



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:46 AM GMT

PDB ID : 2IOB  
Title : E. coli Bifunctional glutathionylspermidine synthetase/amidase Apo protein  
Authors : Pai, C.H.; Chiang, B.Y.; Ko, T.P.; Chou, C.C.; Chong, C.M.; Yen, F.J.; Coward, J.K.; Wang, A.H.-J.; Lin, C.H.  
Deposited on : 2006-10-10  
Resolution : 2.20 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

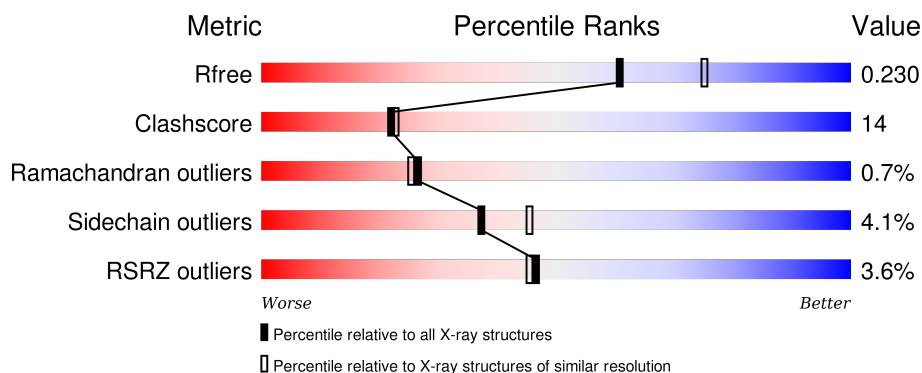
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	619	<div> <div>3%</div> <div> <div></div> <div>69%</div> <div>20%</div> <div>•• 8%</div> </div> </div>
1	B	619	<div> <div>4%</div> <div> <div></div> <div>69%</div> <div>21%</div> <div>• 6%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10550 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 Bifunctional glutathionylspermidine synthetase/amidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	571	Total	C	N	O	S	0	0	0
			4623	2964	787	854	18			
1	B	582	Total	C	N	O	S	0	0	0
			4703	3014	799	872	18			

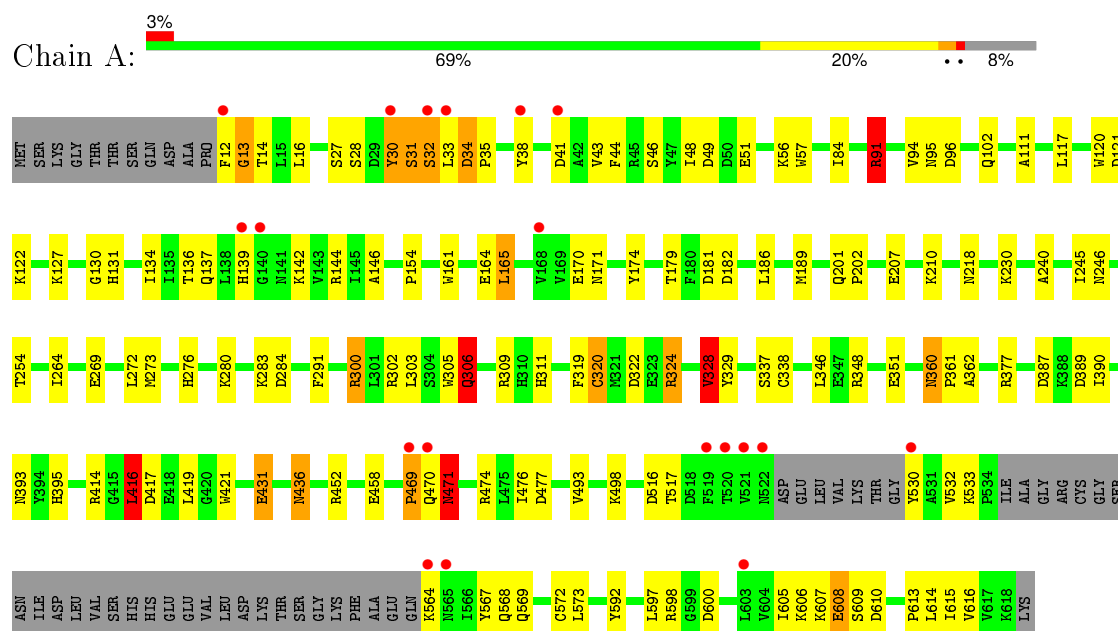
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	596	Total	O	0	0
			596	596		
2	B	628	Total	O	0	0
			628	628		

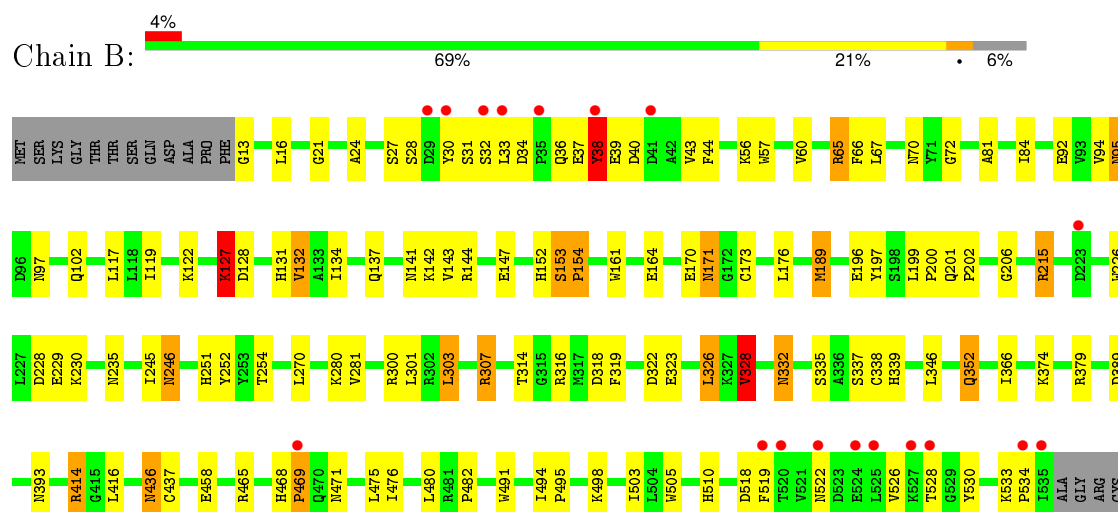
### 3 Residue-property plots

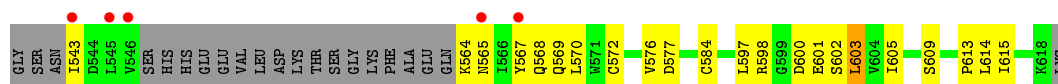
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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



- Molecule 1: Bifunctional glutathionylspermidine synthetase/amidase





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	149.27Å 92.96Å 108.30Å 90.00° 109.37° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 46.77 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.20) 94.7 (46.77-2.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.32 (at 2.20Å)	Xtriage
Refinement program	XTALVIEW	Depositor
R, $R_{free}$	0.175 , 0.236 0.172 , 0.230	Depositor DCC
$R_{free}$ test set	3430 reflections (5.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.8	Xtriage
