



# Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 07:55 pm BST

PDB ID : 1J0H  
Title : Crystal structure of Bacillus stearothermophilus neopullulanase  
Authors : Hondoh, H.; Kuriki, T.; Matsuura, Y.  
Deposited on : 2002-11-14  
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

<https://www.wwpdb.org/validation/2017/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)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

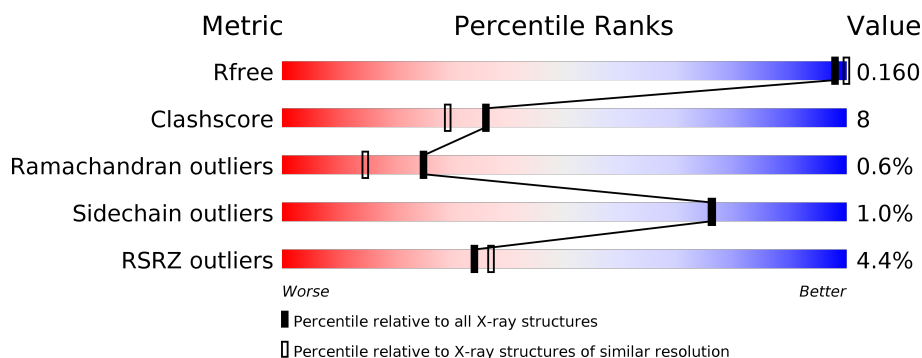
# 1 Overall quality at a glance

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))
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (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 respectively. 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	588	<div> <div>4%</div> <div> <div></div> <div>84%</div> <div>15%</div> </div> <div></div> </div>
1	B	588	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>15%</div> </div> <div></div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11382 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 neopullulanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	588	Total	C	N	O	S	0	0	0
			4889	3158	816	893	22			
1	B	588	Total	C	N	O	S	0	0	0
			4889	3158	816	893	22			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	290	ALA	ARG	SEE REMARK 999	UNP P38940
B	290	ALA	ARG	SEE REMARK 999	UNP P38940

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Ca	0	0
			1	1		
3	A	1	Total	Ca	0	0
			1	1		

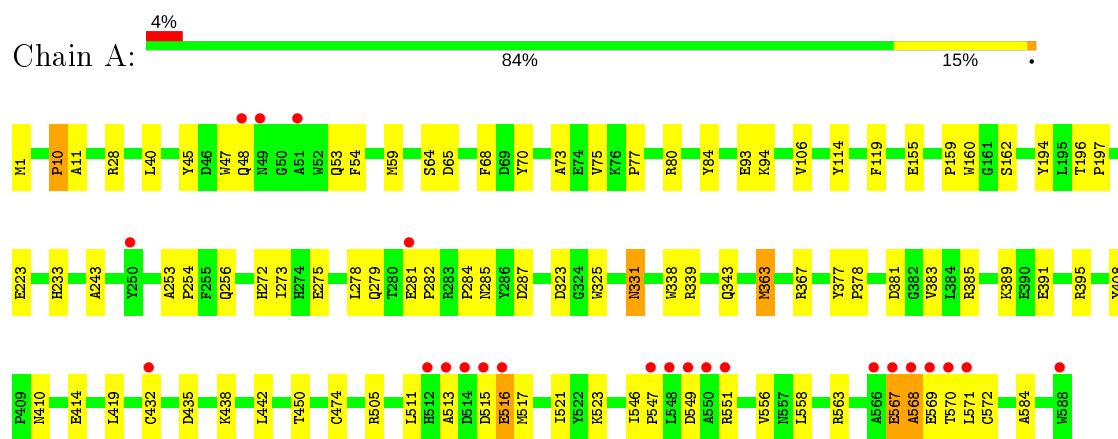
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	814	Total	O	0	0
			814	814		
4	B	787	Total	O	0	0
			787	787		

