
1:A:109:PRO:O	1:A:153:LEU:HD12	2.20	0.41
1:B:207:GLN:O	1:B:210:GLN:HG2	2.20	0.41
1:A:77:HIS:HE1	2:A:320:HOH:O	2.03	0.41
1:A:222:VAL:HG12	1:B:142:CYS:O	2.20	0.41
1:B:113:GLU:HB2	1:B:203:GLN:NE2	2.35	0.41
1:A:133:LYS:HD2	2:A:382:HOH:O	2.20	0.41
1:B:64:VAL:CG1	1:B:65:GLU:N	2.83	0.41
1:A:84:GLN:HG3	1:A:92:MSE:HE1	2.01	0.41
1:B:6:ILE:HB	1:B:42:LEU:CD2	2.51	0.41
1:B:142:CYS:SG	1:B:144:ARG:HG3	2.60	0.41
1:A:19:TYR:CZ	1:A:63:LYS:HE2	2.56	0.41
1:A:141:GLN:NE2	2:A:260:HOH:O	2.51	0.41
1:A:77:HIS:HD2	2:A:264:HOH:O	2.03	0.41
1:B:105:ASN:HB3	2:B:355:HOH:O	2.20	0.41
1:B:124:MSE:CE	1:B:127:LYS:HG3	2.51	0.40
1:B:210:GLN:HG3	1:B:211:GLN:N	2.37	0.40
1:A:99:SER:HB3	1:A:104:VAL:HG21	2.03	0.40
1:A:180:LYS:O	1:A:180:LYS:HG2	2.22	0.40
1:A:238:ILE:HG13	1:B:235:ALA:CB	2.52	0.40
2:A:301:HOH:O	1:B:74:LYS:HE3	2.22	0.40
1:B:175:ALA:HB2	1:B:215:GLU:HB3	2.03	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	244/246 (99%)	232 (95%)	12 (5%)	0	100	100
1	B	243/246 (99%)	223 (92%)	20 (8%)	0	100	100
All	All	487/492 (99%)	455 (93%)	32 (7%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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	207/203 (102%)	200 (97%)	7 (3%)	32	32
1	B	207/203 (102%)	197 (95%)	10 (5%)	21	19
All	All	414/406 (102%)	397 (96%)	17 (4%)	26	25

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	A	88	ARG
1	A	91	ARG
1	A	94	PHE
1	A	118	LYS

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Mol	Chain	Res	Type
1	A	218	LEU
1	A	237	GLN
1	B	20	LEU
1	B	40	LEU
1	B	118	LYS
1	B	124	MSE
1	B	141	GLN
1	B	154	MSE
1	B	164	ASP
1	B	182	LEU
1	B	197	GLU
1	B	243	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
1	A	47	ASN
1	A	77	HIS
1	A	129	GLN
1	A	132	GLN
1	A	141	GLN
1	A	157	GLN
1	A	172	HIS
1	A	203	GLN
1	A	207	GLN
1	A	237	GLN
1	B	15	GLN
1	B	97	GLN
1	B	130	GLN
1	B	132	GLN
1	B	141	GLN
1	B	207	GLN
1	B	210	GLN

### 5.3.3 RNA ⓘ

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 oligosaccharides 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

### 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	242/246 (98%)	0.30	14 (5%) 30 28	16, 28, 52, 69	0
1	B	241/246 (97%)	0.80	37 (15%) 6 5	17, 32, 67, 80	0
All	All	483/492 (98%)	0.55	51 (10%) 13 12	16, 31, 64, 80	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	120	ASP	5.3
1	B	246	ALA	5.2
1	A	119	LEU	4.4
1	B	111	TRP	4.2
1	B	121	ALA	4.1
1	B	117	VAL	4.1
1	A	176	HIS	4.0
1	B	116	GLY	3.9
1	B	202	ALA	3.8
1	A	91	ARG	3.7
1	A	175	ALA	3.7
1	A	88	ARG	3.6
1	B	119	LEU	3.6
1	B	199	GLY	3.4
1	A	90	GLU	3.4
1	B	118	LYS	3.4
1	A	89	GLY	3.4
1	B	198	GLY	3.4
1	B	205	ILE	3.3
1	B	115	CYS	3.3
1	B	164	ASP	3.1
1	B	86	ILE	3.1
1	B	206	ALA	3.1
1	B	87	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	200	LEU	3.0
1	A	118	LYS	2.8
1	B	89	GLY	2.8
1	B	114	ARG	2.7
1	B	210	GLN	2.7
1	B	153	LEU	2.6
1	A	94	PHE	2.5
1	B	94	PHE	2.5
1	B	3	ILE	2.4
1	B	66	ILE	2.4
1	B	60	LYS	2.4
1	B	90	GLU	2.3
1	B	58	ASN	2.3
1	B	122	GLU	2.3
1	B	123	ARG	2.3
1	B	207	GLN	2.3
1	B	67	LEU	2.3
1	B	208	THR	2.3
1	A	174	ARG	2.2
1	A	247	ALA	2.2
1	B	62	VAL	2.2
1	A	205	ILE	2.1
1	B	19	TYR	2.1
1	A	200	LEU	2.1
1	B	163	ASN	2.1
1	B	91	ARG	2.1
1	A	30	ARG	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 monosaccharides 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.