



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 04:44 AM GMT

PDB ID : 2RDY  
Title : Crystal structure of a putative glycoside hydrolase family protein from *Bacillus halodurans*  
Authors : Sugadev, R.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)  
Deposited on : 2007-09-25  
Resolution : 2.03 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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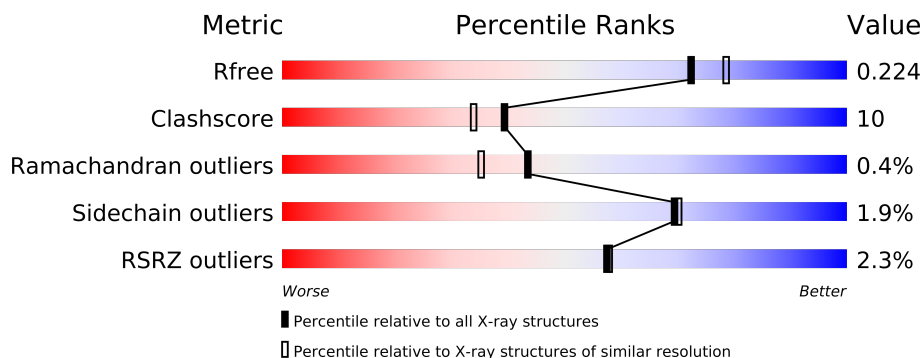
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.03 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))
$R_{free}$	66092	6003 (2.04-2.00)
Clashscore	79885	7467 (2.04-2.00)
Ramachandran outliers	78287	7370 (2.04-2.00)
Sidechain outliers	78261	7368 (2.04-2.00)
RSRZ outliers	66119	6006 (2.04-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	803	
1	B	803	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13037 atoms, of which 0 are hydrogen and 0 are deuterium.

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 BH0842 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	787	Total	C	N	O	S	Se	0	0	0
			6239	3955	1076	1181	9	18			
1	B	787	Total	C	N	O	S	Se	0	0	0
			6239	3955	1076	1181	9	18			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	EXPRESSION TAG	UNP Q9KEL0
A	2	SER	-	EXPRESSION TAG	UNP Q9KEL0
A	3	LEU	-	EXPRESSION TAG	UNP Q9KEL0
A	796	GLU	-	EXPRESSION TAG	UNP Q9KEL0
A	797	GLY	-	EXPRESSION TAG	UNP Q9KEL0
A	798	HIS	-	EXPRESSION TAG	UNP Q9KEL0
A	799	HIS	-	EXPRESSION TAG	UNP Q9KEL0
A	800	HIS	-	EXPRESSION TAG	UNP Q9KEL0
A	801	HIS	-	EXPRESSION TAG	UNP Q9KEL0
A	802	HIS	-	EXPRESSION TAG	UNP Q9KEL0
A	803	HIS	-	EXPRESSION TAG	UNP Q9KEL0
B	1	MSE	-	EXPRESSION TAG	UNP Q9KEL0
B	2	SER	-	EXPRESSION TAG	UNP Q9KEL0
B	3	LEU	-	EXPRESSION TAG	UNP Q9KEL0
B	796	GLU	-	EXPRESSION TAG	UNP Q9KEL0
B	797	GLY	-	EXPRESSION TAG	UNP Q9KEL0
B	798	HIS	-	EXPRESSION TAG	UNP Q9KEL0
B	799	HIS	-	EXPRESSION TAG	UNP Q9KEL0
B	800	HIS	-	EXPRESSION TAG	UNP Q9KEL0
B	801	HIS	-	EXPRESSION TAG	UNP Q9KEL0
B	802	HIS	-	EXPRESSION TAG	UNP Q9KEL0
B	803	HIS	-	EXPRESSION TAG	UNP Q9KEL0

- Molecule 2 is water.