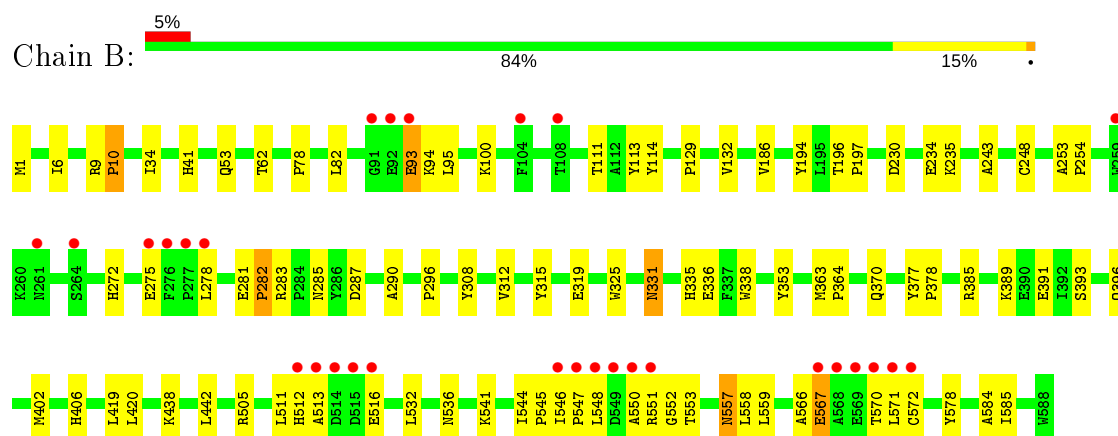
### 3 Residue-property plots [i](#)

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



#### • Molecule 1: neopullulanase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.71Å 72.76Å 123.64Å 90.00° 90.84° 90.00°	Depositor
Resolution (Å)	10.00 – 1.90 35.57 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-1.90) 94.5 (35.57-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.55 (at 1.89Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.163 , 0.203 0.166 , 0.160	Depositor DCC
$R_{free}$ test set	4556 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.3	Xtriage
Anisotropy	0.536	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 54.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11382	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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

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

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	0.32	0/5047	0.59	0/6857
1	B	0.32	0/5047	0.58	1/6857 (0.0%)
All	All	0.32	0/10094	0.59	1/13714 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	114	TYR	N-CA-C	5.30	125.31	111.00

There are no chirality outliers.

There are no planarity outliers.

