



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2017 – 09:59 AM EDT

PDB ID : 2NQO  
Title : Crystal Structure of Helicobacter pylori gamma-Glutamyltranspeptidase  
Authors : Boanca, G.; Sand, A.; Okada, T.; Suzuki, H.; Kumagai, H.; Fukuyama, K.; Barycki, J.J.  
Deposited on : unknown  
Resolution : 1.90 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20030345

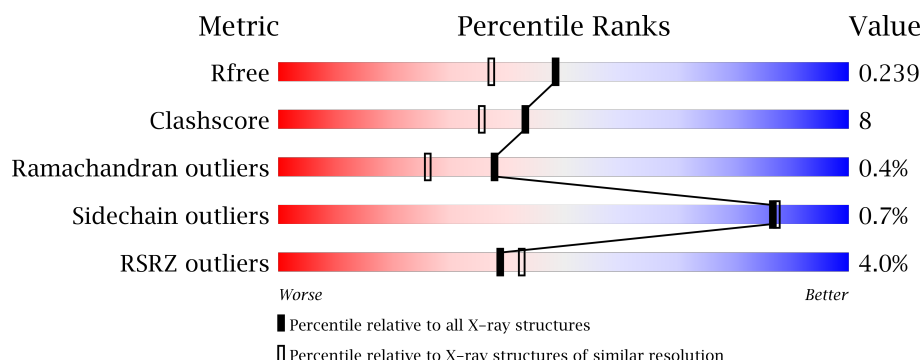
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
$R_{free}$	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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.

Mol	Chain	Length	Quality of chain
1	A	376	<div> <div>7%</div> <div> <div></div> <div>76%</div> <div>16%</div> <div>8%</div> </div> </div>
1	C	376	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>12%</div> <div>7%</div> </div> </div>
2	B	188	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>22%</div> <div>..</div> </div> </div>
2	D	188	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>18%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8679 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 Gamma-glutamyltranspeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	347	Total	C	N	O	S	0	0	0
			2625	1674	450	492	9			
1	C	349	Total	C	N	O	S	0	0	0
			2646	1683	455	499	9			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	MET	-	CLONING ARTIFACT	UNP O25743
A	5	GLY	-	CLONING ARTIFACT	UNP O25743
A	6	SER	-	CLONING ARTIFACT	UNP O25743
A	7	SER	-	CLONING ARTIFACT	UNP O25743
A	8	HIS	-	CLONING ARTIFACT	UNP O25743
A	9	HIS	-	CLONING ARTIFACT	UNP O25743
A	10	HIS	-	CLONING ARTIFACT	UNP O25743
A	11	HIS	-	CLONING ARTIFACT	UNP O25743
A	12	HIS	-	CLONING ARTIFACT	UNP O25743
A	13	HIS	-	CLONING ARTIFACT	UNP O25743
A	14	SER	-	CLONING ARTIFACT	UNP O25743
A	15	SER	-	CLONING ARTIFACT	UNP O25743
A	16	GLY	-	CLONING ARTIFACT	UNP O25743
A	17	LEU	-	CLONING ARTIFACT	UNP O25743
A	18	VAL	-	CLONING ARTIFACT	UNP O25743
A	19	PRO	-	CLONING ARTIFACT	UNP O25743
A	20	ARG	-	CLONING ARTIFACT	UNP O25743
A	21	GLY	-	CLONING ARTIFACT	UNP O25743
A	22	SER	-	CLONING ARTIFACT	UNP O25743
A	23	HIS	-	CLONING ARTIFACT	UNP O25743
A	24	MET	-	CLONING ARTIFACT	UNP O25743
A	25	ALA	-	CLONING ARTIFACT	UNP O25743
A	26	SER	-	CLONING ARTIFACT	UNP O25743
C	4	MET	-	CLONING ARTIFACT	UNP O25743
C	5	GLY	-	CLONING ARTIFACT	UNP O25743

