



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:42 AM GMT

PDB ID : 3FNU  
Title : Crystal structure of KNI-10006 bound histo-aspartic protease (HAP) from Plasmodium falciparum  
Authors : Bhaumik, P.; Gustchina, A.; Wlodawer, A.  
Deposited on : 2008-12-26  
Resolution : 3.00 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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

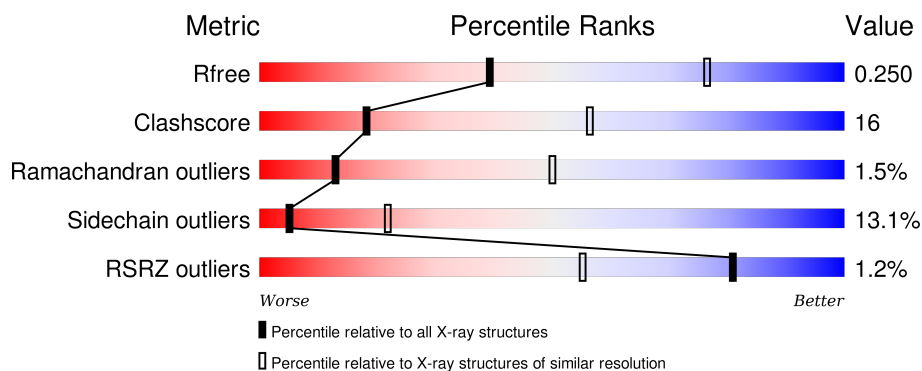
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
$R_{free}$	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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 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	332	<div> <div>%</div> <div> <div></div> <div>70%</div> <div>22%</div> <div>6%</div> <div>.</div> </div> </div>
1	B	332	<div> <div></div> <div>67%</div> <div>26%</div> <div>6%</div> <div>.</div> </div>
1	C	332	<div> <div>2%</div> <div></div> <div>72%</div> <div>21%</div> <div>5%</div> <div>.</div> </div>
1	D	332	<div> <div>%</div> <div></div> <div>72%</div> <div>21%</div> <div>5%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	006	A	329	-	-	-	X
2	006	B	329	-	-	-	X
2	006	C	329	-	-	-	X

## 2 Entry composition [i](#)

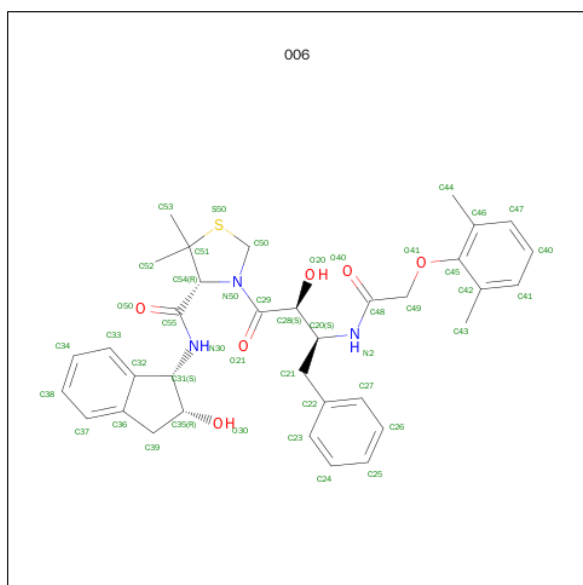
There are 3 unique types of molecules in this entry. The entry contains 10667 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HAP protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	0	0
			2598	1683	403	504	8			
1	B	326	Total	C	N	O	S	0	0	0
			2598	1683	403	504	8			
1	C	326	Total	C	N	O	S	0	0	0
			2598	1683	403	504	8			
1	D	326	Total	C	N	O	S	0	0	0
			2598	1683	403	504	8			

- Molecule 2 is (4R)-3-[(2S,3S)-3-[(2,6-DIMETHYLPHENOXY)ACETYL]AMINO}-2-HYDROXY-4-PHENYLBUTANOYL]-N-[(1S,2R)-2-HYDROXY-2,3-DIHYDRO-1H-INDEN-1-YL]-5,5-DIMETHYL-1,3-THIAZOLIDINE-4-CARBOXAMIDE (three-letter code: 006) (formula: C<sub>35</sub>H<sub>41</sub>N<sub>3</sub>O<sub>6</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			45	35	3	6	1		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			45	35	3	6	1		
2	C	1	Total	C	N	O	S	0	0
			45	35	3	6	1		
2	D	1	Total	C	N	O	S	0	0
			45	35	3	6	1		

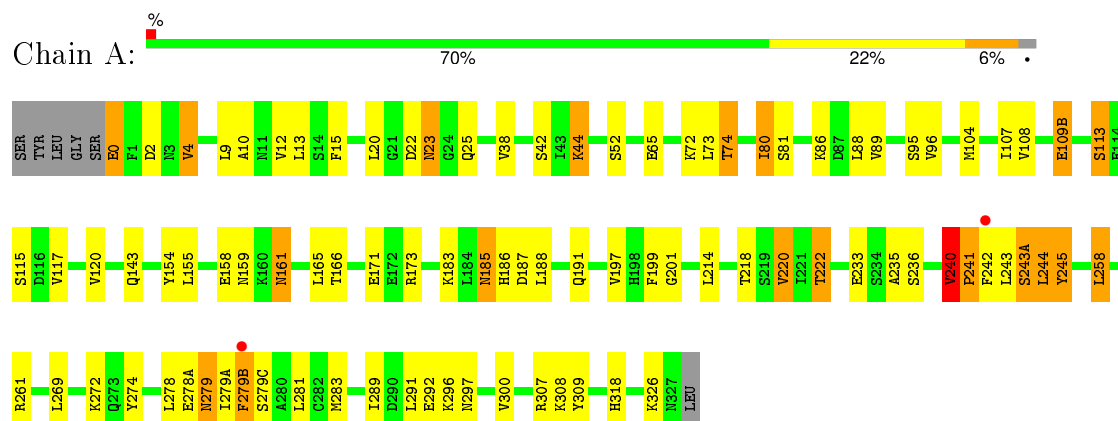
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	25	Total	O	0	0
			25	25		
3	B	31	Total	O	0	0
			31	31		
3	C	14	Total	O	0	0
			14	14		
3	D	25	Total	O	0	0
			25	25		