### 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	4889	0	4642	77	0
1	B	4889	0	4642	77	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	814	0	0	11	0
4	B	787	0	0	11	0
All	All	11382	0	9284	152	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 (152) 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:432:CYS:SG	1:A:438:LYS:HB2	2.05	0.96
1:B:275:GLU:HG3	1:B:285:ASN:HD22	1.42	0.83
1:A:11:ALA:HB1	4:B:2439:HOH:O	1.76	0.83
1:A:511:LEU:HD23	1:A:547:PRO:HG2	1.61	0.81
1:A:546:ILE:HD11	1:A:571:LEU:HB3	1.65	0.79
1:A:556:VAL:HG22	1:A:563:ARG:HG2	1.64	0.77
1:A:279:GLN:HG2	1:A:285:ASN:ND2	2.00	0.77
1:A:389:LYS:HD3	1:A:391:GLU:OE2	1.86	0.76
1:A:546:ILE:HG12	1:A:571:LEU:O	1.87	0.74
1:A:571:LEU:HD13	1:A:572:CYS:N	2.04	0.72
1:B:278:LEU:HA	1:B:285:ASN:HD21	1.55	0.71
1:B:420:LEU:HD12	4:B:2581:HOH:O	1.92	0.70
1:B:281:GLU:HA	1:B:282:PRO:C	2.14	0.68
1:A:331:ASN:N	1:A:331:ASN:HD22	1.92	0.68
1:A:256:GLN:HG3	4:A:2240:HOH:O	1.94	0.67
1:B:331:ASN:HD22	1:B:331:ASN:N	1.91	0.67
1:A:59:MET:HG2	1:A:73:ALA:HB2	1.76	0.66
1:A:253:ALA:HB3	1:A:254:PRO:HD3	1.77	0.66
1:B:571:LEU:HD23	1:B:572:CYS:N	2.14	0.63
1:B:253:ALA:HB3	1:B:254:PRO:HD3	1.81	0.62
1:A:432:CYS:SG	1:A:435:ASP:O	2.58	0.62
1:A:363:MET:HG3	1:B:9:ARG:NH2	2.15	0.61
1:B:331:ASN:HD22	1:B:331:ASN:H	1.47	0.61
1:B:335:HIS:HD2	1:B:370:GLN:OE1	1.86	0.59
1:B:513:ALA:HB1	4:B:2595:HOH:O	2.02	0.59
1:A:432:CYS:SG	1:A:432:CYS:O	2.61	0.58
1:B:557:ASN:HD22	1:B:559:LEU:H	1.49	0.58
1:B:419:LEU:HD23	1:B:419:LEU:H	1.69	0.58
1:B:336:GLU:HG3	4:B:2349:HOH:O	2.03	0.57
1:B:557:ASN:ND2	1:B:559:LEU:H	2.02	0.57
1:A:275:GLU:HG2	1:A:285:ASN:HB2	1.87	0.57
1:A:159:PRO:HB2	1:A:162:SER:HB3	1.86	0.57
1:A:233:HIS:HE1	1:A:323:ASP:OD1	1.86	0.56
1:B:275:GLU:HG2	1:B:285:ASN:HB2	1.87	0.56
1:A:273:ILE:HD13	1:A:278:LEU:HD11	1.87	0.56
1:B:420:LEU:HD13	1:B:442:LEU:HB3	1.87	0.56
1:A:419:LEU:HD23	1:A:419:LEU:H	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:THR:OG1	1:B:406:HIS:HE1	1.89	0.55
1:A:47:TRP:O	1:A:48:GLN:HG3	2.06	0.55
1:B:548:LEU:HD21	1:B:553:THR:HG21	1.89	0.55
1:A:331:ASN:H	1:A:331:ASN:HD22	1.54	0.55
1:A:546:ILE:HG13	1:A:546:ILE:O	2.07	0.54
1:B:545:PRO:O	1:B:547:PRO:HD3	2.06	0.54
1:B:389:LYS:HB3	1:B:391:GLU:HG3	1.90	0.54
1:B:315:TYR:CE1	1:B:319:GLU:HG3	2.43	0.54
1:A:558:LEU:HD21	1:A:584:ALA:HB2	1.88	0.53
1:B:389:LYS:CB	1:B:391:GLU:HG3	2.39	0.53