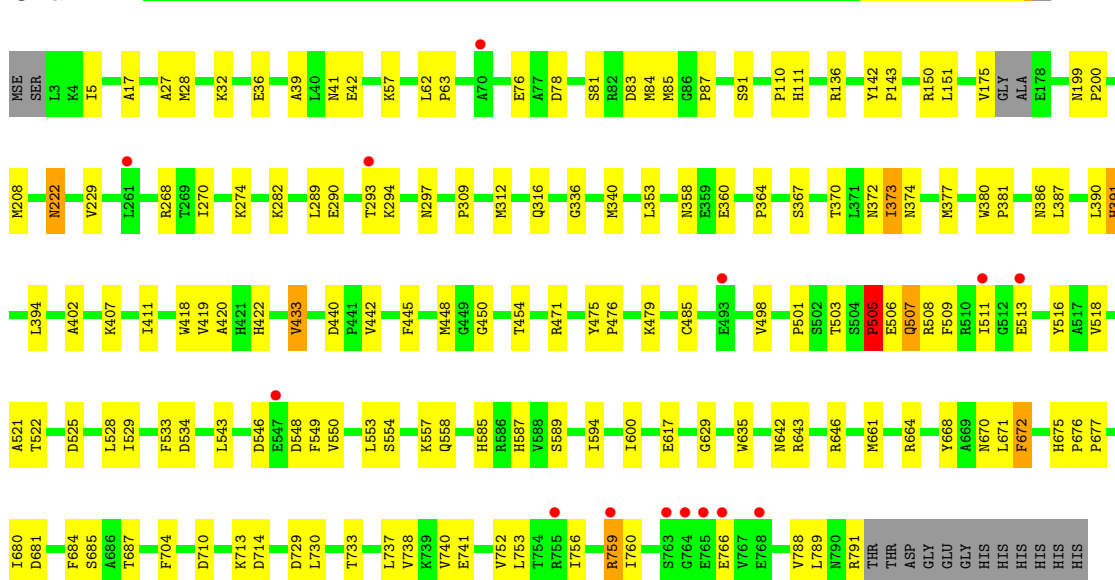
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	275	Total 275	O 275	0	0
2	B	284	Total 284	O 284	0	0

### 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.

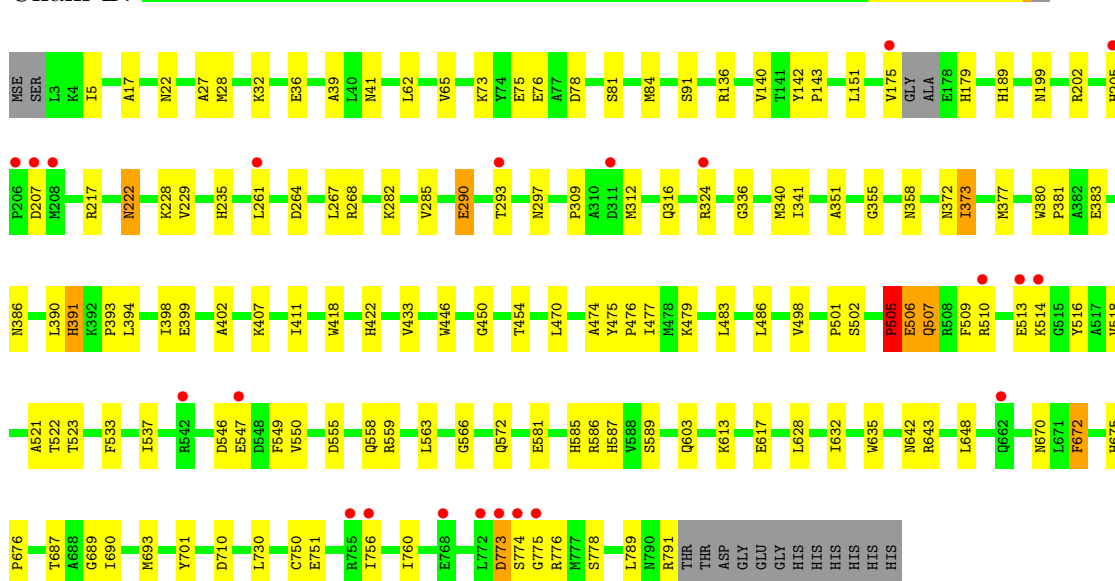
#### • Molecule 1: BH0842 protein

Chain A:



#### • Molecule 1: BH0842 protein

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.61Å 149.07Å 164.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.57 – 2.03 47.57 – 2.03	Depositor EDS
% Data completeness (in resolution range)	93.6 (47.57-2.03) 93.8 (47.57-2.03)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.55 (at 2.03Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.198 , 0.225 0.197 , 0.224	Depositor DCC
$R_{free}$ test set	6536 reflections (6.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	14.9	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 29.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 116001 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13037	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 26.94 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.4057e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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	0.33	0/6378	0.60	2/8621 (0.0%)
1	B	0.34	0/6378	0.60	1/8621 (0.0%)
All	All	0.33	0/12756	0.60	3/17242 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	5	ILE	N-CA-C	-5.28	96.75	111.00
1	A	42	GLU	N-CA-C	-5.14	97.13	111.00
1	A	5	ILE	N-CA-C	-5.10	97.23	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6239	0	6036	123	0
1	B	6239	0	6036	112	0
2	A	275	0	0	5	0
2	B	284	0	0	2	0
All	All	13037	0	12072	235	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

All (235) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:448:MSE:HE2	1:A:525:ASP:HA	1.22	1.17
1:B:690:ILE:HA	1:B:693:MSE:HE3	1.43	0.97
1:B:407:LYS:HE3	1:B:411:ILE:HD11	1.49	0.93
1:B:84:MSE:HE1	1:B:501:PRO:HG2	1.48	0.93
1:A:448:MSE:HE3	1:A:528:LEU:HB2	1.53	0.91
1:B:690:ILE:CA	1:B:693:MSE:HE3	2.02	0.88
1:A:661:MSE:HE2	1:A:664:ARG:HD2	1.56	0.88
1:A:642:ASN:HD21	1:A:710:ASP:H	1.23	0.85
1:A:81:SER:HA	1:A:84:MSE:HE2	1.60	0.83
1:A:448:MSE:HE2	1:A:525:ASP:CA	2.08	0.83
1:B:642:ASN:HD21	1:B:710:ASP:H	1.28	0.82
1:B:632:ILE:CG2	1:B:693:MSE:HE2	2.11	0.80
1:B:81:SER:HA	1:B:84:MSE:HE2	1.65	0.79
1:B:136:ARG:HD3	2:B:821:HOH:O	1.81	0.79
1:A:41:ASN:HD21	1:A:358:ASN:H	1.32	0.77
1:A:506:GLU:HG3	1:A:587:HIS:NE2	2.00	0.77
1:A:407:LYS:HE2	1:A:411:ILE:HD11	1.68	0.75
1:A:448:MSE:CE	1:A:528:LEU:HB2	2.16	0.75
1:B:690:ILE:N	1:B:693:MSE:HE3	2.01	0.74
1:A:222:ASN:HD22	1:A:222:ASN:H	1.37	0.72
1:A:642:ASN:ND2	1:A:710:ASP:H	1.88	0.71