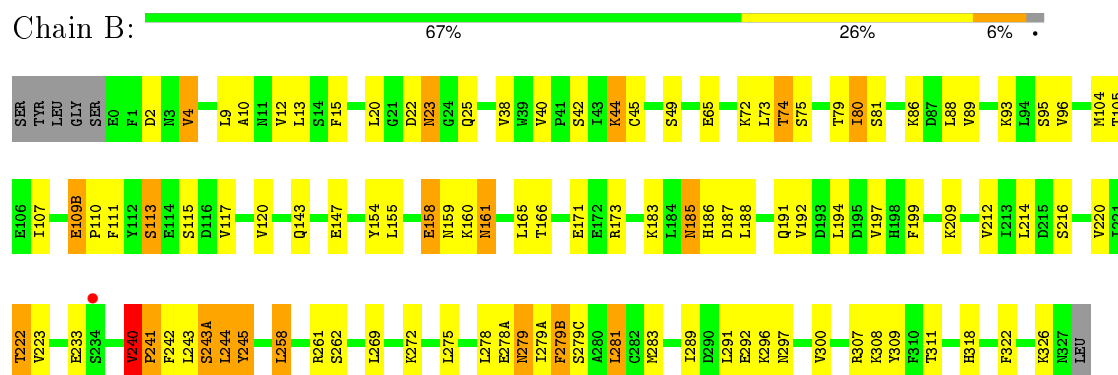
### 3 Residue-property plots

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.

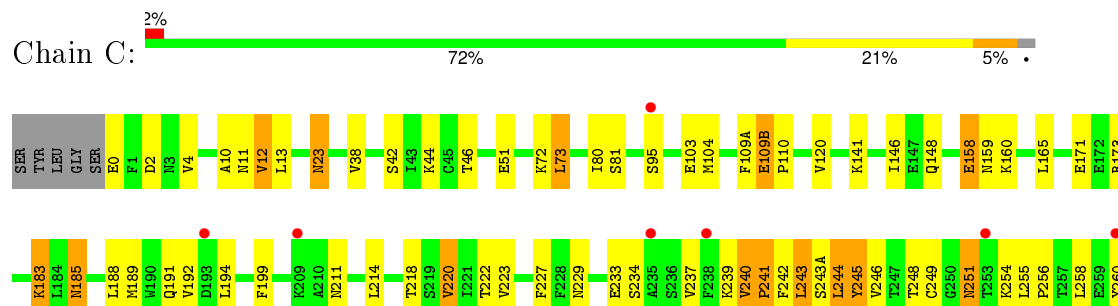
#### • Molecule 1: HAP protein

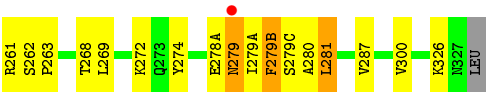


#### • Molecule 1: HAP protein

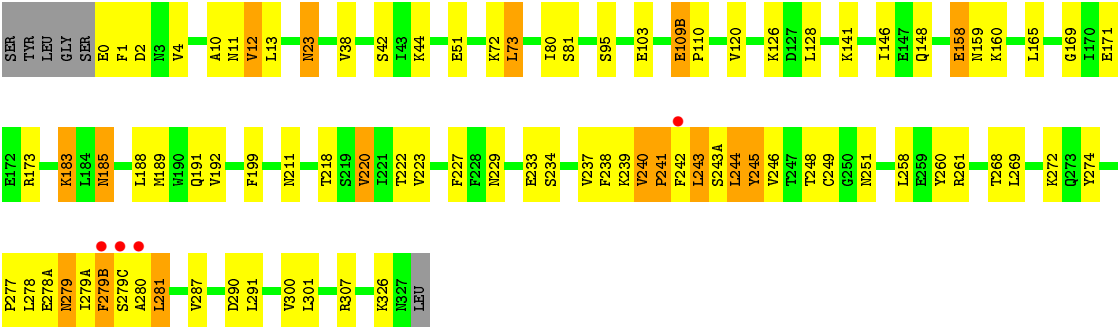


#### • Molecule 1: HAP protein





● Molecule 1: HAP protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	166.10 Å   166.10 Å   276.90 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	30.00 – 3.00 39.87 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-3.00) 100.0 (39.87-3.00)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.35 (at 3.01 Å)	Xtriage
Refinement program	REFMAC 5.4.0057	Depositor
R, $R_{free}$	0.222   ,   0.253 0.218   ,   0.250	Depositor DCC
$R_{free}$ test set	1950 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	100.5	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 65.7	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	0 of 39041 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10667	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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

Bond lengths and bond angles in the following residue types are not validated in this section: 006

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	0.65	1/2663 (0.0%)	0.67	0/3614
1	B	0.53	0/2663	0.66	0/3614
1	C	0.42	0/2663	0.59	0/3614
1	D	0.44	0/2663	0.62	0/3614
All	All	0.52	1/10652 (0.0%)	0.63	0/14456

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	A	0	2
1	B	0	2
1	C	0	1
1	D	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	0	GLU	N-CA	20.46	1.87	1.46

There are no bond angle outliers.

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	VAL	Peptide

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Group
1	A	241	PRO	Peptide
1	B	240	VAL	Peptide
1	B	241	PRO	Peptide
1	C	241	PRO	Peptide
1	D	241	PRO	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	2598	0	2547	77	0
1	B	2598	0	2547	90	0
1	C	2598	0	2547	81	0
1	D	2598	0	2547	80	0
2	A	45	0	41	4	0
2	B	45	0	41	2	0
2	C	45	0	41	6	0
2	D	45	0	41	3	0
3	A	25	0	0	11	0
3	B	31	0	0	18	0
3	C	14	0	0	17	0
3	D	25	0	0	15	0
All	All	10667	0	10352	326	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 (326) 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:0:GLU:CA	1:A:0:GLU:N	1.87	1.37
1:C:279(B):PHE:HB3	1:C:279(C):SER:CB	1.58	1.33
1:B:216:SER:HA	3:B:353:HOH:O	1.27	1.27
1:D:279(B):PHE:HB3	1:D:279(C):SER:CB	1.70	1.19
1:A:279(B):PHE:HB3	1:A:279(C):SER:HA	1.13	1.11
1:B:279(B):PHE:HB3	1:B:279(C):SER:HA	1.19	1.10

