



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:52 PM GMT

PDB ID : 1MIQ  
Title : Crystal structure of proplasmepsin from the human malarial pathogen Plasmodium vivax  
Authors : Bernstein, N.K.; Cherney, M.M.; Yowell, C.A.; Dame, J.B.; James, M.N.  
Deposited on : 2002-08-23  
Resolution : 2.50 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

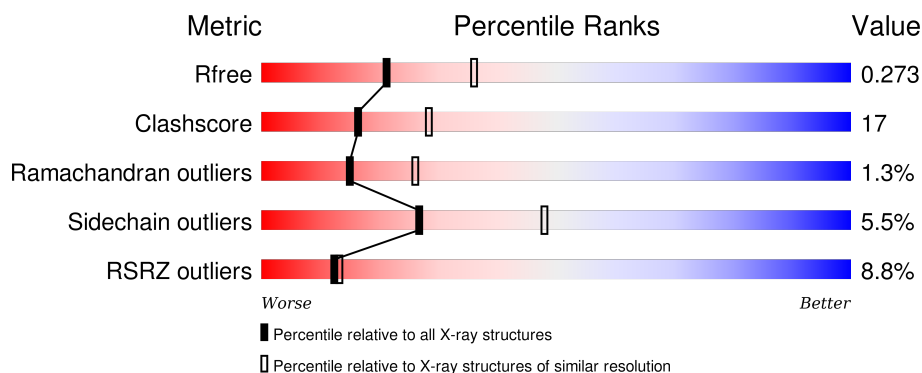
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	375	<div> <div>6%</div> <div>70%</div> <div>26%</div> <div>• •</div> </div>
1	B	375	<div> <div>11%</div> <div>66%</div> <div>29%</div> <div>5%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6032 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 plasmepsin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	373	Total	C	N	O	S	0	0	0
			2976	1927	457	579	13			
1	B	375	Total	C	N	O	S	0	0	0
			2993	1935	460	584	14			

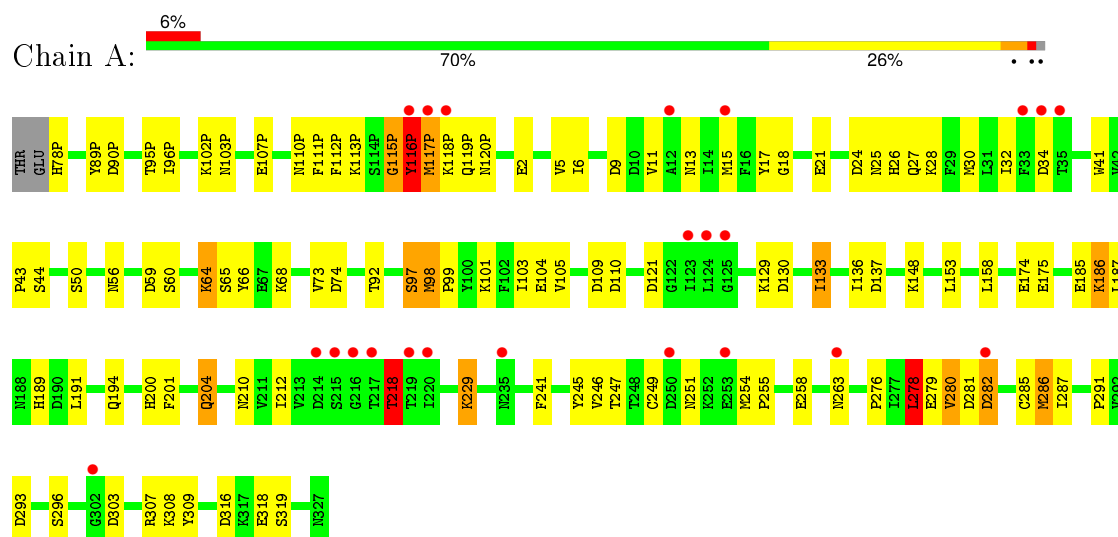
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	49	Total	O	0	0
			49	49		
2	B	14	Total	O	0	0
			14	14		