1:A:737:LEU:HB3	1:A:756:ILE:HD11	1.73	0.71
1:B:751:GLU:OE2	1:B:776:ARG:HD2	1.92	0.70
1:A:661:MSE:HE3	1:A:664:ARG:HB2	1.73	0.69
1:B:701:TYR:CD2	1:B:776:ARG:HD3	2.27	0.69
1:A:635:TRP:CD2	1:A:643:ARG:HG2	2.28	0.69
1:B:642:ASN:ND2	1:B:710:ASP:H	1.90	0.68
1:A:340:MSE:HG2	1:A:390:LEU:HD23	1.75	0.68
1:B:324:ARG:HH11	1:B:324:ARG:HG3	1.61	0.66
1:B:340:MSE:HG2	1:B:390:LEU:HD23	1.78	0.66
1:A:81:SER:CA	1:A:84:MSE:HE2	2.26	0.66
1:A:136:ARG:HD3	2:A:904:HOH:O	1.96	0.66
1:A:525:ASP:O	1:A:529:ILE:HG12	1.95	0.65
1:B:507:GLN:HB2	1:B:585:HIS:CD2	2.31	0.65
1:A:546:ASP:HB3	1:A:549:PHE:HB3	1.79	0.64
1:B:142:TYR:HB3	1:B:143:PRO:HD3	1.79	0.63
1:B:41:ASN:HD21	1:B:358:ASN:H	1.46	0.63
1:A:41:ASN:ND2	1:A:358:ASN:H	1.96	0.62
1:B:62:LEU:O	1:B:65:VAL:HG12	2.00	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:689:GLY:C	1:B:693:MSE:HE3	2.20	0.61
1:B:546:ASP:HB3	1:B:549:PHE:HB3	1.81	0.61
1:B:32:LYS:HB2	1:B:36:GLU:HA	1.83	0.60
1:A:142:TYR:HB3	1:A:143:PRO:HD3	1.81	0.60
1:A:738:VAL:HG12	1:A:791:ARG:CZ	2.31	0.60
1:B:222:ASN:HD22	1:B:222:ASN:H	1.51	0.59
1:A:222:ASN:ND2	1:A:222:ASN:H	2.01	0.59
1:A:136:ARG:HD2	1:A:151:LEU:CD2	2.33	0.59
1:A:293:THR:OG1	1:A:297:ASN:ND2	2.36	0.58
1:B:479:LYS:HG3	1:B:549:PHE:CE2	2.39	0.58
1:B:632:ILE:HG21	1:B:693:MSE:HE2	1.85	0.58
1:B:293:THR:OG1	1:B:297:ASN:ND2	2.36	0.57
1:A:312:MSE:HE2	1:A:316:GLN:NE2	2.19	0.57
1:B:632:ILE:HD13	1:B:648:LEU:HD13	1.87	0.57
1:B:136:ARG:HD2	1:B:151:LEU:CD2	2.35	0.57
1:A:554:SER:O	1:A:558:GLN:HG3	2.04	0.56
1:B:309:PRO:HG2	1:B:312:MSE:HB2	1.85	0.56
1:A:450:GLY:O	1:A:454:THR:HG23	2.04	0.56
1:A:643:ARG:HD3	1:A:646:ARG:HH11	1.70	0.56
1:A:546:ASP:O	1:A:550:VAL:HG23	2.06	0.56
1:A:585:HIS:CD2	1:A:587:HIS:HB2	2.41	0.56
1:A:617:GLU:OE2	1:A:643:ARG:NH2	2.38	0.56
1:B:136:ARG:HD2	1:B:151:LEU:HD22	1.87	0.55
1:B:41:ASN:ND2	1:B:358:ASN:H	2.04	0.55
1:B:222:ASN:ND2	1:B:222:ASN:H	2.04	0.55
1:A:81:SER:CB	1:A:84:MSE:HE2	2.36	0.55
1:B:690:ILE:HA	1:B:693:MSE:CE	2.27	0.55
1:B:585:HIS:CD2	1:B:587:HIS:HB2	2.42	0.54
1:B:760:ILE:HG12	1:B:789:LEU:CD2	2.36	0.54
1:B:199:ASN:ND2	1:B:202:ARG:HG2	2.23	0.54
1:A:507:GLN:HB2	1:A:585:HIS:CD2	2.43	0.54
1:A:505:PRO:HB2	1:A:589:SER:OG	2.08	0.54
1:A:57:LYS:HE3	1:A:83:ASP:HB3	1.90	0.54
1:A:309:PRO:HG2	1:A:312:MSE:HB2	1.89	0.54
1:B:179:HIS:HD2	1:B:217:ARG:HH11	1.56	0.54
1:A:534:ASP:OD1	1:A:557:LYS:HE2	2.09	0.53
1:A:78:ASP:OD1	1:A:518:VAL:HG22	2.09	0.53