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:279(B):PHE:HB3	1:C:279(C):SER:HB3	1.17	1.09
1:D:279(B):PHE:HB3	1:D:279(C):SER:HB3	1.29	1.07
1:D:279(A):ILE:HG13	3:D:346:HOH:O	1.53	1.05
1:A:279(B):PHE:CB	1:A:279(C):SER:HA	1.86	1.05
1:D:281:LEU:HB3	3:D:345:HOH:O	1.56	1.04
1:B:279(B):PHE:CB	1:B:279(C):SER:HA	1.90	1.02
1:C:279(B):PHE:CB	1:C:279(C):SER:HB3	1.89	1.01
1:A:278(A):GLU:HB2	1:A:279(C):SER:HB2	1.47	0.96
1:C:240:VAL:H	1:C:241:PRO:CD	1.82	0.92
1:D:279(B):PHE:CB	1:D:279(C):SER:HB3	2.00	0.91
1:C:23:ASN:H	1:C:23:ASN:HD22	1.16	0.91
1:C:279(B):PHE:HA	3:C:332:HOH:O	1.70	0.91
1:A:279(B):PHE:HB3	1:A:279(C):SER:CA	2.01	0.91
1:D:23:ASN:H	1:D:23:ASN:HD22	1.18	0.91
1:D:240:VAL:H	1:D:241:PRO:CD	1.84	0.90
1:B:10:ALA:N	3:B:354:HOH:O	2.04	0.89
1:B:222:THR:HB	1:B:300:VAL:HB	1.51	0.89
1:A:240:VAL:H	1:A:241:PRO:HD3	1.37	0.89
1:C:279(B):PHE:HB3	1:C:279(C):SER:CA	2.03	0.88
1:B:278(A):GLU:HB2	1:B:279(C):SER:HB2	1.53	0.88
1:A:222:THR:HB	1:A:300:VAL:HB	1.56	0.87
1:C:109(B):GLU:HG3	1:C:110:PRO:HA	1.57	0.86
2:C:329:006:H53	2:C:329:006:H31	1.58	0.86
1:C:279(A):ILE:O	1:C:279(B):PHE:HB2	1.75	0.85
1:D:279(B):PHE:HB3	1:D:279(C):SER:CA	2.05	0.85
1:B:240:VAL:H	1:B:241:PRO:HD3	1.39	0.85
1:D:279(A):ILE:O	1:D:279(B):PHE:HB2	1.74	0.85
1:D:109(B):GLU:HG3	1:D:110:PRO:HA	1.59	0.85
1:D:12:VAL:HG13	3:D:353:HOH:O	1.79	0.83
1:C:0:GLU:HB3	3:C:336:HOH:O	1.77	0.83
1:B:279(B):PHE:HB3	1:B:279(C):SER:CA	2.06	0.81
1:B:23:ASN:H	1:B:23:ASN:HD22	1.28	0.81
1:C:278(A):GLU:HG2	3:C:335:HOH:O	1.79	0.81
1:D:240:VAL:H	1:D:241:PRO:HD3	1.44	0.79
1:A:20:LEU:HD22	1:A:89:VAL:HG22	1.64	0.79
1:B:240:VAL:HB	3:B:331:HOH:O	1.83	0.78
1:C:240:VAL:H	1:C:241:PRO:HD3	1.49	0.77
1:A:9:LEU:HB2	1:A:15:PHE:CE1	2.20	0.77
1:B:279:ASN:N	3:B:344:HOH:O	2.20	0.75
1:D:10:ALA:N	3:D:353:HOH:O	2.18	0.75
1:A:23:ASN:H	1:A:23:ASN:HD22	1.31	0.75

