



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:52 PM GMT

PDB ID : 1YRZ  
Title : Crystal structure of xylan beta-1,4-xylosidase from Bacillus Halodurans C-125  
Authors : Fedorov, A.A.; Fedorov, E.V.; Almo, S.C.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)  
Deposited on : 2005-02-05  
Resolution : 2.00 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

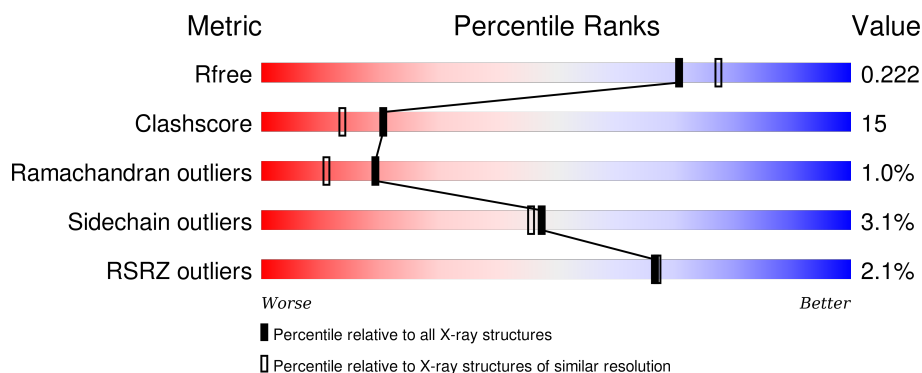
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

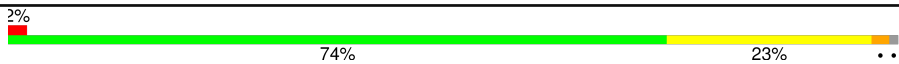

The reported resolution of this entry is 2.00 Å.

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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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. 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	528	 2% 74% 23% ..
1	B	528	 2% 74% 23% ..

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8867 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 xylan beta-1,4-xylosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	522	Total	C	N	O	S	0	0	0
			4229	2693	725	797	14			
1	B	522	Total	C	N	O	S	0	0	0
			4229	2693	725	797	14			

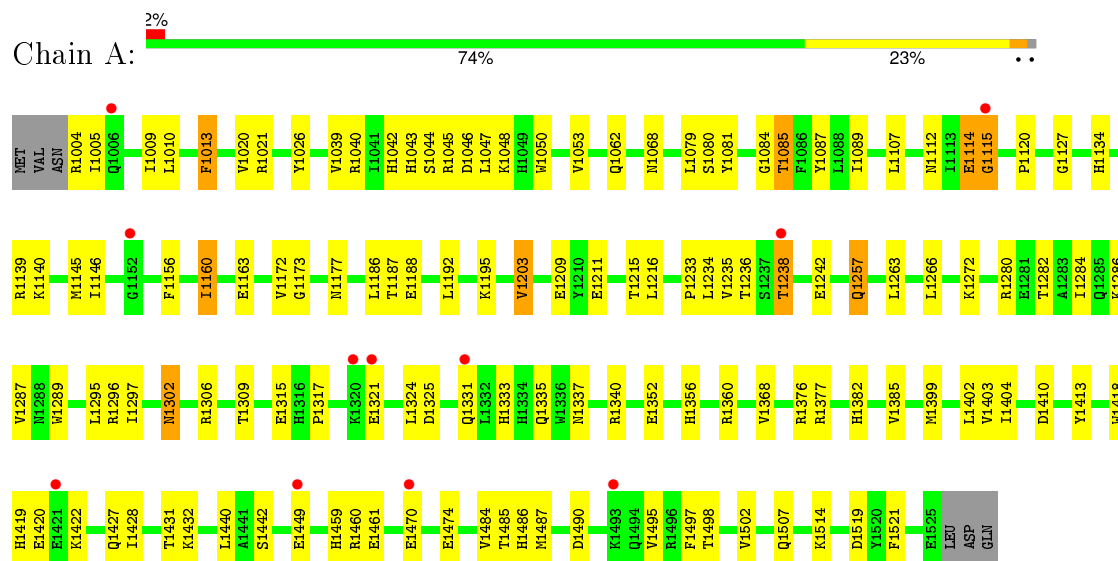
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	198	Total	O	0	0
			198	198		
2	B	211	Total	O	0	0
			211	211		