1:B:81:SER:CA	1:B:84:MSE:HE2	2.38	0.53
1:A:81:SER:HB2	1:A:84:MSE:HE2	1.89	0.53
1:A:675:HIS:N	1:A:676:PRO:HA	2.23	0.53
1:A:377:MSE:SE	1:A:685:SER:HB3	2.58	0.53
1:B:566:GLY:HA2	1:B:572:GLN:HE21	1.74	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:78:ASP:OD1	1:B:518:VAL:HG22	2.09	0.52
1:A:448:MSE:HE1	1:A:529:ILE:HG12	1.92	0.52
1:B:546:ASP:O	1:B:550:VAL:HG23	2.09	0.52
1:B:312:MSE:HE2	1:B:316:GLN:NE2	2.24	0.52
1:A:373:ILE:HG23	1:A:374:ASN:N	2.24	0.52
1:B:510:ARG:HD2	1:B:581:GLU:HG3	1.92	0.52
1:B:506:GLU:HG3	1:B:587:HIS:NE2	2.25	0.51
1:B:523:THR:HG23	1:B:563:LEU:HD22	1.92	0.51
1:B:547:GLU:CD	1:B:547:GLU:H	2.14	0.51
1:A:17:ALA:HB3	1:A:28:MSE:HG3	1.93	0.51
1:B:399:GLU:HG2	1:B:477:ILE:HD11	1.93	0.51
1:B:394:LEU:O	1:B:398:ILE:HG13	2.11	0.50
1:A:675:HIS:H	1:A:676:PRO:HA	1.76	0.50
1:A:675:HIS:HB3	1:A:676:PRO:C	2.31	0.50
1:A:508:ARG:HB3	1:A:516:TYR:O	2.11	0.50
1:B:450:GLY:O	1:B:454:THR:HG23	2.12	0.50
1:B:510:ARG:HH21	1:B:513:GLU:C	2.15	0.50
1:A:336:GLY:HA3	1:A:687:THR:OG1	2.12	0.50
1:A:760:ILE:HG12	1:A:789:LEU:HD22	1.94	0.50
1:B:27:ALA:HA	1:B:39:ALA:O	2.12	0.50
1:A:506:GLU:HG3	1:A:587:HIS:CD2	2.46	0.49
1:A:268:ARG:HB3	1:A:268:ARG:HH11	1.77	0.49
1:A:729:ASP:HB2	1:A:741:GLU:HB2	1.94	0.49
1:B:402:ALA:HA	1:B:418:TRP:CD2	2.48	0.49
1:B:498:VAL:HB	1:B:521:ALA:HB2	1.94	0.49
1:A:360:GLU:OE1	1:A:364:PRO:HD3	2.12	0.49
1:A:84:MSE:HE3	1:A:445:PHE:CE1	2.48	0.49
1:A:372:ASN:O	1:A:373:ILE:HB	2.13	0.48
1:B:756:ILE:CD1	1:B:791:ARG:HG2	2.43	0.48
1:B:261:LEU:HD23	1:B:261:LEU:O	2.13	0.48
1:B:675:HIS:HB3	1:B:676:PRO:C	2.33	0.48
1:B:324:ARG:NH1	1:B:324:ARG:HG3	2.27	0.48
1:A:199:ASN:N	1:A:200:PRO:HD3	2.28	0.48
1:A:402:ALA:HA	1:A:418:TRP:CD2	2.48	0.48
1:B:533:PHE:O	1:B:537:ILE:HG13	2.13	0.48
1:A:643:ARG:HA	1:A:646:ARG:NH1	2.29	0.48
1:A:136:ARG:HD2	1:A:151:LEU:HD22	1.96	0.48
1:B:774:SER:OG	1:B:775:GLY:N	2.44	0.48
1:A:200:PRO:HG3	2:A:813:HOH:O	2.13	0.48
1:A:84:MSE:HE3	1:A:445:PHE:CD1	2.50	0.47
1:B:675:HIS:N	1:B:676:PRO:HA	2.29	0.47
1:B:505:PRO:HB2	1:B:589:SER:OG	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:440:ASP:OD1	1:A:442:VAL:HG12	2.15	0.47
1:B:756:ILE:HD12	1:B:791:ARG:HG2	1.96	0.47
1:A:738:VAL:HG12	1:A:791:ARG:NH2	2.30	0.47
1:B:290:GLU:O	1:B:293:THR:HG22	2.15	0.47
1:B:268:ARG:HB3	1:B:268:ARG:HH11	1.79	0.47
1:A:629:GLY:HA3	1:A:685:SER:OG	2.16	0.46
1:B:205:HIS:ND1	1:B:207:ASP:HB2	2.29	0.46