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:233:GLU:O	3:D:338:HOH:O	2.04	0.75
1:A:289:ILE:HG22	1:A:291:LEU:HD12	1.69	0.75
1:D:278:LEU:HA	3:D:339:HOH:O	1.87	0.74
1:A:241:PRO:HB2	3:A:340:HOH:O	1.87	0.74
1:C:255:LEU:HA	3:C:337:HOH:O	1.87	0.73
1:C:240:VAL:N	1:C:241:PRO:CD	2.51	0.73
2:B:329:006:H31	2:B:329:006:H52	1.71	0.72
1:A:278(A):GLU:HB2	1:A:279(C):SER:CB	2.20	0.72
1:B:9:LEU:HB2	1:B:15:PHE:CE1	2.23	0.71
1:B:278(A):GLU:HB2	1:B:279(C):SER:CB	2.21	0.71
1:A:42:SER:OG	1:A:44:LYS:HD2	1.91	0.71
1:B:242:PHE:HD1	3:B:330:HOH:O	1.71	0.71
1:B:289:ILE:HG22	1:B:291:LEU:HD12	1.72	0.70
1:A:279:ASN:C	3:A:341:HOH:O	2.29	0.70
1:C:223:VAL:HG13	1:C:227:PHE:HB3	1.72	0.70
1:C:256:PRO:HD3	3:C:337:HOH:O	1.91	0.70
1:B:278(A):GLU:C	3:B:344:HOH:O	2.30	0.69
1:D:277:PRO:O	3:D:344:HOH:O	2.10	0.69
2:A:329:006:H52	2:A:329:006:H31	1.74	0.69
1:D:223:VAL:HG13	1:D:227:PHE:HB3	1.73	0.69
1:C:279:ASN:HB2	1:D:238:PHE:CD2	2.29	0.68
1:D:240:VAL:N	1:D:241:PRO:CD	2.51	0.67
1:B:42:SER:OG	1:B:44:LYS:HD2	1.93	0.67
1:C:244:LEU:CB	1:C:245:TYR:HA	2.24	0.67
1:A:241:PRO:HG3	1:A:243(A):SER:N	2.10	0.66
1:A:241:PRO:CG	1:A:243(A):SER:H	2.08	0.66
1:B:241:PRO:HG3	1:B:243(A):SER:N	2.11	0.65
1:B:4:VAL:HG13	1:B:165:LEU:HB3	1.79	0.65
1:C:248:THR:HA	1:C:280:ALA:O	1.96	0.65
1:A:4:VAL:HG13	1:A:165:LEU:HB3	1.78	0.65
2:C:329:006:H21	2:C:329:006:H50	1.79	0.65
1:D:249:CYS:N	1:D:280:ALA:O	2.30	0.65
1:B:241:PRO:CG	1:B:243(A):SER:H	2.10	0.65
1:B:278(A):GLU:CB	3:B:344:HOH:O	2.45	0.65
1:D:244:LEU:CB	1:D:245:TYR:HA	2.27	0.64
1:A:240:VAL:H	1:A:241:PRO:CD	2.10	0.64
1:D:281:LEU:O	3:D:345:HOH:O	2.14	0.64
1:B:279(C):SER:HB2	3:B:344:HOH:O	1.98	0.63
1:D:248:THR:HA	1:D:280:ALA:O	1.98	0.63
1:A:241:PRO:HB2	1:A:243:LEU:N	2.14	0.63
1:A:279(A):ILE:O	1:A:279(B):PHE:HB2	1.97	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:12:VAL:HG11	2:D:329:006:H34	1.81	0.63
1:C:279(B):PHE:HB3	1:C:279(C):SER:HB2	1.74	0.63
1:B:240:VAL:H	1:B:241:PRO:CD	2.12	0.63
1:B:244:LEU:HB2	1:B:245:TYR:HA	1.80	0.63
1:B:279(A):ILE:O	1:B:279(B):PHE:HB2	1.98	0.63
1:A:241:PRO:HG3	1:A:243(A):SER:H	1.64	0.62
1:A:13:LEU:HD22	1:A:155:LEU:HD22	1.80	0.62
1:B:279:ASN:C	3:B:344:HOH:O	2.38	0.61
1:B:93:LYS:O	1:C:46:THR:HG21	2.01	0.61
1:D:279(A):ILE:O	1:D:279(B):PHE:CB	2.49	0.61
1:A:279(B):PHE:CB	1:A:279(C):SER:CA	2.70	0.61
1:B:20:LEU:HD22	1:B:89:VAL:HG22	1.83	0.60
1:B:279(B):PHE:CB	1:B:279(C):SER:CA	2.73	0.60
1:D:281:LEU:CB	3:D:345:HOH:O	2.24	0.60
1:C:191:GLN:HB2	1:C:211:ASN:HD21	1.66	0.60
1:A:244:LEU:HB2	1:A:245:TYR:HA	1.83	0.60
1:B:13:LEU:HD22	1:B:155:LEU:HD22	1.83	0.60
1:C:158:GLU:O	1:C:160:LYS:N	2.32	0.59
1:C:23:ASN:H	1:C:23:ASN:ND2	1.96	0.59
1:C:279(B):PHE:N	3:C:333:HOH:O	2.35	0.59
1:B:109(B):GLU:OE2	1:B:113:SER:HB3	2.01	0.59
1:D:241:PRO:HB2	1:D:243:LEU:N	2.18	0.58
1:D:279(A):ILE:HD12	1:D:279(B):PHE:HD2	1.68	0.58
1:B:241:PRO:HB2	1:B:243:LEU:N	2.18	0.58
1:C:254:LYS:O	3:C:337:HOH:O	2.17	0.58
1:C:245:TYR:N	1:C:245:TYR:CD2	2.71	0.58
1:C:278(A):GLU:HG3	1:C:279(B):PHE:HB2	1.85	0.58
1:B:115:SER:OG	1:B:117:VAL:HG12	2.04	0.57
1:B:241:PRO:HG3	1:B:243(A):SER:H	1.70	0.57
1:A:241:PRO:HB2	1:A:243:LEU:H	1.69	0.57
1:D:12:VAL:HG11	2:D:329:006:C34	2.34	0.57
1:C:279(A):ILE:O	1:C:279(B):PHE:CB	2.49	0.57
1:D:281:LEU:C	3:D:345:HOH:O	2.44	0.56
1:D:191:GLN:HB2	1:D:211:ASN:HD21	1.69	0.56
1:C:240:VAL:N	1:C:241:PRO:HD2	2.20	0.56
1:C:280:ALA:C	3:C:338:HOH:O	2.43	0.56
1:A:115:SER:OG	1:A:117:VAL:HG12	2.05	0.56
1:C:72:LYS:HG3	1:C:81:SER:HB3	1.87	0.56
1:D:158:GLU:O	1:D:160:LYS:N	2.37	0.56
1:D:278(A):GLU:O	1:D:279:ASN:ND2	2.33	0.56
1:B:279:ASN:CA	3:B:344:HOH:O	2.54	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:278(A):GLU:C	1:D:279:ASN:HD22	2.09	0.55
1:B:278(A):GLU:HB2	3:B:344:HOH:O	2.06	0.55
1:C:23:ASN:HD22	1:C:23:ASN:N	1.93	0.55
1:D:245:TYR:CD2	1:D:245:TYR:N	2.72	0.55
1:C:4:VAL:HG13	1:C:165:LEU:HB3	1.88	0.55
1:A:245:TYR:CD2	1:A:245:TYR:N	2.75	0.55
1:D:290:ASP:HA	3:D:347:HOH:O	2.05	0.55
1:D:229:ASN:O	1:D:233:GLU:HB2	2.06	0.55
1:A:10:ALA:HB3	2:A:329:006:H38	1.87	0.55
1:A:72:LYS:HE3	1:A:74:THR:HG21	1.89	0.55
1:B:185:ASN:HD21	1:B:191:GLN:HE21	1.55	0.55
1:A:244:LEU:CB	1:A:245:TYR:HA	2.37	0.54
1:B:242:PHE:HB3	1:B:243:LEU:HD12	1.90	0.54
1:A:245:TYR:HD2	1:A:245:TYR:N	2.06	0.54
1:D:278(A):GLU:HG3	1:D:279(B):PHE:HB2	1.90	0.54
1:A:278(A):GLU:OE1	1:B:281:LEU:HD21	2.07	0.54
1:C:12:VAL:HG11	2:C:329:006:H34	1.90	0.54
1:D:72:LYS:HG3	1:D:81:SER:HB3	1.89	0.54
1:B:241:PRO:HB2	1:B:243:LEU:H	1.73	0.54
1:C:241:PRO:HB2	1:C:243:LEU:N	2.23	0.54