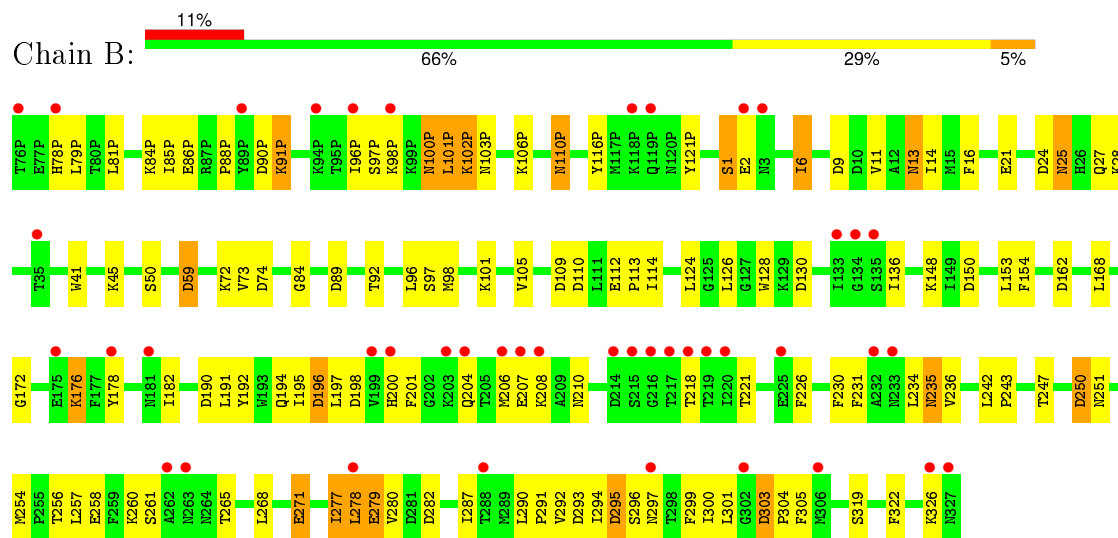
### 3 Residue-property plots [i](#)

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: plasmepsin



#### • Molecule 1: plasmepsin



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	149.41Å 92.73Å 99.13Å 90.00° 130.11° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50 29.84 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.3 (30.00-2.50) 99.4 (29.84-2.50)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.91 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, $R_{free}$	0.203 , 0.245 0.239 , 0.273	Depositor DCC
$R_{free}$ test set	1850 reflections (5.19%)	DCC
Wilson B-factor (Å <sup>2</sup> )	54.2	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 33.3	EDS
Estimated twinning fraction	0.018 for -h-2*k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 35657 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6032	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% 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 ⓘ

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	0.66	0/3049	0.91	12/4131 (0.3%)
1	B	0.54	0/3065	0.86	17/4153 (0.4%)
All	All	0.61	0/6114	0.88	29/8284 (0.4%)