Anisotropy	0.472	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 63.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 67392 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10550	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.76% 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	0.89	3/4744 (0.1%)	0.94	11/6445 (0.2%)
1	B	0.89	3/4823 (0.1%)	0.92	9/6553 (0.1%)
All	All	0.89	6/9567 (0.1%)	0.93	20/12998 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	189	MET	SD-CE	-6.37	1.42	1.77
1	A	320	CYS	CB-SG	6.06	1.92	1.82
1	A	306	GLN	CB-CG	-6.03	1.36	1.52
1	B	328	VAL	CB-CG2	-5.63	1.41	1.52
1	B	601	GLU	CD-OE2	5.25	1.31	1.25
1	A	471	ASN	CB-CG	5.23	1.63	1.51

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	65	ARG	NE-CZ-NH2	-12.79	113.91	120.30
1	B	414	ARG	NE-CZ-NH1	8.84	124.72	120.30
1	A	300	ARG	NE-CZ-NH1	-7.79	116.41	120.30
1	A	328	VAL	CB-CA-C	-7.09	97.94	111.40
1	B	65	ARG	NE-CZ-NH1	7.03	123.81	120.30
1	B	414	ARG	NE-CZ-NH2	-6.43	117.08	120.30
1	A	165	LEU	CA-CB-CG	6.18	129.51	115.30
1	B	322	ASP	CB-CG-OD2	5.78	123.50	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	VAL	CB-CA-C	-5.61	100.75	111.40
1	A	300	ARG	NE-CZ-NH2	5.53	123.06	120.30
1	A	416	LEU	CA-CB-CG	-5.52	102.61	115.30
1	B	328	VAL	CB-CA-C	-5.49	100.97	111.40
1	A	91	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	130	GLY	N-CA-C	-5.42	99.55	113.10
1	A	284	ASP	CB-CG-OD1	5.26	123.03	118.30
1	B	189	MET	CG-SD-CE	-5.23	91.83	100.20
1	A	302	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	A	387	ASP	CB-CG-OD1	5.09	122.88	118.30
1	B	65	ARG	CG-CD-NE	-5.08	101.13	111.80
1	A	598	ARG	NE-CZ-NH1	-5.00	117.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	567	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	4623	0	4486	136	0
1	B	4703	0	4576	123	0
2	A	596	0	0	13	0
2	B	628	0	0	25	0
All	All	10550	0	9062	256	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 14.