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Chain	Residue	Modelled	Actual	Comment	Reference
C	6	SER	-	CLONING ARTIFACT	UNP O25743
C	7	SER	-	CLONING ARTIFACT	UNP O25743
C	8	HIS	-	CLONING ARTIFACT	UNP O25743
C	9	HIS	-	CLONING ARTIFACT	UNP O25743
C	10	HIS	-	CLONING ARTIFACT	UNP O25743
C	11	HIS	-	CLONING ARTIFACT	UNP O25743
C	12	HIS	-	CLONING ARTIFACT	UNP O25743
C	13	HIS	-	CLONING ARTIFACT	UNP O25743
C	14	SER	-	CLONING ARTIFACT	UNP O25743
C	15	SER	-	CLONING ARTIFACT	UNP O25743
C	16	GLY	-	CLONING ARTIFACT	UNP O25743
C	17	LEU	-	CLONING ARTIFACT	UNP O25743
C	18	VAL	-	CLONING ARTIFACT	UNP O25743
C	19	PRO	-	CLONING ARTIFACT	UNP O25743
C	20	ARG	-	CLONING ARTIFACT	UNP O25743
C	21	GLY	-	CLONING ARTIFACT	UNP O25743
C	22	SER	-	CLONING ARTIFACT	UNP O25743
C	23	HIS	-	CLONING ARTIFACT	UNP O25743
C	24	MET	-	CLONING ARTIFACT	UNP O25743
C	25	ALA	-	CLONING ARTIFACT	UNP O25743
C	26	SER	-	CLONING ARTIFACT	UNP O25743

- Molecule 2 is a protein called Gamma-glutamyltranspeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	186	Total	C	N	O	S	0	0	0
			1405	889	238	271	7			
2	D	186	Total	C	N	O	S	0	0	0
			1413	895	240	271	7			

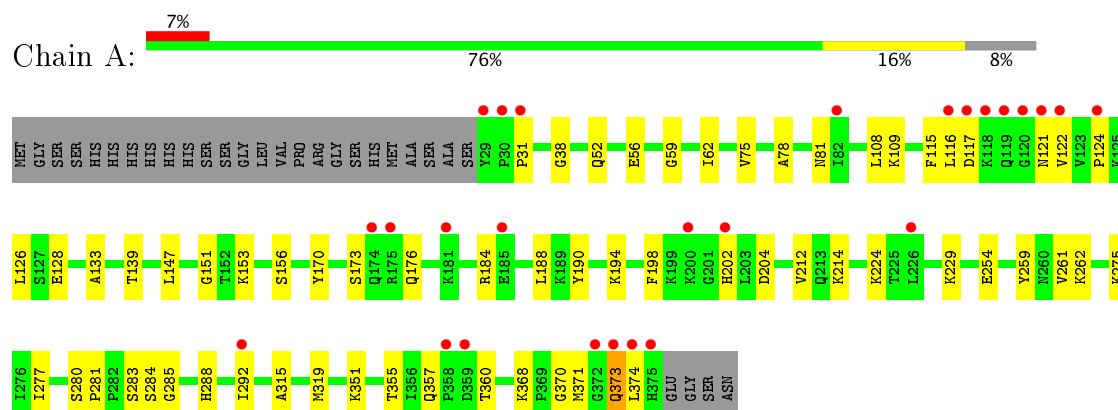
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	124	Total	O	0	0
			124	124		
3	B	97	Total	O	0	0
			97	97		
3	C	239	Total	O	0	0
			239	239		
3	D	130	Total	O	0	0
			130	130		

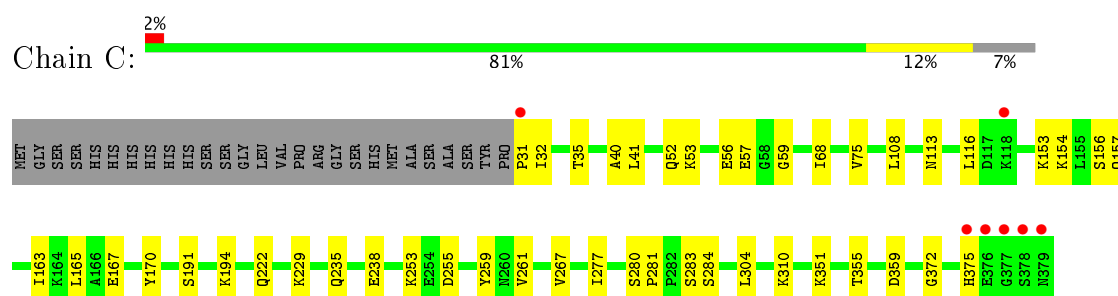
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