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	9	ASP	CB-CG-OD2	7.36	124.92	118.30
1	B	74	ASP	CB-CG-OD2	7.03	124.62	118.30
1	B	150	ASP	CB-CG-OD2	6.79	124.41	118.30
1	B	9	ASP	CB-CG-OD2	6.68	124.32	118.30
1	A	293	ASP	CB-CG-OD2	6.63	124.27	118.30
1	A	121	ASP	CB-CG-OD2	6.60	124.24	118.30
1	B	303	ASP	CB-CG-OD2	6.26	123.94	118.30
1	A	109	ASP	CB-CG-OD2	6.10	123.79	118.30
1	B	59	ASP	CB-CG-OD2	6.00	123.70	118.30
1	A	303	ASP	CB-CG-OD2	5.96	123.67	118.30
1	A	34	ASP	CB-CG-OD2	5.81	123.53	118.30
1	A	90(P)	ASP	CB-CG-OD2	5.75	123.48	118.30
1	A	218	THR	OG1-CB-CG2	-5.61	97.09	110.00
1	B	295	ASP	CB-CG-OD2	5.59	123.34	118.30
1	B	110	ASP	CB-CG-OD2	5.57	123.31	118.30
1	A	316	ASP	CB-CG-OD2	5.56	123.31	118.30
1	A	137	ASP	CB-CG-OD2	5.49	123.24	118.30
1	B	130	ASP	CB-CG-OD2	5.42	123.18	118.30
1	A	98	MET	CG-SD-CE	-5.37	91.60	100.20
1	B	90(P)	ASP	CB-CG-OD2	5.37	123.13	118.30
1	B	293	ASP	CB-CG-OD2	5.23	123.00	118.30
1	B	196	ASP	CB-CG-OD2	5.22	123.00	118.30
1	B	24	ASP	CB-CG-OD2	5.20	122.98	118.30
1	B	89	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	110	ASP	CB-CG-OD2	5.12	122.91	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	162	ASP	CB-CG-OD2	5.09	122.88	118.30
1	B	282	ASP	CB-CG-OD2	5.07	122.86	118.30
1	B	109	ASP	CB-CG-OD2	5.06	122.86	118.30
1	B	250	ASP	CB-CG-OD2	5.01	122.81	118.30

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	2976	0	2877	95	0
1	B	2993	0	2897	104	0
2	A	49	0	0	0	0
2	B	14	0	0	0	0
All	All	6032	0	5774	196	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 17.