1:B:81:SER:HA	1:B:84:MSE:CE	2.42	0.46
1:B:336:GLY:HA3	1:B:687:THR:OG1	2.15	0.46
1:A:62:LEU:N	1:A:63:PRO:HD2	2.30	0.46
1:A:377:MSE:SE	1:A:681:ASP:HB2	2.65	0.46
1:A:290:GLU:O	1:A:293:THR:HG22	2.15	0.46
1:A:509:PHE:CE1	1:A:516:TYR:HB2	2.50	0.46
1:B:603:GLN:CD	1:B:603:GLN:N	2.69	0.46
1:B:760:ILE:HG12	1:B:789:LEU:HD22	1.97	0.46
1:A:440:ASP:OD2	1:A:508:ARG:NH1	2.45	0.46
1:A:448:MSE:HE3	1:A:528:LEU:CB	2.36	0.45
1:A:668:TYR:OH	1:A:677:PRO:HA	2.16	0.45
1:A:270:ILE:HG12	1:A:274:LYS:HE3	1.99	0.45
1:B:264:ASP:HB3	1:B:267:LEU:HD12	1.98	0.45
1:A:353:LEU:HB2	1:A:367:SER:HA	1.98	0.45
1:A:289:LEU:O	1:A:293:THR:HG22	2.16	0.45
1:B:28:MSE:HB2	1:B:39:ALA:HB3	1.98	0.45
1:B:750:CYS:O	1:B:778:SER:HA	2.17	0.45
1:A:136:ARG:HA	1:A:150:ARG:O	2.17	0.45
1:A:479:LYS:HG3	1:A:549:PHE:CE2	2.52	0.45
1:B:179:HIS:CD2	1:B:217:ARG:HD3	2.52	0.45
1:B:635:TRP:CG	1:B:643:ARG:HG2	2.52	0.45
1:A:175:VAL:HG21	1:A:229:VAL:HG13	1.99	0.45
1:A:27:ALA:HA	1:A:39:ALA:O	2.16	0.45
1:A:475:TYR:HB3	1:A:476:PRO:HD3	1.99	0.45
1:B:555:ASP:O	1:B:559:ARG:HG3	2.16	0.45
1:B:373:ILE:HD11	1:B:377:MSE:HE3	1.99	0.45
1:A:282:LYS:HG3	2:A:1006:HOH:O	2.16	0.45
1:A:661:MSE:CE	1:A:664:ARG:HB2	2.46	0.45
1:B:730:LEU:HD12	1:B:730:LEU:C	2.38	0.45
1:B:189:HIS:HD2	2:B:950:HOH:O	1.99	0.45
1:A:380:TRP:N	1:A:381:PRO:CD	2.80	0.45
1:A:87:PRO:O	1:A:433:VAL:HA	2.17	0.44
1:B:635:TRP:CD2	1:B:643:ARG:HG2	2.52	0.44
1:B:380:TRP:N	1:B:381:PRO:CD	2.80	0.44
1:B:774:SER:C	1:B:776:ARG:H	2.20	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:17:ALA:HB3	1:B:28:MSE:HE3	1.99	0.44
1:A:714:ASP:OD1	1:A:733:THR:HA	2.18	0.44
1:B:670:ASN:OD1	1:B:672:PHE:HB2	2.17	0.44
1:B:73:LYS:HD3	1:B:76:GLU:OE2	2.18	0.44
1:A:594:ILE:HD13	1:A:600:ILE:HB	1.99	0.44
1:A:485:CYS:SG	1:A:529:ILE:HD12	2.58	0.44
1:A:370:THR:CG2	1:A:374:ASN:HD22	2.31	0.44
1:B:390:LEU:O	1:B:393:PRO:HD2	2.18	0.44
1:B:475:TYR:HB3	1:B:476:PRO:HD3	2.00	0.44
1:A:76:GLU:HG3	2:A:1052:HOH:O	2.17	0.44
1:B:510:ARG:HG3	1:B:581:GLU:HA	2.00	0.43
1:A:741:GLU:HG2	1:A:788:VAL:HG22	2.00	0.43
1:B:613:LYS:O	1:B:617:GLU:HG3	2.19	0.43
1:A:222:ASN:HD22	1:A:222:ASN:N	2.10	0.43
1:B:175:VAL:HG21	1:B:229:VAL:HG13	2.00	0.43
1:A:110:PRO:O	1:A:111:HIS:HB2	2.18	0.43
1:A:84:MSE:HE1	1:A:501:PRO:HG2	1.99	0.43
1:A:710:ASP:O	1:A:713:LYS:HD2	2.19	0.43
1:A:737:LEU:HD21	1:A:740:VAL:CG2	2.49	0.43
1:B:586:ARG:HG2	1:B:586:ARG:HH11	1.82	0.43
1:B:351:ALA:HB1	1:B:355:GLY:HA2	2.01	0.42