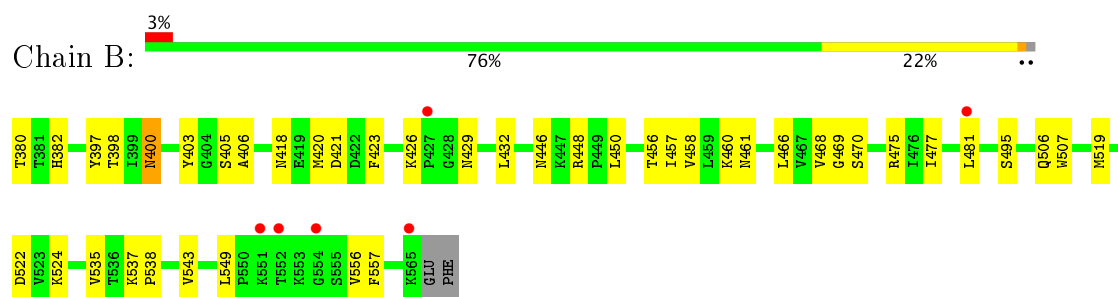
#### • Molecule 1: Gamma-glutamyltranspeptidase



#### • Molecule 1: Gamma-glutamyltranspeptidase

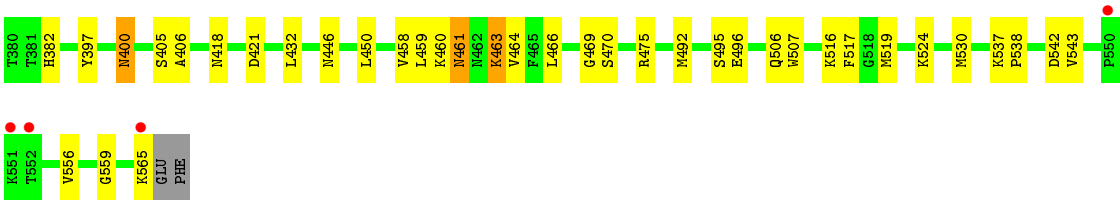


#### • Molecule 2: Gamma-glutamyltranspeptidase



#### • Molecule 2: Gamma-glutamyltranspeptidase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.35Å 105.21Å 91.06Å 90.00° 91.99° 90.00°	Depositor
Resolution (Å)	28.19 – 1.90 28.19 – 1.91	Depositor EDS
% Data completeness (in resolution range)	91.5 (28.19-1.90) 91.7 (28.19-1.91)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.65 (at 1.91Å)	Xtriage
Refinement program	CNS, REFMAC	Depositor
R, $R_{free}$	0.197 , 0.239 0.197 , 0.239	Depositor DCC
$R_{free}$ test set	7385 reflections (10.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.9	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 52.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8679	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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	0.28	0/2672	0.56	0/3600
1	C	0.31	0/2693	0.61	0/3624
2	B	0.31	0/1434	0.65	0/1952
2	D	0.33	0/1442	0.68	0/1960
All	All	0.30	0/8241	0.61	0/11136

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	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	259	TYR	Sidechain
1	C	259	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	A	2625	0	2685	51	0
1	C	2646	0	2702	34	0
2	B	1405	0	1392	33	0
2	D	1413	0	1414	29	0
3	A	124	0	0	3	0
3	B	97	0	0	0	0
3	C	239	0	0	3	0
3	D	130	0	0	1	0
All	All	8679	0	8193	125	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 8.