All (196) 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:194:GLN:NE2	1:A:210:ASN:HB3	1.58	1.16
1:A:194:GLN:HE21	1:A:210:ASN:HB3	1.07	1.02
1:B:278:LEU:H	1:B:278:LEU:CD2	1.72	1.01
1:B:78(P):HIS:CE1	1:B:172:GLY:HA3	1.99	0.98
1:A:189:HIS:HD2	1:A:191:LEU:H	1.05	0.97
1:B:278:LEU:H	1:B:278:LEU:HD23	1.35	0.91
1:A:186:LYS:HD2	1:A:187:LEU:O	1.69	0.91
1:B:235:ASN:O	1:B:247:THR:HG22	1.71	0.90
1:B:191:LEU:C	1:B:192:TYR:HD2	1.77	0.88
1:A:17:TYR:C	1:A:30:MET:HE1	1.97	0.85
1:B:25:ASN:H	1:B:25:ASN:HD22	1.18	0.85
1:B:101:LYS:HD3	1:B:136:ILE:HD11	1.56	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:SER:HB2	1:A:104:GLU:HG2	1.58	0.84
1:A:27:GLN:HE22	1:A:59:ASP:H	1.21	0.84
1:A:247:THR:HG21	1:A:254:MET:CE	2.09	0.82
1:A:116(P):TYR:H	1:A:116(P):TYR:HD1	1.28	0.82
1:B:278:LEU:HD23	1:B:278:LEU:N	1.94	0.81
1:A:189:HIS:CD2	1:A:191:LEU:H	1.96	0.79
1:A:186:LYS:HD3	1:A:187:LEU:N	1.96	0.79
1:B:79(P):LEU:HD22	1:B:96:LEU:HD12	1.64	0.79
1:B:277:ILE:CG2	1:B:280:VAL:HG12	2.15	0.77
1:A:30:MET:HE3	1:A:30:MET:HA	1.68	0.75
1:B:191:LEU:C	1:B:192:TYR:CD2	2.61	0.72
1:B:191:LEU:O	1:B:192:TYR:HD2	1.72	0.72
1:A:11:VAL:O	1:A:218:THR:HG22	1.91	0.71
1:A:279:GLU:OE1	1:A:281:ASP:O	2.09	0.70
1:B:78(P):HIS:ND1	1:B:172:GLY:HA3	2.05	0.70
1:A:287:ILE:N	1:A:287:ILE:HD12	2.07	0.70
1:A:17:TYR:C	1:A:30:MET:CE	2.61	0.69
1:B:101:LYS:HD3	1:B:136:ILE:CD1	2.23	0.69
1:B:45:LYS:NZ	1:B:59:ASP:OD2	2.26	0.67
1:A:245:TYR:O	1:A:286:MET:HA	1.95	0.67
1:A:247:THR:HG21	1:A:254:MET:HE3	1.76	0.66
1:A:249:CYS:SG	1:A:282:ASP:HB3	2.36	0.66
1:B:277:ILE:HG22	1:B:280:VAL:HG12	1.76	0.65
1:B:234:LEU:HD22	1:B:254:MET:HE1	1.78	0.65
1:B:278:LEU:H	1:B:278:LEU:HD22	1.60	0.64
1:A:18:GLY:HA2	1:A:30:MET:HE3	1.79	0.64
1:A:279:GLU:O	1:A:281:ASP:N	2.31	0.64
1:B:86(P):GLU:HG3	1:B:16:PHE:CE1	2.32	0.64
1:A:129:LYS:HE2	1:A:191:LEU:CD1	2.28	0.64
1:A:117(P):MET:O	1:A:119(P):GLN:N	2.29	0.64
1:A:194:GLN:NE2	1:A:210:ASN:CB	2.49	0.63
1:B:13:ASN:HD21	1:B:218:THR:HG23	1.64	0.63
1:B:206:MET:CE	1:B:299:PHE:HE2	2.13	0.61
1:B:236:VAL:HA	1:B:247:THR:HG23	1.82	0.60
1:B:206:MET:HE3	1:B:297:ASN:HB2	1.82	0.60
1:B:192:TYR:N	1:B:192:TYR:CD2	2.68	0.60
1:A:247:THR:HG22	1:A:287:ILE:HD11	1.82	0.60