All (256) 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:B:24:ALA:O	1:B:65:ARG:NH2	2.00	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:SER:HG	1:A:30:TYR:HE1	1.11	0.92
1:A:269:GLU:HG2	1:A:273:MET:CE	1.99	0.92
1:A:269:GLU:HG2	1:A:273:MET:HE2	1.51	0.91
1:B:534:PRO:HA	1:B:565:ASN:ND2	1.86	0.89
1:A:516:ASP:H	1:A:569:GLN:HE21	0.90	0.88
1:B:316:ARG:HD3	1:B:584:CYS:HB3	1.58	0.83
1:B:533:LYS:HG2	1:B:543:ILE:HD12	1.63	0.80
1:A:33:LEU:HG	1:A:34:ASP:H	1.48	0.79
1:A:516:ASP:H	1:A:569:GLN:NE2	1.76	0.78
1:A:416:LEU:HD23	1:A:419:LEU:HD12	1.64	0.78
1:B:84:ILE:HG22	1:B:189:MET:CE	2.14	0.78
1:A:280:LYS:HE2	2:A:841:HOH:O	1.83	0.78
1:A:84:ILE:HG22	1:A:189:MET:CE	2.14	0.78
1:A:322:ASP:OD2	1:A:324:ARG:NH1	2.18	0.77
1:B:229:GLU:O	1:B:235:ASN:HB2	1.84	0.77
1:B:142:LYS:HE3	1:B:164:GLU:HG2	1.65	0.77
1:A:516:ASP:N	1:A:569:GLN:HE21	1.75	0.75
1:B:28:SER:H	1:B:152:HIS:HE1	1.33	0.74
1:B:40:ASP:O	1:B:43:VAL:HG22	1.90	0.71
1:B:303:LEU:HD13	1:B:307:ARG:NH1	2.05	0.71
1:A:139:HIS:ND1	1:A:144:ARG:NH2	2.38	0.71
1:A:84:ILE:HG22	1:A:189:MET:HE1	1.74	0.69
1:B:543:ILE:HG12	2:B:900:HOH:O	1.92	0.69
1:A:41:ASP:HB3	1:A:43:VAL:HG22	1.74	0.68
1:B:332:ASN:HD21	1:B:335:SER:H	1.41	0.68
1:B:141:ASN:HB3	2:B:662:HOH:O	1.94	0.68
1:B:144:ARG:HD3	1:B:161:TRP:CD1	2.29	0.67
1:B:13:GLY:N	2:B:940:HOH:O	2.26	0.67
1:A:311:HIS:HE2	1:A:377:ARG:NH2	1.91	0.67
1:A:170:GLU:HG2	1:A:171:ASN:ND2	2.10	0.66
1:B:84:ILE:HG22	1:B:189:MET:HE1	1.75	0.66
1:B:576:VAL:O	2:B:1069:HOH:O	2.13	0.65
1:A:606:LYS:CD	1:A:607:LYS:H	2.09	0.65
1:A:144:ARG:HD2	1:A:161:TRP:CD1	2.31	0.65
1:A:306:GLN:NE2	2:A:1036:HOH:O	2.29	0.65
1:B:84:ILE:HG22	1:B:189:MET:HE3	1.78	0.65
1:A:606:LYS:NZ	1:A:607:LYS:NZ	2.45	0.64
1:A:393:ASN:HD21	1:A:414:ARG:HE	1.45	0.64
1:A:171:ASN:HA	2:A:837:HOH:O	1.97	0.64
1:B:534:PRO:HA	1:B:565:ASN:HD22	1.62	0.64
1:B:534:PRO:HD2	1:B:543:ILE:HD13	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:SER:OG	1:A:30:TYR:HE1	1.80	0.64
1:A:121:ASP:OD1	1:A:122:LYS:N	2.28	0.63
1:A:322:ASP:OD1	1:A:324:ARG:HG3	1.99	0.63
1:A:564:LYS:HE3	2:A:1137:HOH:O	1.98	0.63
1:A:329:TYR:HE1	1:A:573:LEU:HD21	1.63	0.63
1:A:181:ASP:HB2	2:A:939:HOH:O	1.98	0.63
1:A:269:GLU:HG2	1:A:273:MET:HE1	1.79	0.62
1:B:28:SER:H	1:B:152:HIS:CE1	2.15	0.62
1:B:95:ASN:ND2	2:B:864:HOH:O	2.32	0.61