1:B:41:HIS:HB2	1:B:82:LEU:HD11	1.91	0.53
1:B:567:GLU:OE1	1:B:571:LEU:HG	2.09	0.53
1:A:410:ASN:O	1:A:414:GLU:HG3	2.08	0.53
1:B:557:ASN:C	1:B:557:ASN:HD22	2.12	0.53
1:B:53:GLN:HG2	4:B:2043:HOH:O	2.09	0.52
1:B:385:ARG:HD2	4:B:1452:HOH:O	2.09	0.52
1:B:111:THR:HB	1:B:113:TYR:CE1	2.44	0.52
1:A:568:ALA:C	1:A:570:THR:H	2.13	0.51
1:A:233:HIS:HD2	4:A:1340:HOH:O	1.93	0.51
1:A:432:CYS:SG	1:A:435:ASP:HB3	2.51	0.51
1:B:511:LEU:HD12	1:B:511:LEU:N	2.26	0.51
1:B:536:ASN:O	1:B:578:TYR:HA	2.11	0.50
1:B:1:MET:HE3	1:B:6:ILE:HD11	1.93	0.50
1:A:160:TRP:CE2	1:A:474:CYS:HB3	2.48	0.49
1:B:281:GLU:HA	1:B:283:ARG:N	2.28	0.49
1:B:275:GLU:CG	1:B:285:ASN:HD22	2.18	0.49
1:B:272:HIS:HB2	1:B:287:ASP:HB2	1.95	0.49
1:B:1:MET:HG2	1:B:34:ILE:CD1	2.43	0.49
4:A:1652:HOH:O	1:B:335:HIS:HE1	1.96	0.49
1:B:557:ASN:HD21	1:B:559:LEU:HB2	1.78	0.49
1:B:196:THR:HB	1:B:197:PRO:CD	2.43	0.48
1:A:339:ARG:O	1:A:343:GLN:HG3	2.13	0.48
1:A:571:LEU:HD11	4:A:2536:HOH:O	2.12	0.48
1:A:65:ASP:HB2	4:A:1001:HOH:O	2.14	0.47
1:A:567:GLU:C	1:A:569:GLU:H	2.17	0.47
1:A:363:MET:O	1:A:363:MET:HE2	2.14	0.47
1:B:230:ASP:O	1:B:234:GLU:HG3	2.15	0.47
1:B:548:LEU:CD2	1:B:585:ILE:HD12	2.45	0.47
1:A:513:ALA:HB2	1:A:521:ILE:HD12	1.95	0.47
1:B:505:ARG:HD3	4:B:1434:HOH:O	2.15	0.47
1:A:48:GLN:OE1	1:A:53:GLN:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:ILE:CD1	1:A:571:LEU:HB3	2.39	0.47
1:B:548:LEU:HD22	1:B:585:ILE:HD12	1.97	0.47
1:A:196:THR:HB	1:A:197:PRO:CD	2.45	0.46
1:B:331:ASN:ND2	1:B:331:ASN:N	2.62	0.46
1:A:272:HIS:HB2	1:A:287:ASP:HB2	1.97	0.46
1:A:567:GLU:HG3	4:A:2534:HOH:O	2.14	0.46
1:A:243:ALA:HB2	1:A:325:TRP:CE3	2.51	0.46
1:A:551:ARG:NE	1:A:551:ARG:HA	2.31	0.46
1:A:511:LEU:N	1:A:511:LEU:HD12	2.31	0.46
1:A:505:ARG:HB3	4:A:1613:HOH:O	2.14	0.46
1:A:523:LYS:NZ	1:A:523:LYS:CB	2.79	0.45
1:B:1:MET:HE2	1:B:95:LEU:HD12	1.97	0.45
1:A:279:GLN:NE2	4:A:2504:HOH:O	2.49	0.45
1:B:186:VAL:HG21	1:B:235:LYS:HD3	1.99	0.45
1:B:1:MET:CE	1:B:95:LEU:HD12	2.47	0.45
1:B:308:TYR:O	1:B:312:VAL:HG23	2.17	0.45
1:A:338:TRP:HA	1:A:338:TRP:CE3	2.52	0.44
1:A:64:SER:HB2	1:A:68:PHE:O	2.18	0.44
1:B:278:LEU:HD12	1:B:278:LEU:N	2.33	0.44
1:B:544:ILE:HA	1:B:545:PRO:HD3	1.82	0.44
1:B:10:PRO:HB3	4:B:2538:HOH:O	2.16	0.44
1:B:93:GLU:CD	1:B:94:LYS:H	2.20	0.44
1:A:367:ARG:NH2	4:A:2440:HOH:O	2.50	0.44
1:A:383:VAL:HG12	1:A:442:LEU:CD2	2.47	0.44