1:A:186:LYS:HD3	1:A:187:LEU:H	1.65	0.60
1:B:295:ASP:O	1:B:297:ASN:N	2.29	0.60
1:B:11:VAL:HG12	1:B:11:VAL:O	2.01	0.60
1:B:101(P):LEU:O	1:B:103(P):ASN:N	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:GLU:HG2	1:A:28:LYS:HD3	1.84	0.60
1:B:201:PHE:CD1	1:B:257:LEU:HD22	2.36	0.59
1:B:178:TYR:O	1:B:326:LYS:HE3	2.03	0.59
1:B:235:ASN:O	1:B:247:THR:CG2	2.50	0.59
1:A:102(P):LYS:HB2	1:A:278:LEU:HD21	1.83	0.59
1:A:17:TYR:O	1:A:30:MET:CE	2.51	0.58
1:B:301:LEU:HD22	1:B:305:PHE:CD2	2.39	0.58
1:A:279:GLU:C	1:A:281:ASP:N	2.57	0.58
1:B:278:LEU:CD2	1:B:278:LEU:N	2.47	0.57
1:A:153:LEU:C	1:A:153:LEU:HD12	2.25	0.57
1:B:201:PHE:HB2	1:B:204:GLN:HB2	1.86	0.56
1:A:194:GLN:HE21	1:A:210:ASN:CB	1.98	0.56
1:A:186:LYS:CD	1:A:187:LEU:N	2.68	0.56
1:A:18:GLY:N	1:A:30:MET:HE1	2.21	0.56
1:A:116(P):TYR:CD1	1:A:116(P):TYR:N	2.63	0.56
1:A:89(P):TYR:OH	1:A:278:LEU:HB3	2.06	0.56
1:B:13:ASN:ND2	1:B:218:THR:HG23	2.20	0.56
1:B:98:MET:HB3	1:B:148:LYS:HE3	1.88	0.56
1:B:128:TRP:HB2	1:B:191:LEU:O	2.06	0.56
1:B:206:MET:HE2	1:B:299:PHE:HE2	1.71	0.56
1:B:153:LEU:HD12	1:B:153:LEU:C	2.27	0.55
1:B:201:PHE:CD2	1:B:226:PHE:HE1	2.24	0.55
1:B:197:LEU:HD23	1:B:261:SER:HB3	1.89	0.55
1:A:112(P):PHE:HB2	1:A:116(P):TYR:OH	2.07	0.55
1:A:110(P):ASN:O	1:A:113(P):LYS:HG2	2.07	0.55
1:B:25:ASN:N	1:B:25:ASN:HD22	1.87	0.54
1:A:15:MET:O	1:A:32:ILE:HA	2.07	0.54
1:B:194:GLN:HE22	1:B:210:ASN:HD21	1.56	0.54
1:B:25:ASN:HD21	1:B:27:GLN:HE21	1.54	0.54
1:B:14:ILE:HD13	1:B:14:ILE:N	2.23	0.54
1:A:2:GLU:H	1:A:2:GLU:CD	2.10	0.54
1:B:277:ILE:HB	1:B:280:VAL:CG1	2.38	0.53
1:B:200:HIS:HB2	1:B:258:GLU:HB2	1.89	0.53
1:A:249:CYS:CB	1:A:282:ASP:HB3	2.38	0.53
1:A:92:THR:HG1	1:A:97:SER:HG	1.56	0.53
1:B:196:ASP:O	1:B:197:LEU:HG	2.08	0.53
1:A:111(P):PHE:HD2	1:A:116(P):TYR:CE1	2.27	0.53
1:B:86(P):GLU:HG3	1:B:16:PHE:HE1	1.73	0.52
1:A:111(P):PHE:HD2	1:A:116(P):TYR:HE1	1.57	0.52
1:B:41:TRP:CE3	1:B:105:VAL:HG21	2.45	0.52
1:B:81(P):LEU:HD12	1:B:168:LEU:HD23	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:25:ASN:ND2	1:B:25:ASN:H	1.98	0.52
1:A:129:LYS:HE2	1:A:191:LEU:HD13	1.92	0.51
1:B:98(P):LYS:O	1:B:102(P):LYS:HB3	2.10	0.51
1:A:279:GLU:C	1:A:281:ASP:H	2.13	0.51
1:A:308:LYS:HD3	1:A:309:TYR:CE1	2.46	0.51