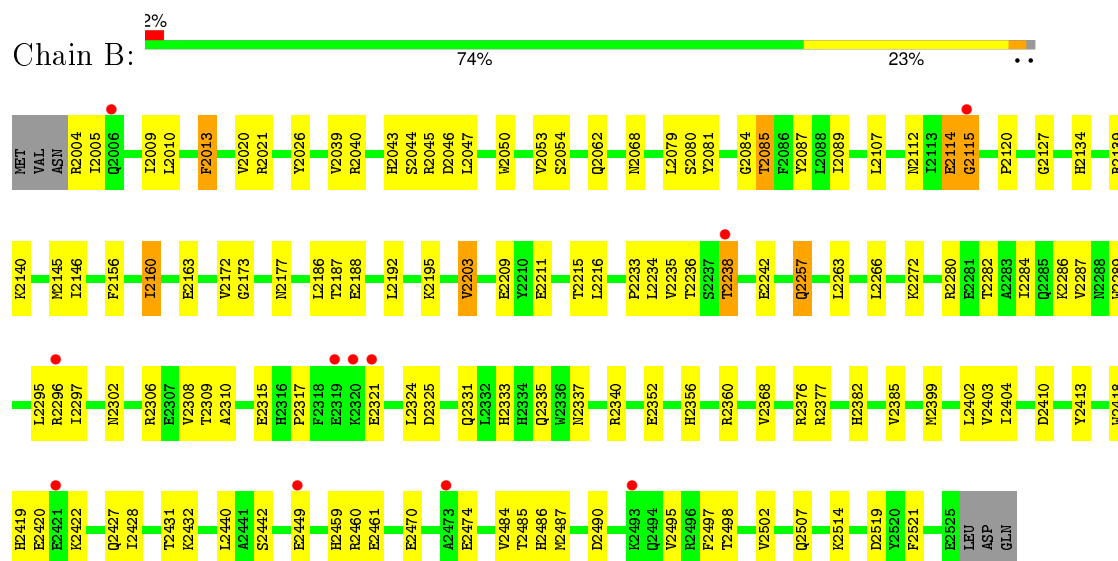
### 3 Residue-property plots

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: xylan beta-1,4-xylosidase



- Molecule 1: xylan beta-1,4-xylosidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.06 Å 125.82 Å 97.13 Å 90.00° 95.08° 90.00°	Depositor
Resolution (Å)	24.87 – 2.00 29.91 – 1.99	Depositor EDS
% Data completeness (in resolution range)	96.0 (24.87-2.00) 95.6 (29.91-1.99)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.26 (at 1.98 Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.207 , 0.224 0.206 , 0.222	Depositor DCC
$R_{free}$ test set	4213 reflections (5.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	18.1	Xtriage
Anisotropy	0.600	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 56.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 88594 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8867	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.28% 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 [i](#)

### 5.1 Standard geometry [i](#)

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	0/4362	0.69	4/5934 (0.1%)
1	B	0.34	0/4362	0.70	4/5934 (0.1%)
All	All	0.33	0/8724	0.69	8/11868 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2460	ARG	NE-CZ-NH2	-13.11	113.75	120.30
1	B	2460	ARG	NE-CZ-NH1	12.61	126.61	120.30
1	A	1460	ARG	NE-CZ-NH1	-12.55	114.02	120.30
1	A	1460	ARG	NE-CZ-NH2	11.83	126.22	120.30
1	B	2460	ARG	CD-NE-CZ	6.21	132.29	123.60
1	A	1460	ARG	CD-NE-CZ	5.88	131.83	123.60
1	A	1404	ILE	N-CA-C	-5.64	95.78	111.00
1	B	2404	ILE	N-CA-C	-5.60	95.88	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4229	0	4009	117	0
1	B	4229	0	4009	122	0
2	A	198	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	211	0	0	4	0
All	All	8867	0	8018	239	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 15.