1:A:635:TRP:CG	1:A:643:ARG:HG2	2.55	0.42
1:A:387:LEU:HD22	1:A:390:LEU:HD22	2.02	0.42
1:A:759:ARG:O	1:A:789:LEU:HA	2.19	0.42
1:A:391:HIS:HE1	1:A:394:LEU:HD23	1.85	0.42
1:B:689:GLY:O	1:B:693:MSE:HG3	2.19	0.42
1:B:483:LEU:HD23	1:B:486:LEU:HD12	2.01	0.42
1:B:502:SER:OG	1:B:522:THR:HG23	2.19	0.42
1:A:670:ASN:OD1	1:A:672:PHE:HB2	2.19	0.42
1:B:383:GLU:OE2	1:B:391:HIS:HD2	2.02	0.42
1:B:75:GLU:OE1	1:B:514:LYS:HE2	2.18	0.42
1:B:22:ASN:HB3	1:B:140:VAL:HG12	2.01	0.42
1:B:509:PHE:CE1	1:B:516:TYR:HB2	2.55	0.42
1:A:753:LEU:HD23	1:A:753:LEU:C	2.39	0.42
1:A:680:ILE:HG12	1:A:684:PHE:CE2	2.55	0.42
1:A:293:THR:HG23	1:A:294:LYS:N	2.34	0.42
1:B:341:ILE:HA	1:B:390:LEU:HD21	2.02	0.42
1:B:372:ASN:O	1:B:373:ILE:HB	2.20	0.42
1:A:380:TRP:N	1:A:381:PRO:HD2	2.34	0.42
1:B:380:TRP:N	1:B:381:PRO:HD2	2.35	0.42
1:A:498:VAL:HB	1:A:521:ALA:HB2	2.02	0.42
1:A:471:ARG:HB2	1:A:543:LEU:HD22	2.02	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:671:LEU:HD12	1:A:671:LEU:HA	1.86	0.41
1:A:533:PHE:CD1	1:A:553:LEU:HD22	2.55	0.41
1:A:511:ILE:HB	1:A:516:TYR:HE2	1.85	0.41
1:B:628:LEU:O	1:B:632:ILE:HG13	2.20	0.41
1:A:32:LYS:HE2	1:A:32:LYS:HB3	1.83	0.41
1:A:222:ASN:ND2	1:A:222:ASN:N	2.68	0.41
1:B:773:ASP:CG	1:B:774:SER:N	2.75	0.41
1:B:585:HIS:NE2	1:B:587:HIS:HB2	2.36	0.41
1:B:537:ILE:HG23	1:B:550:VAL:HG13	2.03	0.41
1:A:419:VAL:HG22	1:A:420:ALA:N	2.36	0.41
1:A:759:ARG:HG2	2:A:1050:HOH:O	2.20	0.41
1:B:372:ASN:HA	1:B:446:TRP:CH2	2.56	0.41
1:A:85:MSE:HB3	1:A:433:VAL:O	2.19	0.41
1:A:32:LYS:HB2	1:A:36:GLU:HA	2.02	0.41
1:B:228:LYS:HG2	1:B:235:HIS:HB2	2.03	0.41
1:B:282:LYS:HA	1:B:285:VAL:HG12	2.03	0.41
1:B:470:LEU:HA	1:B:474:ALA:HB3	2.03	0.40
1:A:704:PHE:HE1	1:A:752:VAL:HB	1.85	0.40
1:B:282:LYS:O	1:B:285:VAL:HG12	2.21	0.40
1:A:664:ARG:O	1:A:676:PRO:HD3	2.21	0.40
1:B:773:ASP:CG	1:B:774:SER:H	2.24	0.40
1:A:635:TRP:CE2	1:A:643:ARG:HG2	2.56	0.40
1:A:420:ALA:HB3	1:A:450:GLY:N	2.36	0.40
1:B:142:TYR:N	1:B:143:PRO:CD	2.85	0.40
1:A:759:ARG:HH11	1:A:759:ARG:HG3	1.86	0.40
1:A:503:THR:C	1:A:522:THR:HG21	2.41	0.40
1:A:387:LEU:HB3	1:A:390:LEU:HD22	2.03	0.40
1:B:730:LEU:HD12	1:B:730:LEU:O	2.22	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	783/803 (98%)	749 (96%)	31 (4%)	3 (0%)	43 35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	783/803 (98%)	750 (96%)	29 (4%)	4 (0%)	38	28
All	All	1566/1606 (98%)	1499 (96%)	60 (4%)	7 (0%)	43	35