1:B:194:GLN:CD	1:B:210:ASN:OD1	2.49	0.51
1:B:206:MET:HE1	1:B:297:ASN:HA	1.92	0.50
1:A:187:LEU:HG	1:A:318:GLU:O	2.11	0.50
1:B:11:VAL:CG1	1:B:11:VAL:O	2.59	0.50
1:B:112:GLU:HB3	1:B:113:PRO:HA	1.93	0.50
1:A:96(P):ILE:HD12	1:A:96(P):ILE:N	2.27	0.50
1:B:6:ILE:HD12	1:B:291:PRO:HD2	1.94	0.50
1:B:198:ASP:OD2	1:B:208:LYS:HD2	2.11	0.50
1:B:6:ILE:CD1	1:B:290:LEU:HD22	2.42	0.50
1:B:176:LYS:H	1:B:176:LYS:HZ3	1.59	0.49
1:B:231:PHE:O	1:B:234:LEU:N	2.42	0.49
1:A:194:GLN:HG3	1:A:212:ILE:HG13	1.94	0.49
1:A:130:ASP:OD2	1:A:136:ILE:HB	2.13	0.48
1:A:158:LEU:HB3	1:A:307:ARG:CZ	2.43	0.48
1:A:78(P):HIS:HB2	1:A:174:GLU:OE1	2.13	0.48
1:A:279:GLU:O	1:A:280:VAL:C	2.50	0.48
1:A:200:HIS:HB2	1:A:258:GLU:HB2	1.96	0.48
1:A:21:GLU:OE2	1:A:28:LYS:HE3	2.14	0.48
1:A:291:PRO:HG2	1:A:291:PRO:O	2.13	0.48
1:A:11:VAL:C	1:A:218:THR:HG22	2.33	0.48
1:A:251:ASN:HB3	1:A:254:MET:HG2	1.95	0.48
1:A:287:ILE:CD1	1:A:287:ILE:N	2.75	0.48
1:B:88(P):PRO:HD2	1:B:218:THR:HG21	1.96	0.48
1:A:103(P):ASN:O	1:A:107(P):GLU:HB2	2.14	0.47
1:B:96(P):ILE:HG23	1:B:96(P):ILE:O	2.15	0.47
1:B:84(P):LYS:HD3	1:B:85(P):ILE:N	2.29	0.47
1:A:278:LEU:HD23	1:A:279:GLU:H	1.79	0.47
1:A:73:VAL:HG21	1:A:103:ILE:HD13	1.96	0.47
1:A:60:SER:HB2	1:A:66:TYR:CG	2.49	0.47
1:B:13:ASN:C	1:B:14:ILE:HD13	2.35	0.47
1:A:111(P):PHE:O	1:A:115(P):GLY:N	2.42	0.47
1:B:221:THR:OG1	1:B:300:ILE:HB	2.15	0.47
1:B:250:ASP:OD1	1:B:250:ASP:C	2.53	0.47
1:A:11:VAL:HG12	1:A:11:VAL:O	2.14	0.46
1:A:5:VAL:HG12	1:A:6:ILE:N	2.30	0.46
1:B:124:LEU:HD23	1:B:124:LEU:C	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:GLN:OE1	1:A:229:LYS:HG2	2.16	0.46
1:B:101(P):LEU:HG	1:B:102(P):LYS:H	1.81	0.46
1:B:271:GLU:HG3	1:B:271:GLU:H	1.50	0.46
1:B:114:ILE:HD12	1:B:114:ILE:C	2.36	0.46
1:A:254:MET:HA	1:A:255:PRO:HD3	1.80	0.46
1:A:279:GLU:CD	1:A:281:ASP:O	2.55	0.45
1:A:194:GLN:HG3	1:A:212:ILE:CG1	2.45	0.45
1:B:182:ILE:HA	1:B:322:PHE:O	2.17	0.45
1:A:247:THR:HG21	1:A:254:MET:HE2	1.96	0.45
1:B:206:MET:HE1	1:B:299:PHE:HE2	1.81	0.45
1:B:257:LEU:HD12	1:B:268:LEU:HD23	1.99	0.45
1:A:117(P):MET:C	1:A:119(P):GLN:N	2.70	0.45
1:B:91(P):LYS:HB3	1:B:91(P):LYS:HE3	1.87	0.44
1:A:43:PRO:HG2	1:A:56:ASN:O	2.18	0.44
1:A:25:ASN:O	1:A:26:HIS:HB2	2.17	0.44