1:A:185:ASN:HD21	1:A:191:GLN:HE21	1.56	0.54
1:C:281:LEU:N	3:C:338:HOH:O	2.41	0.53
2:D:329:006:H31	2:D:329:006:H52	1.90	0.53
1:C:279(B):PHE:CE1	1:D:279(B):PHE:HE1	2.27	0.53
1:B:244:LEU:CB	1:B:245:TYR:HA	2.38	0.53
1:B:158:GLU:HB3	3:B:346:HOH:O	2.09	0.53
1:A:0:GLU:HB2	3:A:330:HOH:O	2.09	0.53
1:B:241:PRO:CG	1:B:243(A):SER:N	2.70	0.53
1:B:23:ASN:HD21	1:B:25:GLN:HE21	1.56	0.53
1:C:248:THR:HB	1:C:251:ASN:HB2	1.90	0.53
1:B:23:ASN:HD22	1:B:23:ASN:N	2.03	0.52
1:C:279(A):ILE:HD12	1:C:279(B):PHE:HD2	1.75	0.52
1:D:279(A):ILE:CG1	3:D:346:HOH:O	2.31	0.52
1:C:279(B):PHE:HE1	1:D:279(B):PHE:HE1	1.56	0.52
1:C:249:CYS:N	1:C:280:ALA:O	2.43	0.52
1:B:245:TYR:CD2	1:B:245:TYR:N	2.78	0.52
1:C:280:ALA:CB	3:C:341:HOH:O	2.57	0.52
1:D:222:THR:HB	1:D:300:VAL:HB	1.92	0.52
1:D:0:GLU:HA	3:D:342:HOH:O	2.09	0.52
1:B:199:PHE:CE1	1:B:258:LEU:HG	2.45	0.52
1:C:244:LEU:HB2	1:C:245:TYR:HA	1.90	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:280:ALA:HB1	3:C:341:HOH:O	2.09	0.51
2:A:329:006:H21A	3:A:349:HOH:O	2.10	0.51
1:D:4:VAL:HG13	1:D:165:LEU:HB3	1.91	0.51
1:C:279(B):PHE:CB	1:C:279(C):SER:CB	2.52	0.51
1:C:229:ASN:O	1:C:233:GLU:HB2	2.10	0.51
1:D:185:ASN:HD21	1:D:191:GLN:HE21	1.59	0.51
1:C:222:THR:HB	1:C:300:VAL:HB	1.93	0.51
1:A:241:PRO:CG	1:A:243(A):SER:N	2.70	0.50
1:D:199:PHE:CZ	1:D:258:LEU:HG	2.45	0.50
1:D:278(A):GLU:CD	1:D:279(C):SER:HB3	2.31	0.50
1:D:23:ASN:ND2	1:D:23:ASN:H	1.98	0.50
1:B:185:ASN:HD22	1:B:186:HIS:N	2.10	0.50
1:D:23:ASN:HD22	1:D:23:ASN:N	1.95	0.50
1:B:96:VAL:HG21	1:B:143:GLN:HG3	1.94	0.50
1:C:279(B):PHE:CE1	1:D:279(B):PHE:CE1	3.00	0.50
1:D:278(A):GLU:OE2	1:D:279(C):SER:OG	2.28	0.50
1:A:96:VAL:HG21	1:A:143:GLN:HG3	1.93	0.50
1:C:278(A):GLU:C	1:C:279:ASN:HD22	2.16	0.49
1:D:239:LYS:HD3	1:D:245:TYR:CE1	2.47	0.49
1:D:258:LEU:HD13	1:D:274:TYR:CE1	2.48	0.49
1:B:96:VAL:CG2	1:B:143:GLN:HG3	2.42	0.49
1:C:80:ILE:HD11	1:C:104:MET:SD	2.52	0.49
1:D:277:PRO:C	3:D:344:HOH:O	2.50	0.49
1:C:280:ALA:N	3:C:338:HOH:O	2.26	0.49
1:B:161:ASN:N	1:B:161:ASN:OD1	2.46	0.49
1:B:65:GLU:HB2	1:B:86:LYS:HB3	1.94	0.49
1:A:241:PRO:CB	3:A:340:HOH:O	2.53	0.49
1:B:278:LEU:CB	1:B:278(A):GLU:OE2	2.61	0.49
1:D:243(A):SER:O	1:D:244:LEU:HB2	2.13	0.49
1:C:278(A):GLU:CG	3:C:335:HOH:O	2.47	0.49
1:C:185:ASN:HD21	1:C:191:GLN:HE21	1.59	0.49
1:B:72:LYS:HE3	1:B:74:THR:HG21	1.95	0.49
1:C:278(A):GLU:HG3	1:C:279(A):ILE:O	2.13	0.49
1:A:241:PRO:HG3	1:A:243(A):SER:CA	2.42	0.49
1:B:194:LEU:HD12	1:B:212:VAL:HG21	1.95	0.49
1:B:199:PHE:CZ	1:B:258:LEU:HG	2.48	0.49
1:C:239:LYS:HD3	1:C:245:TYR:CE1	2.48	0.48
1:A:185:ASN:HD22	1:A:186:HIS:N	2.09	0.48
1:D:218:THR:HG22	1:D:220:VAL:H	1.78	0.48
1:A:235:ALA:HB2	3:A:337:HOH:O	2.12	0.48
1:A:52:SER:HB3	3:A:352:HOH:O	2.12	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:240:VAL:N	1:D:241:PRO:HD2	2.26	0.48
1:C:280:ALA:CA	3:C:338:HOH:O	2.61	0.48
1:B:245:TYR:N	1:B:245:TYR:HD2	2.11	0.48
1:A:52:SER:CB	3:A:352:HOH:O	2.61	0.48
1:A:187:ASP:OD2	1:A:318:HIS:HD2	1.96	0.48
1:A:242:PHE:HB3	1:A:243:LEU:HD12	1.94	0.48
1:C:244:LEU:CB	1:C:245:TYR:CA	2.91	0.48
1:D:244:LEU:HB3	1:D:245:TYR:CA	2.43	0.48
1:D:258:LEU:O	1:D:268:THR:HA	2.14	0.48
1:D:278(A):GLU:HG3	1:D:279(A):ILE:O	2.14	0.48
1:A:279(A):ILE:C	3:A:341:HOH:O	2.52	0.48
1:A:161:ASN:OD1	1:A:161:ASN:N	2.47	0.48
1:B:75:SER:HB2	3:B:341:HOH:O	2.13	0.48
1:D:244:LEU:HB2	1:D:245:TYR:HA	1.96	0.48
1:A:199:PHE:CE1	1:A:258:LEU:HG	2.49	0.48
1:A:279(A):ILE:O	1:A:279(B):PHE:CB	2.62	0.47
1:A:96:VAL:CG2	1:A:143:GLN:HG3	2.44	0.47
1:B:49:SER:HB3	3:B:348:HOH:O	2.15	0.47
1:B:241:PRO:HG3	1:B:243(A):SER:CA	2.44	0.47
1:A:23:ASN:HD21	1:A:25:GLN:HE21	1.62	0.47
1:D:244:LEU:CB	1:D:245:TYR:CA	2.92	0.47
1:B:110:PRO:O	1:B:111:PHE:C	2.53	0.47
1:B:65:GLU:OE2	1:B:86:LYS:HD3	2.15	0.47
1:B:240:VAL:N	1:B:241:PRO:CD	2.77	0.47
1:B:279(A):ILE:O	1:B:279(B):PHE:CB	2.63	0.46
1:A:279(C):SER:HB2	3:A:341:HOH:O	2.15	0.46
1:A:72:LYS:HG3	1:A:81:SER:HB3	1.97	0.46
1:D:278:LEU:HA	3:D:344:HOH:O	2.15	0.46
1:A:308:LYS:HD3	1:A:309:TYR:CE2	2.50	0.46
1:B:279:ASN:HB3	3:B:343:HOH:O	2.14	0.46
1:C:243:LEU:HB2	3:C:343:HOH:O	2.15	0.46
1:B:292:GLU:O	1:B:296:LYS:C	2.54	0.46
1:D:278(A):GLU:CD	1:D:279(C):SER:HG	2.17	0.46
1:A:240:VAL:N	1:A:241:PRO:CD	2.74	0.46
1:D:239:LYS:HD3	1:D:245:TYR:HE1	1.80	0.46
1:A:185:ASN:HD22	1:A:185:ASN:C	2.18	0.46
1:C:244:LEU:HB3	1:C:245:TYR:CA	2.45	0.46
1:C:199:PHE:CZ	1:C:258:LEU:HG	2.50	0.46
1:B:45:CYS:HA	1:B:105:THR:O	2.16	0.46
2:C:329:006:C53	2:C:329:006:H31	2.38	0.45
1:B:185:ASN:C	1:B:185:ASN:HD22	2.19	0.45