1:A:606:LYS:HD2	1:A:607:LYS:H	1.65	0.61
1:A:84:ILE:HG22	1:A:189:MET:HE3	1.81	0.61
1:B:300:ARG:NH1	2:B:1181:HOH:O	2.34	0.61
1:B:498:LYS:HE3	1:B:534:PRO:O	2.00	0.60
1:B:494:ILE:HB	1:B:495:PRO:HD3	1.84	0.60
1:A:303:LEU:HD21	1:B:72:GLY:HA3	1.83	0.60
1:A:12:PHE:CG	1:A:13:GLY:N	2.62	0.60
1:B:119:ILE:CD1	1:B:132:VAL:HG13	2.32	0.59
1:B:366:ILE:HG12	2:B:1143:HOH:O	2.03	0.59
1:A:240:ALA:HB2	1:A:390:ILE:HG22	1.84	0.58
1:B:122:LYS:HB2	1:B:127:LYS:O	2.02	0.58
1:A:431:GLU:HG2	2:A:1103:HOH:O	2.03	0.58
1:B:21:GLY:HA3	1:B:70:ASN:HD21	1.68	0.58
1:A:416:LEU:HD23	1:A:419:LEU:CD1	2.33	0.58
1:B:465:ARG:HD3	2:B:1016:HOH:O	2.03	0.58
1:B:605:ILE:HG23	1:B:609:SER:OG	2.03	0.58
1:B:34:ASP:OD2	1:B:36:GLN:HB3	2.03	0.57
1:B:246:ASN:H	1:B:246:ASN:HD22	1.52	0.57
1:A:31:SER:O	1:A:33:LEU:N	2.38	0.57
1:B:206:GLY:O	1:B:323:GLU:HA	2.05	0.56
1:A:416:LEU:HD13	2:A:976:HOH:O	2.05	0.56
1:A:121:ASP:HB2	1:A:186:LEU:HG	1.88	0.56
1:B:81:ALA:HB1	1:B:132:VAL:HG22	1.87	0.55
1:B:436:ASN:HD22	1:B:436:ASN:C	2.10	0.55
1:A:469:PRO:CB	1:A:470:GLN:HE22	2.19	0.55
1:B:572:CYS:HB3	1:B:603:LEU:HD21	1.88	0.55
1:B:603:LEU:HD22	2:B:790:HOH:O	2.07	0.55
1:A:38:TYR:HA	1:A:44:PHE:CD1	2.42	0.55
1:A:207:GLU:OE2	1:A:210:LYS:HE2	2.06	0.54
1:B:173:CYS:HB2	2:B:742:HOH:O	2.07	0.54
1:A:38:TYR:HA	1:A:44:PHE:CE1	2.43	0.54
1:A:474:ARG:HB2	1:A:477:ASP:OD2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:HIS:HE1	1:B:577:ASP:OD2	1.90	0.54
1:B:498:LYS:HG2	2:B:764:HOH:O	2.06	0.54
1:B:600:ASP:OD1	1:B:602:SER:HB3	2.08	0.54
1:A:606:LYS:HZ1	1:A:607:LYS:NZ	2.06	0.53
1:B:92:GLU:HG2	2:B:864:HOH:O	2.07	0.53
1:B:27:SER:HB2	1:B:152:HIS:ND1	2.23	0.53
1:B:66:PHE:CE2	1:B:134:ILE:HG21	2.43	0.53
1:A:606:LYS:NZ	1:A:607:LYS:HZ1	2.05	0.53
1:A:606:LYS:HZ1	1:A:607:LYS:HZ1	1.55	0.53
1:B:316:ARG:HD2	1:B:318:ASP:OD1	2.07	0.53
1:A:517:THR:HG23	1:A:568:GLN:HB2	1.90	0.53
1:B:131:HIS:HE1	1:B:147:GLU:OE1	1.92	0.53
1:B:143:VAL:HG21	1:B:176:LEU:HD21	1.91	0.53
1:A:320:CYS:HB2	1:A:329:TYR:CZ	2.44	0.52
1:B:131:HIS:HD2	2:B:879:HOH:O	1.92	0.52
1:B:568:GLN:HG2	2:B:1117:HOH:O	2.10	0.52
1:B:228:ASP:OD1	1:B:230:LYS:N	2.35	0.52
1:B:337:SER:O	1:B:338:CYS:HB2	2.08	0.52
1:B:522:ASN:O	1:B:526:VAL:HG23	2.09	0.52
1:A:606:LYS:NZ	1:A:607:LYS:HZ2	2.08	0.52
1:B:280:LYS:HD3	1:B:503:ILE:HG23	1.90	0.52
1:B:60:VAL:HG12	2:B:685:HOH:O	2.09	0.52