1:B:21:GLU:OE1	1:B:28:LYS:NZ	2.51	0.44
1:A:18:GLY:CA	1:A:30:MET:HE3	2.44	0.44
1:B:198:ASP:HA	1:B:207:GLU:HA	1.98	0.44
1:A:246:VAL:HA	1:A:285:CYS:O	2.17	0.44
1:A:98:MET:HB3	1:A:148:LYS:HE3	2.00	0.43
1:A:276:PRO:HG3	1:A:282:ASP:OD2	2.18	0.43
1:A:107(P):GLU:HG2	1:B:103(P):ASN:HB3	2.00	0.43
1:B:279:GLU:H	1:B:279:GLU:HG2	1.59	0.43
1:B:96(P):ILE:CG2	1:B:96(P):ILE:O	2.66	0.43
1:B:97(P):SER:O	1:B:100(P):ASN:OD1	2.36	0.43
1:A:201:PHE:O	1:A:204:GLN:HB2	2.19	0.43
1:B:235:ASN:C	1:B:247:THR:CG2	2.88	0.43
1:A:185:GLU:O	1:A:319:SER:HB3	2.19	0.43
1:B:260:LYS:HG2	1:B:265:THR:HG23	2.01	0.43
1:A:41:TRP:CE3	1:A:105:VAL:HG21	2.54	0.43
1:B:277:ILE:CG2	1:B:280:VAL:CG1	2.91	0.42
1:A:133:ILE:CG1	1:A:133:ILE:O	2.66	0.42
1:B:292:VAL:HG12	1:B:294:ILE:HG13	2.01	0.42
1:A:98:MET:HA	1:A:99:PRO:HD3	1.85	0.42
1:B:72:LYS:HD3	1:B:84:GLY:O	2.19	0.42
1:B:235:ASN:HD22	1:B:235:ASN:HA	1.63	0.42
1:A:95(P):THR:HB	1:A:96(P):ILE:HD12	2.02	0.42
1:A:11:VAL:CG1	1:A:11:VAL:O	2.68	0.42
1:B:257:LEU:HD12	1:B:268:LEU:HB3	2.02	0.42
1:B:297:ASN:N	1:B:297:ASN:OD1	2.53	0.41
1:A:282:ASP:N	1:A:282:ASP:OD1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96(P):ILE:HD11	1:B:116(P):TYR:HB2	2.02	0.41
1:A:13:ASN:ND2	1:A:218:THR:HB	2.35	0.41
1:A:25:ASN:O	1:A:26:HIS:CB	2.65	0.41
1:B:92:THR:HG23	1:B:97:SER:HB3	2.02	0.41
1:B:303:ASP:HB3	1:B:304:PRO:HD3	2.03	0.41
1:B:236:VAL:HG13	1:B:287:ILE:HD13	2.03	0.41
1:B:79(P):LEU:CD2	1:B:96:LEU:HD12	2.43	0.41
1:B:126:LEU:HB3	1:B:154:PHE:CZ	2.55	0.41
1:A:101:LYS:HE2	1:A:101:LYS:HB2	1.84	0.41
1:B:1:SER:OG	1:B:2:GLU:N	2.54	0.41
1:B:106(P):LYS:O	1:B:110(P):ASN:HB2	2.21	0.41
1:B:257:LEU:HB2	1:B:268:LEU:HB3	2.03	0.40
1:B:242:LEU:HA	1:B:243:PRO:HD3	1.87	0.40
1:A:24:ASP:OD2	1:A:64:LYS:HG2	2.22	0.40
1:B:231:PHE:CD2	1:B:236:VAL:HG11	2.56	0.40
1:A:73:VAL:O	1:A:74:ASP:OD2	2.39	0.40
1:B:201:PHE:HB3	1:B:230:PHE:CD1	2.57	0.40
1:B:194:GLN:NE2	1:B:210:ASN:HD21	2.17	0.40
1:B:6:ILE:HD13	1:B:290:LEU:HD22	2.03	0.40
1:A:241:PHE:CZ	1:B:121(P):TYR:CG	3.09	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	371/375 (99%)	348 (94%)	17 (5%)	6 (2%)	12	21
1	B	373/375 (100%)	343 (92%)	26 (7%)	4 (1%)	17	31
All	All	744/750 (99%)	691 (93%)	43 (6%)	10 (1%)	15	26