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:279(B):PHE:HB2	1:C:279(C):SER:HB3	1.92	0.45
1:C:245:TYR:N	1:C:245:TYR:HD2	2.15	0.45
1:B:80:ILE:HD11	1:B:104:MET:SD	2.57	0.45
1:C:279(A):ILE:C	3:C:333:HOH:O	2.55	0.45
1:B:278:LEU:HD21	1:B:283:MET:HB2	1.98	0.45
1:C:194:LEU:HD13	1:C:260:TYR:HB3	1.98	0.45
1:C:243(A):SER:O	1:C:244:LEU:HB2	2.16	0.44
1:A:240:VAL:N	1:A:241:PRO:HD3	2.17	0.44
1:B:10:ALA:HB3	2:B:329:006:H38	1.98	0.44
1:A:108:VAL:HG11	1:B:79:THR:HG22	1.99	0.44
1:A:292:GLU:O	1:A:296:LYS:C	2.56	0.44
1:B:240:VAL:N	1:B:241:PRO:HD3	2.20	0.44
1:B:192:VAL:HG12	1:B:194:LEU:HG	2.00	0.44
1:C:42:SER:HB2	1:C:103:GLU:HB3	2.00	0.44
1:A:279:ASN:HD22	1:A:279:ASN:HA	1.70	0.44
1:A:278:LEU:CB	1:A:278(A):GLU:OE2	2.66	0.43
1:A:278:LEU:HD21	1:A:283:MET:HB2	1.99	0.43
1:B:147:GLU:HG2	3:B:338:HOH:O	2.18	0.43
1:A:9:LEU:HB2	1:A:15:PHE:CD1	2.52	0.43
1:C:258:LEU:O	1:C:268:THR:HA	2.17	0.43
1:A:243(A):SER:HB3	3:A:331:HOH:O	2.18	0.43
1:B:9:LEU:HB2	1:B:15:PHE:CD1	2.54	0.43
1:B:244:LEU:CB	1:B:245:TYR:CA	2.96	0.43
1:A:154:TYR:O	1:A:155:LEU:HD23	2.19	0.43
1:B:209:LYS:HG3	3:B:357:HOH:O	2.17	0.43
1:D:278(A):GLU:CD	1:D:279(C):SER:CB	2.87	0.43
1:C:218:THR:HG22	1:C:220:VAL:H	1.83	0.43
1:A:65:GLU:OE2	1:A:86:LYS:HD3	2.18	0.43
1:B:278:LEU:HB2	1:B:278(A):GLU:OE2	2.18	0.43
1:C:73:LEU:HB3	1:C:80:ILE:HG23	2.00	0.43
1:C:183:LYS:O	1:C:192:VAL:HG23	2.19	0.43
1:A:65:GLU:HB2	1:A:86:LYS:HB3	2.00	0.43
1:D:42:SER:HB2	1:D:103:GLU:HB3	2.01	0.43
1:B:187:ASP:OD2	1:B:318:HIS:HD2	2.01	0.43
1:A:218:THR:HG22	1:A:220:VAL:H	1.84	0.43
1:B:278:LEU:HB3	1:B:278(A):GLU:OE2	2.19	0.42
1:A:80:ILE:HD11	1:A:104:MET:SD	2.59	0.42
1:A:278:LEU:O	1:B:240:VAL:HG21	2.20	0.42
1:B:23:ASN:ND2	1:B:23:ASN:H	2.06	0.42
1:D:244:LEU:HD23	1:D:244:LEU:HA	1.91	0.42
1:A:244:LEU:HA	1:A:244:LEU:HD23	1.90	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:241:PRO:HB2	1:D:243:LEU:H	1.85	0.42
1:C:109(A):PHE:CE1	2:C:329:006:H49A	2.55	0.42
1:B:308:LYS:HD3	1:B:309:TYR:CE2	2.54	0.42
1:C:279(A):ILE:HD12	1:C:279(A):ILE:O	2.20	0.42
1:C:258:LEU:HD13	1:C:274:TYR:CE1	2.53	0.42
1:D:73:LEU:HB3	1:D:80:ILE:HG23	2.01	0.42
1:B:72:LYS:HG3	1:B:81:SER:HB3	2.01	0.42
1:C:244:LEU:HB3	1:C:245:TYR:HA	1.98	0.42
1:B:160:LYS:HE2	1:D:126:LYS:HZ1	1.84	0.42
1:D:188:LEU:HB3	1:D:189:MET:H	1.69	0.42
1:A:244:LEU:CB	1:A:245:TYR:CA	2.98	0.42
1:B:209:LYS:HE3	3:B:357:HOH:O	2.20	0.42
1:A:258:LEU:HD13	1:A:274:TYR:CE1	2.56	0.41
1:C:239:LYS:HD3	1:C:245:TYR:HE1	1.84	0.41
1:D:244:LEU:HB3	1:D:245:TYR:HA	1.98	0.41
1:D:183:LYS:O	1:D:192:VAL:HG23	2.21	0.41
1:A:240:VAL:HG21	1:B:278:LEU:O	2.20	0.41
1:D:1:PHE:CZ	1:D:169:GLY:HA3	2.56	0.41
1:C:10:ALA:HB3	2:C:329:006:H38	2.03	0.41
1:D:291:LEU:HD12	1:D:291:LEU:H	1.86	0.41
1:C:109(B):GLU:CG	1:C:110:PRO:HA	2.39	0.41
1:A:23:ASN:N	1:A:23:ASN:HD22	2.07	0.41
1:C:158:GLU:HG3	3:C:330:HOH:O	2.20	0.41
1:A:80:ILE:HG21	1:A:80:ILE:HD13	1.69	0.41
1:D:245:TYR:N	1:D:245:TYR:HD2	2.17	0.41
1:A:109(B):GLU:OE2	1:A:113:SER:HB3	2.21	0.41
1:D:128:LEU:HG	1:D:128:LEU:O	2.22	0.40
1:D:260:TYR:CZ	1:D:301:LEU:HD21	2.56	0.40
1:B:311:THR:HG22	1:B:322:PHE:CD1	2.57	0.40
1:C:188:LEU:HB3	1:C:189:MET:H	1.74	0.40
1:C:262:SER:HB2	1:C:263:PRO:HD2	2.02	0.40
2:A:329:006:H28	2:A:329:006:H50A	1.85	0.40
1:B:154:TYR:O	1:B:155:LEU:HD23	2.21	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	324/332 (98%)	294 (91%)	24 (7%)	6 (2%)	10	43
1	B	324/332 (98%)	294 (91%)	25 (8%)	5 (2%)	13	50
1	C	324/332 (98%)	298 (92%)	22 (7%)	4 (1%)	16	56
1	D	324/332 (98%)	299 (92%)	21 (6%)	4 (1%)	16	56
All	All	1296/1328 (98%)	1185 (91%)	92 (7%)	19 (2%)	13	50