1:B:30:TYR:O	1:B:33:LEU:HB2	2.09	0.52
1:B:389:ASP:C	1:B:389:ASP:OD2	2.46	0.52
1:A:469:PRO:CB	1:A:470:GLN:NE2	2.73	0.51
1:A:139:HIS:CG	1:A:144:ARG:HH21	2.27	0.51
1:A:245:ILE:HG23	1:A:246:ASN:N	2.25	0.51
1:A:606:LYS:O	1:A:609:SER:HB2	2.10	0.51
1:B:352:GLN:NE2	1:B:352:GLN:HA	2.26	0.51
1:A:96:ASP:O	1:A:276:HIS:CE1	2.63	0.51
1:B:31:SER:C	1:B:33:LEU:H	2.14	0.51
1:A:56:LYS:HD3	1:A:57:TRP:CZ2	2.45	0.51
1:B:56:LYS:NZ	2:B:682:HOH:O	2.44	0.51
1:B:300:ARG:NH2	1:B:482:PRO:HG3	2.27	0.50
1:B:171:ASN:ND2	1:B:171:ASN:O	2.44	0.50
1:B:119:ILE:HD13	1:B:132:VAL:HG13	1.93	0.50
1:B:122:LYS:NZ	2:B:886:HOH:O	2.43	0.50
1:B:393:ASN:OD1	1:B:414:ARG:NH1	2.45	0.50
1:A:324:ARG:HH11	1:A:324:ARG:CG	2.25	0.50
1:A:498:LYS:HD3	1:A:533:LYS:HD3	1.94	0.50
1:A:96:ASP:O	1:A:276:HIS:HE1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:ILE:HG23	1:B:246:ASN:N	2.27	0.49
1:A:361:PRO:HD3	1:A:616:VAL:HG23	1.94	0.49
1:B:171:ASN:C	1:B:171:ASN:HD22	2.15	0.49
1:A:91:ARG:HD3	1:A:272:LEU:HD21	1.94	0.49
1:A:305:TRP:CH2	1:A:309:ARG:HD3	2.47	0.49
1:A:56:LYS:HB3	1:A:57:TRP:CE2	2.46	0.49
1:A:51:GLU:OE1	1:A:91:ARG:NH2	2.46	0.49
1:A:476:ILE:O	1:A:476:ILE:HG13	2.12	0.49
1:B:228:ASP:OD1	1:B:228:ASP:C	2.50	0.49
1:B:352:GLN:HE21	1:B:352:GLN:CA	2.25	0.49
1:A:142:LYS:HB3	1:A:164:GLU:HG2	1.95	0.49
1:A:254:THR:HA	1:A:615:ILE:O	2.13	0.48
1:A:30:TYR:O	1:A:32:SER:N	2.46	0.48
1:B:314:THR:OG1	1:B:339:HIS:HE1	1.95	0.48
1:A:532:VAL:HG22	1:A:567:TYR:CD2	2.48	0.48
1:A:30:TYR:N	1:A:30:TYR:CD1	2.79	0.48
1:B:246:ASN:N	1:B:246:ASN:HD22	2.09	0.48
1:A:324:ARG:HG3	1:A:324:ARG:HH11	1.78	0.48
1:B:303:LEU:HD13	1:B:307:ARG:HH11	1.76	0.48
1:A:16:LEU:HD21	1:A:27:SER:HB3	1.96	0.48
1:A:469:PRO:HB3	1:A:470:GLN:HE22	1.78	0.48
1:B:215:ARG:NH1	2:B:632:HOH:O	2.34	0.48
1:A:337:SER:O	1:A:338:CYS:HB2	2.14	0.48
1:A:117:LEU:HD23	1:A:134:ILE:CD1	2.44	0.48
1:A:240:ALA:CB	1:A:390:ILE:HG22	2.44	0.47
1:B:597:LEU:HG	1:B:614:LEU:HD22	1.95	0.47
1:A:56:LYS:HB3	1:A:57:TRP:CD2	2.49	0.47
1:B:332:ASN:HD22	1:B:332:ASN:C	2.18	0.47
1:A:137:GLN:NE2	1:B:458:GLU:OE2	2.46	0.47
1:B:56:LYS:HB3	1:B:57:TRP:CD2	2.49	0.47
1:A:319:PHE:CE2	1:A:328:VAL:HG13	2.49	0.47
1:B:94:VAL:HG23	2:B:923:HOH:O	2.14	0.47
1:B:319:PHE:CD2	1:B:326:LEU:HD22	2.49	0.47
1:A:30:TYR:O	1:A:31:SER:C	2.53	0.47
1:B:505:TRP:CH2	1:B:510:HIS:HA	2.50	0.47