All (125) 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:D:463:LYS:HE3	2:D:464:VAL:H	1.14	1.07
2:D:463:LYS:HE3	2:D:464:VAL:N	1.77	1.00
1:C:154:LYS:HD2	1:C:157:GLN:HE22	1.38	0.88
1:C:32:ILE:HD11	1:C:41:LEU:HD21	1.58	0.86
1:A:275:LYS:HE2	1:A:277:ILE:HD11	1.61	0.83
1:A:31:PRO:HG3	2:B:495:SER:HB2	1.62	0.80
1:A:292:ILE:HG21	2:B:481:LEU:HD11	1.65	0.77
1:A:373:GLN:HG2	1:A:374:LEU:H	1.52	0.72
1:C:52:GLN:O	1:C:56:GLU:HG3	1.93	0.69
2:D:460:LYS:HG3	2:D:460:LYS:O	1.94	0.68
1:A:108:LEU:HD23	2:B:446:ASN:HD21	1.60	0.67
2:B:519:MET:SD	2:B:524:LYS:HG2	2.34	0.66
1:A:292:ILE:CG2	2:B:481:LEU:HD11	2.25	0.66
2:B:470:SER:HB2	2:B:543:VAL:HG22	1.78	0.65
1:A:108:LEU:CD2	2:B:446:ASN:HD21	2.12	0.62
1:C:31:PRO:HG3	2:D:495:SER:HB2	1.82	0.61
2:D:460:LYS:O	2:D:461:ASN:HB2	2.01	0.61
2:B:382:HIS:CE1	2:B:469:GLY:HA3	2.36	0.61
2:D:400:ASN:HB3	2:D:418:ASN:OD1	2.02	0.60
1:A:31:PRO:HG3	2:B:495:SER:CB	2.32	0.59
1:A:373:GLN:HG2	1:A:374:LEU:N	2.18	0.59
1:A:75:VAL:HA	1:A:170:TYR:CZ	2.38	0.58
1:C:32:ILE:CD1	1:C:41:LEU:HD21	2.32	0.57
1:A:52:GLN:O	1:A:56:GLU:HG3	2.04	0.57
1:C:35:THR:HG22	2:D:556:VAL:HA	1.87	0.56
1:A:285:GLY:HA2	2:B:477:ILE:HG12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:351:LYS:O	1:C:355:THR:HG23	2.06	0.56
2:B:458:VAL:HB	2:B:466:LEU:HB2	1.87	0.56
1:C:372:GLY:HA2	1:C:375:HIS:CD2	2.41	0.56
1:A:188:LEU:O	1:A:194:LYS:HD2	2.06	0.55
1:C:154:LYS:HD2	1:C:157:GLN:NE2	2.17	0.55
1:A:198:PHE:HB3	1:A:202:HIS:HA	1.87	0.54
1:A:357:GLN:HB2	1:A:360:THR:HG22	1.89	0.54
1:C:108:LEU:HD23	2:D:446:ASN:OD1	2.06	0.54
1:A:281:PRO:HA	1:A:283:SER:N	2.23	0.54
1:C:229:LYS:HG3	3:C:567:HOH:O	2.07	0.53
2:B:380:THR:HA	2:B:398:THR:HB	1.90	0.53
2:D:565:LYS:HD3	3:D:584:HOH:O	2.08	0.53
1:A:117:ASP:OD2	1:A:121:ASN:HB2	2.09	0.53
1:A:357:GLN:CB	1:A:360:THR:HG22	2.39	0.53
1:A:190:TYR:O	1:A:194:LYS:HG3	2.11	0.51
1:C:163:ILE:O	1:C:167:GLU:HG3	2.10	0.51
1:C:59:GLY:CA	1:C:153:LYS:HE3	2.40	0.51
1:C:156:SER:HB3	1:C:157:GLN:OE1	2.10	0.51
1:C:277:ILE:HD11	2:D:459:LEU:HD11	1.91	0.51
1:A:262:LYS:HG3	2:B:448:ARG:NH2	2.26	0.51
2:D:542:ASP:OD1	2:D:565:LYS:HB2	2.11	0.51
2:D:537:LYS:HB3	2:D:538:PRO:HD2	1.92	0.51
1:C:277:ILE:HD11	2:D:459:LEU:CD1	2.41	0.50
1:C:41:LEU:HD11	2:D:559:GLY:HA3	1.92	0.50
2:B:426:LYS:O	2:B:429:ASN:HB3	2.11	0.50
2:D:421:ASP:OD2	2:D:432:LEU:HG	2.11	0.50
1:A:128:GLU:OE1	2:B:432:LEU:HD21	2.12	0.49
1:A:116:LEU:HD23	1:A:122:VAL:HA	1.94	0.49
2:D:516:LYS:HE2	2:D:517:PHE:CZ	2.48	0.49
1:A:133:ALA:O	2:B:418:ASN:HA	2.12	0.49
1:C:53:LYS:O	1:C:57:GLU:HG3	2.11	0.49
1:A:184:ARG:O	1:A:188:LEU:HG	2.12	0.49
2:D:458:VAL:HB	2:D:466:LEU:HB2	1.95	0.49
1:C:284:SER:HB3	2:D:450:LEU:HD11	1.95	0.48
2:D:519:MET:SD	2:D:524:LYS:HG2	2.53	0.48
1:A:62:ILE:HD12	1:A:62:ILE:N	2.28	0.48
1:A:115:PHE:HA	1:A:126:LEU:HD23	1.96	0.48
2:D:537:LYS:HB3	2:D:538:PRO:CD	2.43	0.48
2:B:400:ASN:HB3	2:B:418:ASN:OD1	2.14	0.47
1:C:53:LYS:HD3	3:C:494:HOH:O	2.14	0.47