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	ASN
1	A	240	VAL
1	A	244	LEU
1	A	279(B)	PHE
1	B	159	ASN
1	B	240	VAL
1	B	244	LEU
1	B	279(B)	PHE
1	C	159	ASN
1	C	240	VAL
1	C	244	LEU
1	C	279(B)	PHE
1	D	159	ASN
1	D	240	VAL
1	D	244	LEU
1	D	279(B)	PHE
1	A	243(A)	SER
1	B	243(A)	SER
1	A	201	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	A	296/301 (98%)	256 (86%)	40 (14%)	5	20
1	B	296/301 (98%)	253 (86%)	43 (14%)	4	18
1	C	296/301 (98%)	260 (88%)	36 (12%)	6	25
1	D	296/301 (98%)	260 (88%)	36 (12%)	6	25
All	All	1184/1204 (98%)	1029 (87%)	155 (13%)	5	22

All (155) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASP
1	A	4	VAL
1	A	12	VAL
1	A	22	ASP
1	A	23	ASN
1	A	38	VAL
1	A	44	LYS
1	A	73	LEU
1	A	74	THR
1	A	80	ILE
1	A	88	LEU
1	A	95	SER
1	A	107	ILE
1	A	109(B)	GLU
1	A	113	SER
1	A	120	VAL
1	A	158	GLU
1	A	161	ASN
1	A	166	THR
1	A	171	GLU
1	A	173	ARG
1	A	183	LYS
1	A	185	ASN
1	A	188	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	197	VAL
1	A	214	LEU
1	A	220	VAL
1	A	222	THR
1	A	233	GLU
1	A	236	SER
1	A	245	TYR
1	A	258	LEU
1	A	261	ARG
1	A	269	LEU
1	A	272	LYS
1	A	279	ASN
1	A	281	LEU
1	A	297	ASN
1	A	307	ARG
1	A	326	LYS
1	B	2	ASP
1	B	4	VAL
1	B	12	VAL
1	B	22	ASP
1	B	23	ASN
1	B	38	VAL
1	B	40	VAL
1	B	44	LYS
1	B	73	LEU
1	B	74	THR
1	B	80	ILE
1	B	88	LEU
1	B	95	SER
1	B	107	ILE
1	B	109(B)	GLU
1	B	113	SER
1	B	120	VAL
1	B	158	GLU
1	B	161	ASN
1	B	166	THR
1	B	171	GLU
1	B	173	ARG
1	B	183	LYS
1	B	185	ASN
1	B	188	LEU
1	B	197	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	214	LEU
1	B	220	VAL
1	B	222	THR
1	B	223	VAL
1	B	233	GLU
1	B	245	TYR
1	B	258	LEU
1	B	261	ARG
1	B	262	SER
1	B	269	LEU
1	B	272	LYS
1	B	275	LEU
1	B	279	ASN
1	B	281	LEU
1	B	297	ASN
1	B	307	ARG
1	B	326	LYS
1	C	2	ASP
1	C	11	ASN
1	C	12	VAL
1	C	13	LEU
1	C	23	ASN
1	C	38	VAL
1	C	44	LYS
1	C	51	GLU
1	C	73	LEU
1	C	95	SER
1	C	109(B)	GLU
1	C	120	VAL
1	C	141	LYS
1	C	146	ILE
1	C	148	GLN
1	C	158	GLU
1	C	171	GLU
1	C	173	ARG
1	C	183	LYS
1	C	185	ASN
1	C	214	LEU
1	C	220	VAL
1	C	234	SER
1	C	237	VAL
1	C	242	PHE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	243	LEU
1	C	245	TYR
1	C	246	VAL
1	C	251	ASN
1	C	261	ARG
1	C	269	LEU
1	C	272	LYS
1	C	279	ASN
1	C	281	LEU
1	C	287	VAL
1	C	326	LYS
1	D	2	ASP
1	D	11	ASN
1	D	12	VAL
1	D	13	LEU
1	D	23	ASN
1	D	38	VAL
1	D	44	LYS
1	D	51	GLU
1	D	73	LEU
1	D	95	SER
1	D	109(B)	GLU
1	D	120	VAL
1	D	141	LYS
1	D	146	ILE
1	D	148	GLN
1	D	158	GLU
1	D	171	GLU
1	D	173	ARG
1	D	183	LYS
1	D	185	ASN
1	D	220	VAL
1	D	234	SER
1	D	237	VAL
1	D	242	PHE
1	D	243	LEU
1	D	245	TYR
1	D	246	VAL
1	D	251	ASN
1	D	261	ARG
1	D	269	LEU
1	D	272	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	279	ASN
1	D	281	LEU
1	D	287	VAL
1	D	307	ARG
1	D	326	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	148	GLN
1	A	185	ASN
1	A	203	ASN
1	A	211	ASN
1	A	229	ASN
1	A	279	ASN
1	A	297	ASN
1	A	318	HIS
1	B	23	ASN
1	B	148	GLN
1	B	185	ASN
1	B	203	ASN
1	B	211	ASN
1	B	229	ASN
1	B	279	ASN
1	B	318	HIS
1	C	23	ASN
1	C	25	GLN
1	C	185	ASN
1	C	186	HIS
1	C	203	ASN
1	C	211	ASN
1	C	251	ASN
1	D	23	ASN
1	D	25	GLN
1	D	185	ASN
1	D	186	HIS
1	D	203	ASN
1	D	211	ASN
1	D	279	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 ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	006	A	329	-	49,49,49	1.24	4 (8%)	65,71,71	1.60	10 (15%)
2	006	B	329	-	49,49,49	1.29	4 (8%)	65,71,71	1.62	9 (13%)
2	006	C	329	-	49,49,49	1.31	4 (8%)	65,71,71	1.43	9 (13%)
2	006	D	329	-	49,49,49	1.13	5 (10%)	65,71,71	1.56	9 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	006	A	329	-	-	0/33/61/61	0/5/5/5
2	006	B	329	-	-	0/33/61/61	0/5/5/5
2	006	C	329	-	-	0/33/61/61	0/5/5/5
2	006	D	329	-	-	0/33/61/61	0/5/5/5