1:A:33:LEU:HD12	2:A:1148:HOH:O	2.15	0.47
1:B:543:ILE:CG1	2:B:900:HOH:O	2.58	0.47
1:B:303:LEU:HD23	1:B:303:LEU:HA	1.73	0.46
1:A:458:GLU:O	1:B:137:GLN:HA	2.16	0.46
1:A:324:ARG:NH1	1:A:324:ARG:HG3	2.30	0.46
1:B:323:GLU:HG2	2:B:668:HOH:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:TYR:O	1:A:530:TYR:CG	2.67	0.46
1:A:597:LEU:HG	1:A:614:LEU:HD22	1.98	0.46
1:A:606:LYS:CG	1:A:607:LYS:N	2.78	0.46
1:A:56:LYS:HA	1:A:57:TRP:HA	1.74	0.46
1:A:102:GLN:O	1:A:189:MET:HA	2.15	0.46
1:A:393:ASN:ND2	1:A:414:ARG:HE	2.09	0.46
1:A:469:PRO:HD3	2:B:931:HOH:O	2.14	0.46
1:A:144:ARG:HD3	1:A:161:TRP:CE2	2.51	0.46
1:B:95:ASN:ND2	1:B:97:ASN:OD1	2.48	0.46
1:A:395:HIS:HE1	2:A:894:HOH:O	1.98	0.45
1:A:94:VAL:HG23	2:A:1006:HOH:O	2.16	0.45
1:B:352:GLN:NE2	1:B:352:GLN:CA	2.79	0.45
1:B:196:GLU:HG2	1:B:197:TYR:CD1	2.51	0.45
1:A:12:PHE:O	1:A:14:THR:N	2.50	0.45
1:A:360:ASN:ND2	1:A:362:ALA:H	2.14	0.45
1:B:530:TYR:HA	1:B:570:LEU:HG	1.99	0.45
1:A:322:ASP:CG	1:A:324:ARG:NH1	2.70	0.45
1:B:170:GLU:O	1:B:171:ASN:HB3	2.16	0.45
1:B:38:TYR:CD2	1:B:44:PHE:CE2	3.05	0.45
1:B:584:CYS:SG	1:B:598:ARG:HD3	2.56	0.45
1:A:532:VAL:HG22	1:A:567:TYR:HD2	1.82	0.45
1:B:270:LEU:HD13	1:B:328:VAL:CG2	2.47	0.45
1:B:603:LEU:CD2	2:B:790:HOH:O	2.65	0.45
1:A:111:ALA:HB2	1:A:174:TYR:CE1	2.52	0.45
1:B:518:ASP:OD1	1:B:519:PHE:N	2.50	0.45
1:B:92:GLU:CG	2:B:864:HOH:O	2.64	0.44
1:A:605:ILE:HG23	1:A:609:SER:CB	2.47	0.44
1:B:533:LYS:HG2	1:B:543:ILE:CD1	2.40	0.44
1:B:16:LEU:HD21	1:B:27:SER:HB3	1.99	0.44
1:B:416:LEU:HD21	1:B:475:LEU:HA	1.99	0.44
1:B:67:LEU:HD11	1:B:117:LEU:HD21	1.99	0.44
1:B:468:HIS:CG	1:B:469:PRO:HD2	2.53	0.44
1:A:165:LEU:CD2	1:A:179:THR:HG23	2.48	0.44
1:B:252:TYR:HB2	1:B:613:PRO:HB2	2.00	0.44
1:A:28:SER:HB2	1:A:57:TRP:O	2.18	0.44
1:A:91:ARG:CD	1:A:272:LEU:HD21	2.48	0.44
1:A:348:ARG:NE	1:A:348:ARG:HA	2.33	0.44
1:A:421:TRP:HE3	1:A:471:ASN:ND2	2.16	0.44
1:A:142:LYS:HB3	1:A:164:GLU:CG	2.48	0.44
1:A:120:TRP:HB2	1:A:131:HIS:HB3	2.00	0.44
1:A:33:LEU:HG	1:A:34:ASP:N	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:ARG:NH1	2:A:858:HOH:O	2.50	0.43
1:B:226:TRP:HB2	1:B:352:GLN:HG2	1.98	0.43
1:B:199:LEU:HA	1:B:200:PRO:HD3	1.87	0.43
1:A:136:THR:HG21	1:A:146:ALA:HB2	2.01	0.43
1:B:301:LEU:CD1	1:B:491:TRP:HA	2.49	0.43
1:A:324:ARG:NH2	1:A:572:CYS:O	2.49	0.43