2:D:460:LYS:O	2:D:461:ASN:CB	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:420:MET:O	2:B:423:PHE:HB2	2.15	0.47
2:B:537:LYS:HB3	2:B:538:PRO:HD2	1.96	0.47
2:D:506:GLN:O	2:D:507:TRP:HB3	2.14	0.47
1:C:222:GLN:NE2	1:C:235:GLN:OE1	2.48	0.46
2:D:470:SER:HB2	2:D:543:VAL:HG22	1.95	0.46
1:A:38:GLY:HA2	2:B:557:PHE:CD2	2.51	0.46
2:B:537:LYS:HB3	2:B:538:PRO:CD	2.46	0.46
2:D:382:HIS:CE1	2:D:469:GLY:HA3	2.49	0.46
1:A:108:LEU:HD13	1:A:254:GLU:OE2	2.16	0.46
2:D:492:MET:HB3	2:D:496:GLU:HB2	1.98	0.45
1:C:191:SER:HA	1:C:194:LYS:HE3	1.97	0.45
1:A:373:GLN:CG	1:A:374:LEU:H	2.21	0.45
1:A:108:LEU:HD23	2:B:446:ASN:ND2	2.30	0.45
1:C:75:VAL:HA	1:C:170:TYR:CZ	2.51	0.45
1:A:59:GLY:CA	1:A:153:LYS:HE3	2.47	0.45
1:C:304:LEU:HD12	1:C:310:LYS:HB3	1.99	0.45
1:C:310:LYS:C	1:C:310:LYS:HD3	2.38	0.44
1:A:184:ARG:HG3	1:A:184:ARG:HH11	1.82	0.44
1:A:156:SER:HA	1:A:224:LYS:HG3	1.99	0.44
2:D:463:LYS:CE	2:D:464:VAL:H	2.04	0.44
1:A:368:LYS:HE2	3:A:469:HOH:O	2.16	0.44
2:B:405:SER:O	2:B:406:ALA:HB3	2.18	0.44
1:C:238:GLU:OE2	1:C:253:LYS:HD2	2.17	0.44
1:A:198:PHE:HE1	1:A:204:ASP:OD1	2.01	0.44
1:A:109:LYS:O	1:A:109:LYS:HG3	2.16	0.44
1:C:267:VAL:HG13	1:C:280:SER:HB3	1.99	0.43
2:D:463:LYS:CE	2:D:464:VAL:N	2.65	0.43
1:A:351:LYS:O	1:A:355:THR:HG23	2.18	0.43
1:A:370:GLY:O	1:A:371:MET:HB2	2.18	0.43
1:C:113:ASN:HB3	1:C:116:LEU:HD12	2.00	0.43
1:A:261:VAL:HG22	3:A:503:HOH:O	2.19	0.43
1:C:108:LEU:HG	1:C:255:ASP:OD1	2.18	0.43
1:C:75:VAL:CG1	1:C:165:LEU:HD13	2.49	0.43
1:A:81:ASN:O	1:A:139:THR:HG21	2.19	0.42
1:A:147:LEU:HD12	1:A:151:GLY:HA3	2.00	0.42
2:B:481:LEU:HD23	2:B:481:LEU:C	2.39	0.42
1:C:281:PRO:HA	1:C:283:SER:N	2.34	0.42
1:C:40:ALA:HB1	1:C:68:ILE:HD11	2.02	0.42
1:A:212:VAL:HG11	1:A:214:LYS:HE2	2.01	0.42
2:B:506:GLN:O	2:B:507:TRP:HB3	2.20	0.42
1:A:284:SER:HB3	2:B:450:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:460:LYS:O	2:B:461:ASN:HB2	2.20	0.42
2:D:405:SER:O	2:D:406:ALA:HB3	2.20	0.42
2:B:421:ASP:OD2	2:B:432:LEU:HG	2.20	0.41
2:B:468:VAL:HG22	2:B:469:GLY:N	2.35	0.41
2:B:456:THR:HG22	2:B:457:ILE:N	2.35	0.41
2:B:535:VAL:HG23	2:B:535:VAL:O	2.21	0.41
1:C:359:ASP:O	2:D:530:MET:HG2	2.21	0.41
1:A:173:SER:OG	1:A:176:GLN:HG3	2.21	0.41
1:A:280:SER:HB2	1:A:281:PRO:CD	2.50	0.40
1:C:261:VAL:HG22	3:C:536:HOH:O	2.21	0.40
1:A:229:LYS:HG3	3:A:497:HOH:O	2.20	0.40
1:A:315:ALA:O	1:A:319:MET:HG3	2.22	0.40
1:A:262:LYS:HE2	1:A:262:LYS:HB3	1.99	0.40
1:A:78:ALA:HB2	2:B:403:TYR:CZ	2.56	0.40
1:A:122:VAL:O	1:A:124:PRO:HD3	2.21	0.40
1:A:288:HIS:O	1:A:292:ILE:HG13	2.21	0.40
2:B:549:LEU:HB2	2:B:556:VAL:CG1	2.52	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	345/376 (92%)	329 (95%)	15 (4%)	1 (0%)	44	34
1	C	347/376 (92%)	337 (97%)	10 (3%)	0	100	100
2	B	184/188 (98%)	177 (96%)	6 (3%)	1 (0%)	32	20
2	D	184/188 (98%)	174 (95%)	8 (4%)	2 (1%)	17	6
All	All	1060/1128 (94%)	1017 (96%)	39 (4%)	4 (0%)	38	26