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	101(P)	LEU
1	B	102(P)	LYS
1	B	296	SER
1	A	115(P)	GLY
1	A	278	LEU
1	A	117(P)	MET
1	B	251	ASN
1	A	118(P)	LYS
1	A	280	VAL
1	A	116(P)	TYR

### 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	332/340 (98%)	314 (95%)	18 (5%)	27	49
1	B	335/340 (98%)	316 (94%)	19 (6%)	25	46
All	All	667/680 (98%)	630 (94%)	37 (6%)	27	48

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116(P)	TYR
1	A	120(P)	ASN
1	A	50	SER
1	A	64	LYS
1	A	65	SER
1	A	68	LYS
1	A	97	SER
1	A	133	ILE
1	A	175	GLU
1	A	186	LYS
1	A	204	GLN
1	A	218	THR
1	A	229	LYS
1	A	263	ASN

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Mol	Chain	Res	Type
1	A	278	LEU
1	A	282	ASP
1	A	286	MET
1	A	296	SER
1	B	91(P)	LYS
1	B	100(P)	ASN
1	B	110(P)	ASN
1	B	1	SER
1	B	6	ILE
1	B	13	ASN
1	B	25	ASN
1	B	50	SER
1	B	73	VAL
1	B	176	LYS
1	B	190	ASP
1	B	195	ILE
1	B	235	ASN
1	B	256	THR
1	B	271	GLU
1	B	277	ILE
1	B	278	LEU
1	B	279	GLU
1	B	319	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100(P)	ASN
1	A	120(P)	ASN
1	A	3	ASN
1	A	13	ASN
1	A	27	GLN
1	A	189	HIS
1	A	194	GLN
1	A	275	ASN
1	B	103(P)	ASN
1	B	13	ASN
1	B	25	ASN
1	B	146	GLN
1	B	194	GLN
1	B	235	ASN
1	B	275	ASN

### 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 [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	373/375 (99%)	0.33	23 (6%) 24 27	2, 11, 28, 53	0
1	B	375/375 (100%)	0.70	43 (11%) 6 6	5, 20, 42, 59	0
All	All	748/750 (99%)	0.51	66 (8%) 12 13	2, 15, 40, 59	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	133	ILE	6.6
1	B	76(P)	THR	5.4
1	A	282	ASP	4.9
1	B	94(P)	LYS	4.7
1	A	118(P)	LYS	4.4
1	B	98(P)	LYS	4.3
1	A	116(P)	TYR	3.9
1	B	220	ILE	3.8
1	B	327	ASN	3.8
1	B	215	SER	3.5
1	A	117(P)	MET	3.4
1	B	203	LYS	3.4
1	B	208	LYS	3.4
1	B	89(P)	TYR	3.4
1	B	119(P)	GLN	3.2
1	B	134	GLY	3.2
1	B	178	TYR	3.1
1	A	216	GLY	3.1
1	A	15	MET	3.1
1	B	233	ASN	3.1
1	B	3	ASN	3.0
1	A	235	ASN	3.0
1	B	219	THR	2.9
1	A	302	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	278	LEU	2.9
1	B	217	THR	2.8
1	B	218	THR	2.8
1	A	125	GLY	2.7
1	A	217	THR	2.6
1	A	263	ASN	2.6
1	B	199	VAL	2.6
1	B	96(P)	ILE	2.6
1	A	123	ILE	2.6
1	B	262	ALA	2.5
1	B	302	GLY	2.5
1	A	124	LEU	2.5
1	A	253	GLU	2.4
1	B	232	ALA	2.4
1	B	263	ASN	2.4
1	B	204	GLN	2.4
1	A	215	SER	2.4
1	B	297	ASN	2.4
1	A	214	ASP	2.4
1	B	118(P)	LYS	2.4
1	A	219	THR	2.4
1	B	207	GLU	2.3
1	B	225	GLU	2.3
1	B	326	LYS	2.3
1	A	34	ASP	2.3
1	B	306	MET	2.2
1	B	288	THR	2.2
1	B	206	MET	2.2
1	A	12	ALA	2.2
1	B	214	ASP	2.2
1	A	35	THR	2.2
1	B	35	THR	2.2
1	B	175	GLU	2.2
1	A	33	PHE	2.2
1	B	216	GLY	2.1
1	A	220	ILE	2.1
1	B	135	SER	2.1
1	B	200	HIS	2.1
1	B	2	GLU	2.1
1	B	181	ASN	2.0
1	A	250	ASP	2.0
1	B	78(P)	HIS	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.