1:B:248:CYS:SG	1:B:296:PRO:HG2	2.57	0.44
1:B:550:ALA:O	1:B:552:GLY:N	2.51	0.44
1:A:363:MET:HG2	1:A:408:TYR:CD1	2.52	0.44
1:B:550:ALA:HA	1:B:566:ALA:HB3	2.00	0.44
1:B:558:LEU:HD21	1:B:584:ALA:HB2	2.00	0.44
1:A:377:TYR:N	1:A:378:PRO:CD	2.81	0.44
1:B:532:LEU:HD21	1:B:546:ILE:HG23	2.00	0.44
1:A:40:LEU:HD11	1:A:106:VAL:HG11	2.00	0.44
1:A:523:LYS:NZ	1:A:523:LYS:HB3	2.32	0.44
1:B:393:SER:OG	1:B:396:GLN:HG3	2.17	0.43
1:B:278:LEU:HA	1:B:285:ASN:ND2	2.28	0.43
1:B:377:TYR:N	1:B:378:PRO:CD	2.80	0.43
1:B:438:LYS:NZ	4:B:2583:HOH:O	2.50	0.43
1:A:84:TYR:O	1:A:114:TYR:HB3	2.18	0.43
1:A:450:THR:HG23	1:A:505:ARG:HA	1.99	0.43
1:A:28:ARG:HB3	1:A:70:TYR:CE1	2.54	0.43
1:B:129:PRO:O	1:B:132:VAL:HG22	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:ARG:O	1:A:119:PHE:HA	2.19	0.42
1:A:395:ARG:HB2	1:A:516:GLU:HB3	2.00	0.42
1:A:40:LEU:HG	1:A:54:PHE:CD2	2.54	0.42
1:A:570:THR:O	1:A:570:THR:HG23	2.19	0.42
1:B:363:MET:HB3	1:B:364:PRO:HD3	2.00	0.42
1:B:541:LYS:HE2	4:B:2151:HOH:O	2.18	0.42
1:A:1:MET:CE	1:A:93:GLU:HG2	2.50	0.42
1:B:78:PRO:HD2	4:B:2551:HOH:O	2.19	0.42
1:B:281:GLU:CA	1:B:282:PRO:C	2.85	0.42
1:B:243:ALA:HB2	1:B:325:TRP:CE3	2.54	0.42
1:A:10:PRO:O	1:A:11:ALA:HB2	2.19	0.42
1:A:549:ASP:OD1	1:A:551:ARG:HG2	2.18	0.42
1:A:75:VAL:O	1:A:77:PRO:HD3	2.19	0.42
1:A:331:ASN:ND2	1:A:331:ASN:H	2.17	0.42
1:B:132:VAL:HG11	1:B:353:TYR:CD1	2.55	0.42
1:B:338:TRP:HA	1:B:338:TRP:CE3	2.55	0.42
1:A:381:ASP:O	1:A:385:ARG:HG3	2.20	0.41
1:B:331:ASN:ND2	1:B:331:ASN:H	2.13	0.41
1:B:402:MET:O	1:B:406:HIS:HD2	2.03	0.41
1:A:515:ASP:C	1:A:517:MET:H	2.23	0.41
1:A:281:GLU:HA	1:A:282:PRO:C	2.40	0.41
1:A:279:GLN:O	1:A:284:PRO:HA	2.21	0.41
1:A:568:ALA:C	1:A:570:THR:N	2.73	0.41
1:A:567:GLU:HG2	1:A:568:ALA:N	2.36	0.41
1:A:94:LYS:HB3	4:A:2459:HOH:O	2.19	0.41
1:B:196:THR:HB	1:B:197:PRO:HD2	2.02	0.41
1:B:570:THR:HG23	1:B:570:THR:O	2.21	0.41
1:A:363:MET:HE3	1:A:363:MET:HA	2.03	0.41
1:A:223:GLU:HG2	4:A:2236:HOH:O	2.21	0.40
1:B:9:ARG:HA	1:B:10:PRO:HD3	1.83	0.40
1:B:557:ASN:HD22	1:B:559:LEU:N	2.17	0.40
1:A:45:TYR:CG	1:B:290:ALA:HA	2.57	0.40
1:B:512:HIS:ND1	1:B:516:GLU:OE1	2.51	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	586/588 (100%)	563 (96%)	20 (3%)	3 (0%)	29	18
1	B	586/588 (100%)	562 (96%)	20 (3%)	4 (1%)	22	12
All	All	1172/1176 (100%)	1125 (96%)	40 (3%)	7 (1%)	25	15