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	329	006	C51-S50	-5.01	1.75	1.85
2	B	329	006	C51-S50	-4.78	1.75	1.85
2	A	329	006	C51-S50	-4.74	1.75	1.85
2	D	329	006	C51-S50	-4.48	1.76	1.85
2	C	329	006	C32-C31	-3.55	1.48	1.51
2	A	329	006	C32-C31	-3.43	1.48	1.51
2	B	329	006	C32-C31	-3.17	1.48	1.51
2	B	329	006	C50-S50	-2.84	1.75	1.82
2	D	329	006	C50-S50	-2.84	1.75	1.82
2	A	329	006	C50-S50	-2.82	1.75	1.82
2	C	329	006	C50-S50	-2.75	1.75	1.82
2	D	329	006	C32-C31	-2.71	1.48	1.51
2	D	329	006	C28-C29	-2.04	1.51	1.53
2	D	329	006	C54-N50	3.38	1.49	1.46
2	A	329	006	C54-N50	4.61	1.50	1.46
2	C	329	006	C54-N50	4.86	1.50	1.46
2	B	329	006	C54-N50	5.15	1.50	1.46

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	329	006	C21-C20-N2	-5.00	104.67	110.14
2	C	329	006	C21-C20-N2	-4.97	104.70	110.14
2	D	329	006	C22-C21-C20	-4.79	105.86	113.48
2	B	329	006	C22-C21-C20	-4.25	106.72	113.48
2	A	329	006	C32-C31-N30	-3.90	108.94	114.36
2	A	329	006	C21-C20-N2	-3.39	106.43	110.14
2	D	329	006	O50-C55-N30	-3.24	116.57	122.93
2	A	329	006	O50-C55-N30	-3.20	116.65	122.93
2	D	329	006	C21-C20-N2	-3.19	106.65	110.14
2	B	329	006	C32-C31-N30	-2.90	110.32	114.36
2	D	329	006	C32-C31-N30	-2.83	110.42	114.36
2	B	329	006	O50-C55-N30	-2.81	117.42	122.93
2	A	329	006	C34-C33-C32	-2.66	117.56	121.02
2	B	329	006	C34-C33-C32	-2.53	117.72	121.02
2	C	329	006	C34-C33-C32	-2.50	117.77	121.02
2	C	329	006	C32-C31-N30	-2.46	110.93	114.36
2	D	329	006	C34-C33-C32	-2.26	118.08	121.02
2	C	329	006	O50-C55-N30	-2.13	118.75	122.93
2	A	329	006	C38-C37-C36	-2.10	117.66	120.90
2	C	329	006	C31-N30-C55	2.08	127.32	121.86
2	A	329	006	C51-C54-C55	2.49	118.41	113.28

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	329	006	C49-O41-C45	2.50	122.01	114.79
2	C	329	006	S50-C50-N50	2.54	109.08	105.26
2	C	329	006	C47-C46-C45	2.57	121.57	117.67
2	D	329	006	C51-C54-C55	2.74	118.92	113.28
2	A	329	006	C49-O41-C45	3.02	123.51	114.79
2	B	329	006	C31-N30-C55	3.13	130.06	121.86
2	C	329	006	C54-C55-N30	3.15	120.99	115.73
2	A	329	006	C51-C54-N50	3.21	111.25	106.44
2	D	329	006	C31-N30-C55	3.31	130.54	121.86
2	D	329	006	C51-C54-N50	3.37	111.49	106.44
2	A	329	006	C31-N30-C55	3.53	131.12	121.86
2	B	329	006	C51-C54-N50	3.82	112.16	106.44
2	C	329	006	C51-C54-N50	4.06	112.53	106.44
2	B	329	006	C54-C55-N30	4.33	122.96	115.73
2	D	329	006	C54-C55-N30	5.16	124.35	115.73
2	A	329	006	C54-C55-N30	5.42	124.78	115.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	329	006	4	0
2	B	329	006	2	0
2	C	329	006	6	0
2	D	329	006	3	0

## 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	326/332 (98%)	-0.34	2 (0%) 90 73	42, 51, 58, 61	0
1	B	326/332 (98%)	-0.31	1 (0%) 94 84	42, 51, 58, 61	0
1	C	326/332 (98%)	0.06	8 (2%) 61 30	41, 51, 57, 59	0
1	D	326/332 (98%)	-0.11	4 (1%) 81 55	41, 51, 57, 59	0
All	All	1304/1328 (98%)	-0.18	15 (1%) 81 55	41, 51, 58, 61	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	279(B)	PHE	5.4
1	D	279(C)	SER	5.0
1	C	238	PHE	3.6
1	D	280	ALA	3.4
1	C	253	THR	2.9
1	C	279	ASN	2.8
1	A	242	PHE	2.7
1	B	234	SER	2.7
1	C	95	SER	2.5
1	C	193	ASP	2.5
1	D	242	PHE	2.5
1	C	209	LYS	2.4
1	C	235	ALA	2.4
1	A	279(B)	PHE	2.1
1	C	260	TYR	2.0

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

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	006	C	329	45/45	0.75	0.39	4.75	190,200,202,202	0
2	006	B	329	45/45	0.79	0.33	4.05	132,160,166,167	0
2	006	A	329	45/45	0.79	0.32	2.58	145,170,176,176	0
2	006	D	329	45/45	0.81	0.35	1.88	151,171,175,175	0

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

There are no such residues in this entry.