1:A:417:ASP:HB2	2:A:1183:HOH:O	2.18	0.43
1:A:600:ASP:HB2	1:A:605:ILE:HD13	2.01	0.43
1:B:37:GLU:C	1:B:39:GLU:H	2.21	0.43
1:B:254:THR:HA	1:B:615:ILE:O	2.19	0.43
1:B:564:LYS:HA	1:B:564:LYS:HD2	1.81	0.43
1:B:31:SER:O	1:B:33:LEU:N	2.52	0.43
1:A:117:LEU:HD23	1:A:134:ILE:HD13	2.00	0.43
1:A:95:ASN:HB2	2:A:871:HOH:O	2.17	0.43
1:A:606:LYS:HG3	1:A:608:GLU:H	1.84	0.42
1:B:436:ASN:HD22	1:B:437:CYS:N	2.17	0.42
1:A:606:LYS:HZ2	1:A:607:LYS:NZ	2.15	0.42
1:A:102:GLN:HA	1:A:102:GLN:HE21	1.84	0.42
1:B:252:TYR:CB	1:B:613:PRO:HB2	2.49	0.42
1:A:436:ASN:C	1:A:436:ASN:HD22	2.21	0.42
1:A:46:SER:HB2	1:A:56:LYS:HG2	2.02	0.42
1:A:469:PRO:HB2	1:A:470:GLN:NE2	2.33	0.42
1:B:56:LYS:HB3	1:B:57:TRP:CE2	2.55	0.42
1:B:102:GLN:O	1:B:189:MET:HA	2.19	0.42
1:B:301:LEU:HD11	1:B:491:TRP:HA	2.02	0.42
1:A:142:LYS:HG3	1:A:164:GLU:OE1	2.19	0.42
1:A:182:ASP:N	1:A:182:ASP:OD1	2.50	0.42
1:A:48:ILE:O	1:A:49:ASP:HB2	2.20	0.41
1:B:300:ARG:HH22	1:B:482:PRO:HG3	1.85	0.41
1:A:393:ASN:HD21	1:A:414:ARG:HH21	1.68	0.41
1:A:498:LYS:CE	1:A:533:LYS:HD3	2.50	0.41
1:B:153:SER:O	1:B:154:PRO:C	2.58	0.41
1:B:528:THR:HG21	1:B:569:GLN:HB2	2.02	0.41
1:A:606:LYS:HG3	1:A:607:LYS:N	2.35	0.41
1:A:230:LYS:HB2	1:A:230:LYS:HE3	1.72	0.41
1:A:393:ASN:HA	1:A:393:ASN:HD22	1.65	0.41
1:A:329:TYR:HE1	1:A:573:LEU:CD2	2.30	0.41
1:B:281:VAL:HG22	1:B:503:ILE:HD13	2.01	0.41
1:A:218:ASN:C	1:A:218:ASN:OD1	2.59	0.41
1:B:476:ILE:O	1:B:476:ILE:HG13	2.20	0.41
1:A:291:PHE:CD1	1:A:291:PHE:N	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:ILE:CG2	1:A:246:ASN:N	2.84	0.40
1:B:201:GLN:HA	1:B:202:PRO:HD3	2.00	0.40
1:A:264:ILE:HG12	1:A:592:TYR:CD2	2.57	0.40
1:A:165:LEU:HD23	1:A:179:THR:HG23	2.03	0.40
1:B:316:ARG:HD3	1:B:584:CYS:CB	2.39	0.40
1:B:374:LYS:CE	2:B:1158:HOH:O	2.70	0.40
1:A:346:LEU:HD22	1:A:613:PRO:HA	2.02	0.40
1:A:201:GLN:HA	1:A:202:PRO:HD3	1.84	0.40
1:B:346:LEU:HD23	1:B:346:LEU:HA	1.78	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	565/619 (91%)	539 (95%)	21 (4%)	5 (1%)	21	19
1	B	576/619 (93%)	548 (95%)	25 (4%)	3 (0%)	34	35
All	All	1141/1238 (92%)	1087 (95%)	46 (4%)	8 (1%)	26	25

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	GLY
1	A	31	SER
1	A	32	SER
1	A	127	LYS
1	B	127	LYS
1	B	32	SER
1	A	35	PRO
1	B	38	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	490/530 (92%)	470 (96%)	20 (4%)	37	45