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	551	ARG
1	B	567	GLU
1	A	10	PRO
1	B	10	PRO
1	A	516	GLU
1	A	568	ALA
1	B	282	PRO

### 5.3.2 Protein sidechains [i](#)

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	521/521 (100%)	516 (99%)	5 (1%)	76	76
1	B	521/521 (100%)	516 (99%)	5 (1%)	76	76
All	All	1042/1042 (100%)	1032 (99%)	10 (1%)	76	76

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	155	GLU
1	A	194	TYR
1	A	331	ASN
1	A	363	MET
1	A	567	GLU
1	B	93	GLU
1	B	100	LYS
1	B	194	TYR
1	B	331	ASN
1	B	557	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	121	HIS
1	A	139	GLN
1	A	233	HIS
1	A	279	GLN
1	A	331	ASN
1	A	446	GLN
1	A	499	GLN
1	B	49	ASN
1	B	139	GLN
1	B	176	GLN
1	B	261	ASN
1	B	272	HIS
1	B	331	ASN
1	B	335	HIS
1	B	343	GLN
1	B	370	GLN
1	B	406	HIS
1	B	446	GLN
1	B	481	GLN
1	B	499	GLN
1	B	557	ASN

### 5.3.3 RNA ⓘ

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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	588/588 (100%)	0.02	23 (3%)	39 42	8, 15, 37, 67	0
1	B	588/588 (100%)	0.09	29 (4%)	29 33	9, 17, 41, 67	0
All	All	1176/1176 (100%)	0.06	52 (4%)	34 37	8, 16, 39, 67	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	571	LEU	9.6
1	A	570	THR	8.8
1	B	568	ALA	7.8
1	A	568	ALA	7.3
1	B	570	THR	7.3
1	A	514	ASP	7.1
1	B	514	ASP	7.1
1	B	569	GLU	6.3
1	A	551	ARG	6.2
1	A	547	PRO	6.1
1	B	547	PRO	6.1
1	A	569	GLU	5.5
1	B	548	LEU	5.4
1	B	551	ARG	5.0
1	B	92	GLU	4.7
1	B	515	ASP	4.6
1	A	567	GLU	4.5
1	B	549	ASP	4.5
1	A	49	ASN	4.3
1	B	567	GLU	4.2
1	A	571	LEU	4.2
1	B	93	GLU	4.0
1	A	513	ALA	3.9
1	A	51	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	546	ILE	3.5
1	A	516	GLU	3.4
1	A	550	ALA	3.3
1	A	512	HIS	3.3
1	B	572	CYS	3.3
1	B	512	HIS	3.3
1	B	104	PHE	3.2
1	A	515	ASP	3.0
1	B	513	ALA	3.0
1	B	550	ALA	3.0
1	A	48	GLN	3.0
1	A	432	CYS	2.8
1	A	250	TYR	2.8
1	A	548	LEU	2.7
1	A	549	ASP	2.7
1	B	275	GLU	2.5
1	B	259	TRP	2.4
1	B	108	THR	2.4
1	B	516	GLU	2.3
1	B	277	PRO	2.3
1	A	566	ALA	2.3
1	A	281	GLU	2.2
1	B	276	PHE	2.2
1	B	261	ASN	2.2
1	B	264	SER	2.1
1	B	278	LEU	2.1
1	B	91	GLY	2.1
1	A	588	TRP	2.1

## 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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CA	A	601	1/1	0.99	0.20	24,24,24,24	0
3	CA	B	602	1/1	1.00	0.21	25,25,25,25	0
2	CL	A	600	1/1	1.00	0.04	17,17,17,17	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.