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	373	ILE
1	B	373	ILE
1	A	505	PRO
1	B	505	PRO
1	B	773	ASP
1	A	433	VAL
1	B	433	VAL

### 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	661/654 (101%)	647 (98%)	14 (2%)	66	66
1	B	661/654 (101%)	650 (98%)	11 (2%)	73	74
All	All	1322/1308 (101%)	1297 (98%)	25 (2%)	69	70

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	SER
1	A	208	MSE
1	A	222	ASN
1	A	386	ASN
1	A	391	HIS
1	A	422	HIS
1	A	505	PRO
1	A	507	GLN
1	A	513	GLU
1	A	548	ASP
1	A	672	PHE

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Mol	Chain	Res	Type
1	A	730	LEU
1	A	759	ARG
1	A	766	GLU
1	B	91	SER
1	B	222	ASN
1	B	290	GLU
1	B	386	ASN
1	B	391	HIS
1	B	422	HIS
1	B	505	PRO
1	B	506	GLU
1	B	507	GLN
1	B	558	GLN
1	B	672	PHE

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	24	ASN
1	A	41	ASN
1	A	104	HIS
1	A	179	HIS
1	A	222	ASN
1	A	288	HIS
1	A	297	ASN
1	A	374	ASN
1	A	386	ASN
1	A	391	HIS
1	A	423	ASN
1	A	642	ASN
1	A	679	GLN
1	A	699	GLN
1	B	24	ASN
1	B	41	ASN
1	B	133	GLN
1	B	179	HIS
1	B	189	HIS
1	B	222	ASN
1	B	288	HIS
1	B	297	ASN
1	B	316	GLN
1	B	386	ASN

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Mol	Chain	Res	Type
1	B	391	HIS
1	B	507	GLN
1	B	558	GLN
1	B	572	GLN
1	B	642	ASN
1	B	662	GLN
1	B	679	GLN
1	B	699	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no ligands in this entry.

### 5.7 Other polymers ⓘ

There are no such residues in this entry.

### 5.8 Polymer linkage issues

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	787/803 (98%)	0.02	14 (1%) 65 66	7, 14, 28, 44	0
1	B	787/803 (98%)	0.07	22 (2%) 50 50	6, 14, 30, 49	0
All	All	1574/1606 (98%)	0.05	36 (2%) 57 58	6, 14, 28, 49	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	775	GLY	5.5
1	B	774	SER	4.3
1	B	773	ASP	4.1
1	B	261	LEU	4.0
1	A	763	SER	4.0
1	B	208	MSE	4.0
1	B	207	ASP	3.8
1	B	756	ILE	3.7
1	B	755	ARG	3.5
1	B	205	HIS	3.4
1	A	765	GLU	3.2
1	A	768	GLU	3.2
1	A	755	ARG	2.9
1	B	206	PRO	2.9
1	A	766	GLU	2.8
1	A	261	LEU	2.7
1	A	759	ARG	2.7
1	A	547	GLU	2.5
1	B	513	GLU	2.5
1	B	542	ARG	2.5
1	A	764	GLY	2.4
1	A	70	ALA	2.4
1	A	513	GLU	2.4
1	B	510	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	772	LEU	2.2
1	B	175	VAL	2.2
1	B	311	ASP	2.2
1	A	293	THR	2.1
1	B	662	GLN	2.1
1	B	293	THR	2.1
1	B	514	LYS	2.1
1	B	547	GLU	2.1
1	A	511	ILE	2.1
1	B	324	ARG	2.1
1	B	768	GLU	2.0
1	A	493	GLU	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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.