1	B	500/530 (94%)	479 (96%)	21 (4%)	36	44
All	All	990/1060 (93%)	949 (96%)	41 (4%)	37	45

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	TYR
1	A	34	ASP
1	A	91	ARG
1	A	154	PRO
1	A	283	LYS
1	A	300	ARG
1	A	306	GLN
1	A	324	ARG
1	A	328	VAL
1	A	351	GLU
1	A	360	ASN
1	A	389	ASP
1	A	416	LEU
1	A	431	GLU
1	A	436	ASN
1	A	469	PRO
1	A	471	ASN
1	A	493	VAL
1	A	608	GLU
1	A	610	ASP
1	B	38	TYR
1	B	95	ASN
1	B	127	LYS
1	B	128	ASP
1	B	153	SER
1	B	154	PRO
1	B	171	ASN

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Mol	Chain	Res	Type
1	B	215	ARG
1	B	246	ASN
1	B	303	LEU
1	B	307	ARG
1	B	326	LEU
1	B	328	VAL
1	B	332	ASN
1	B	352	GLN
1	B	379	ARG
1	B	436	ASN
1	B	469	PRO
1	B	471	ASN
1	B	480	LEU
1	B	603	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	97	ASN
1	A	102	GLN
1	A	149	ASN
1	A	171	ASN
1	A	201	GLN
1	A	268	ASN
1	A	360	ASN
1	A	386	GLN
1	A	393	ASN
1	A	395	HIS
1	A	436	ASN
1	A	470	GLN
1	A	471	ASN
1	A	569	GLN
1	B	70	ASN
1	B	95	ASN
1	B	131	HIS
1	B	171	ASN
1	B	201	GLN
1	B	246	ASN
1	B	261	GLN
1	B	268	ASN
1	B	332	ASN

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Mol	Chain	Res	Type
1	B	339	HIS
1	B	352	GLN
1	B	367	ASN
1	B	401	GLN
1	B	405	GLN
1	B	436	ASN
1	B	471	ASN
1	B	565	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	571/619 (92%)	-0.09	19 (3%) 50 49	18, 33, 69, 106	0
1	B	582/619 (94%)	-0.08	23 (3%) 42 41	17, 32, 67, 104	0
All	All	1153/1238 (93%)	-0.09	42 (3%) 46 45	17, 33, 69, 106	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	38	TYR	10.0
1	A	530	TYR	5.3
1	B	543	ILE	4.7
1	A	32	SER	4.6
1	A	521	VAL	4.3
1	B	545	LEU	4.3
1	A	30	TYR	4.0
1	A	33	LEU	4.0
1	A	564	LYS	4.0
1	B	520	THR	3.8
1	B	535	ILE	3.6
1	B	32	SER	3.4
1	B	519	PHE	3.4
1	B	522	ASN	3.4
1	B	469	PRO	3.3
1	A	38	TYR	3.3
1	B	30	TYR	3.2
1	B	524	GLU	3.1
1	B	528	THR	3.0
1	A	469	PRO	3.0
1	B	527	LYS	3.0
1	A	520	THR	2.9
1	B	29	ASP	2.9
1	B	525	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	567	TYR	2.9
1	A	519	PHE	2.6
1	B	41	ASP	2.4
1	A	565	ASN	2.4
1	A	139	HIS	2.4
1	B	33	LEU	2.3
1	B	565	ASN	2.3
1	A	41	ASP	2.2
1	A	470	GLN	2.2
1	A	522	ASN	2.2
1	B	35	PRO	2.2
1	B	223	ASP	2.2
1	A	603	LEU	2.1
1	A	140	GLY	2.1
1	A	168	VAL	2.1
1	B	534	PRO	2.1
1	B	546	VAL	2.0
1	A	12	PHE	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.