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	373	GLN
2	B	400	ASN
2	D	461	ASN
2	D	400	ASN

### 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	272/297 (92%)	272 (100%)	0	100	100
1	C	275/297 (93%)	275 (100%)	0	100	100
2	B	155/159 (98%)	152 (98%)	3 (2%)	62	57
2	D	157/159 (99%)	154 (98%)	3 (2%)	62	57
All	All	859/912 (94%)	853 (99%)	6 (1%)	87	87

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	397	TYR
2	B	475	ARG
2	B	522	ASP
2	D	397	TYR
2	D	463	LYS
2	D	475	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	GLN
1	A	168	ASN
2	B	446	ASN
2	B	461	ASN
2	B	462	ASN
1	C	168	ASN
1	C	174	GLN

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Mol	Chain	Res	Type
1	C	233	GLN
1	C	379	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	347/376 (92%)	0.46	26 (7%) 15 17	21, 35, 55, 73	0
1	C	349/376 (92%)	-0.04	7 (2%) 65 69	15, 27, 42, 74	0
2	B	186/188 (98%)	0.30	6 (3%) 48 51	20, 30, 51, 68	0
2	D	186/188 (98%)	0.07	4 (2%) 62 66	15, 23, 42, 60	0
All	All	1068/1128 (94%)	0.20	43 (4%) 39 43	15, 29, 51, 74	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	375	HIS	6.7
1	A	29	TYR	5.2
2	B	552	THR	5.1
1	A	122	VAL	4.7
1	A	373	GLN	4.7
1	C	378	SER	4.6
1	A	374	LEU	4.6
1	A	30	PRO	4.3
1	C	31	PRO	4.1
1	C	379	ASN	3.9
1	A	116	LEU	3.8
1	A	124	PRO	3.5
2	D	552	THR	3.5
1	A	119	GLN	3.5
1	A	175	ARG	3.4
1	A	120	GLY	3.4
2	B	565	LYS	3.3
1	A	200	LYS	3.2
1	A	226	LEU	3.2
1	A	372	GLY	3.0
1	A	31	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	118	LYS	2.8
1	A	118	LYS	2.8
1	C	375	HIS	2.7
1	A	121	ASN	2.7
2	D	565	LYS	2.7
2	B	554	GLY	2.7
1	C	377	GLY	2.6
2	B	551	LYS	2.4
2	B	481	LEU	2.4
2	D	551	LYS	2.4
1	A	181	LYS	2.4
1	A	359	ASP	2.3
2	B	427	PRO	2.3
1	A	185	GLU	2.2
1	A	292	ILE	2.2
1	A	358	PRO	2.1
2	D	550	PRO	2.1
1	A	202	HIS	2.1
1	C	376	GLU	2.1
1	A	82	ILE	2.1
1	A	117	ASP	2.1
1	A	174	GLN	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.