All (239) 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:2385:VAL:HG21	1:B:2502:VAL:HG21	1.30	1.12
1:A:1385:VAL:HG21	1:A:1502:VAL:HG21	1.30	1.10
1:A:1427:GLN:HE21	1:A:1428:ILE:H	1.08	1.01
1:B:2427:GLN:HE21	1:B:2428:ILE:H	1.06	0.94
1:B:2399:MET:HB2	1:B:2507:GLN:HE21	1.31	0.94
1:A:1399:MET:HB2	1:A:1507:GLN:HE21	1.33	0.93
1:B:2257:GLN:HE21	1:B:2257:GLN:H	0.89	0.88
1:B:2146:ILE:HD13	1:B:2160:ILE:HD13	1.55	0.88
1:A:1257:GLN:H	1:A:1257:GLN:NE2	1.73	0.86
1:A:1146:ILE:HD13	1:A:1160:ILE:HD13	1.57	0.86
1:A:1257:GLN:N	1:A:1257:GLN:HE21	1.74	0.86
1:A:1257:GLN:H	1:A:1257:GLN:HE21	0.89	0.84
1:B:2257:GLN:NE2	1:B:2257:GLN:H	1.74	0.84
1:B:2484:VAL:HG13	1:B:2487:MET:HE3	1.60	0.82
1:A:1403:VAL:HG12	1:A:1413:TYR:CD2	2.16	0.81
1:B:2403:VAL:HG12	1:B:2413:TYR:CD2	2.16	0.80
1:B:2257:GLN:HE21	1:B:2257:GLN:N	1.75	0.79
1:A:1484:VAL:HG13	1:A:1487:MET:HE3	1.66	0.78
1:B:2484:VAL:HG13	1:B:2487:MET:CE	2.15	0.77
1:A:1382:HIS:HD2	1:A:1459:HIS:HD2	1.34	0.75
1:A:1484:VAL:HG13	1:A:1487:MET:CE	2.16	0.75
1:B:2337:ASN:HD21	1:B:2377:ARG:HH12	1.33	0.75
1:B:2382:HIS:HD2	1:B:2459:HIS:HD2	1.34	0.73
1:A:1337:ASN:HD21	1:A:1377:ARG:HH12	1.34	0.71
1:A:1337:ASN:ND2	1:A:1377:ARG:HH12	1.89	0.70
1:B:2235:VAL:HG22	1:B:2297:ILE:HD11	1.71	0.70
1:B:2188:GLU:O	1:B:2203:VAL:HG22	1.91	0.69
1:B:2287:VAL:HG21	1:B:2295:LEU:HB3	1.73	0.69
1:B:2139:ARG:HD2	1:B:2163:GLU:OE2	1.92	0.69
1:A:1235:VAL:HG22	1:A:1297:ILE:HD11	1.72	0.69
1:A:1188:GLU:O	1:A:1203:VAL:HG22	1.92	0.68
1:A:1287:VAL:HG21	1:A:1295:LEU:HB3	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1236:THR:OG1	1:A:1238:THR:HG23	1.94	0.68
1:B:2236:THR:OG1	1:B:2238:THR:HG23	1.93	0.68
1:A:1139:ARG:HD2	1:A:1163:GLU:OE2	1.93	0.67
1:B:2009:ILE:HD13	1:B:2050:TRP:HE1	1.59	0.67
1:B:2337:ASN:ND2	1:B:2377:ARG:HH12	1.91	0.67
1:B:2004:ARG:HD3	1:B:2310:ALA:HB3	1.77	0.67
1:B:2484:VAL:HG12	1:B:2484:VAL:O	1.96	0.66
1:A:1009:ILE:HD13	1:A:1050:TRP:HE1	1.61	0.66
1:A:1484:VAL:HG12	1:A:1484:VAL:O	1.97	0.65
1:B:2045:ARG:HG2	2:B:3263:HOH:O	1.96	0.65
1:A:1010:LEU:HB2	1:A:1282:THR:HB	1.79	0.64
1:A:1368:VAL:HG12	1:A:1368:VAL:O	1.98	0.64
1:B:2368:VAL:O	1:B:2368:VAL:HG12	1.98	0.64
1:A:1306:ARG:HG2	1:A:1306:ARG:HH11	1.63	0.63
1:B:2306:ARG:HH11	1:B:2306:ARG:HG2	1.63	0.63
1:B:2010:LEU:HB2	1:B:2282:THR:HB	1.79	0.62
1:B:2422:LYS:HZ1	1:B:2442:SER:HB3	1.64	0.62
1:B:2020:VAL:HG21	1:B:2079:LEU:O	1.99	0.62
1:B:2009:ILE:HG23	1:B:2050:TRP:CD1	2.35	0.61
1:A:1385:VAL:HG13	1:A:1521:PHE:CZ	2.35	0.61
1:A:1009:ILE:HG23	1:A:1050:TRP:CD1	2.35	0.61
1:A:1020:VAL:HG21	1:A:1079:LEU:O	2.01	0.61
1:B:2385:VAL:HG13	1:B:2521:PHE:CZ	2.36	0.60
1:A:1427:GLN:HE22	1:A:1440:LEU:HB2	1.66	0.60
1:A:1160:ILE:HD12	1:A:1177:ASN:HA	1.84	0.60
1:B:2382:HIS:CD2	1:B:2459:HIS:HD2	2.19	0.60
1:B:2160:ILE:HD12	1:B:2177:ASN:HA	1.84	0.60
1:A:1427:GLN:NE2	1:A:1428:ILE:H	1.90	0.59
1:B:2112:ASN:HB2	1:B:2115:GLY:HA3	1.84	0.59
1:A:1146:ILE:HG23	1:A:1160:ILE:HB	1.85	0.59
1:B:2427:GLN:NE2	1:B:2428:ILE:H	1.88	0.59
1:A:1112:ASN:HB2	1:A:1115:GLY:HA3	1.84	0.59
1:A:1382:HIS:HD2	1:A:1459:HIS:CD2	2.19	0.59
1:A:1280:ARG:NH2	1:A:1497:PHE:HB3	2.18	0.59
1:B:2427:GLN:HE22	1:B:2440:LEU:HB2	1.67	0.58
1:B:2382:HIS:HD2	1:B:2459:HIS:CD2	2.20	0.58
1:B:2287:VAL:HG22	1:B:2295:LEU:HD22	1.86	0.58
1:B:2399:MET:HB2	1:B:2507:GLN:NE2	2.12	0.58
1:B:2146:ILE:HG23	1:B:2160:ILE:HB	1.86	0.58
1:A:1382:HIS:CD2	1:A:1459:HIS:HD2	2.18	0.58
1:B:2385:VAL:CG1	1:B:2402:LEU:HD11	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2280:ARG:NH2	1:B:2497:PHE:HB3	2.19	0.57
1:B:2134:HIS:HD2	1:B:2140:LYS:NZ	2.02	0.57
1:A:1385:VAL:CG1	1:A:1402:LEU:HD11	2.34	0.57
1:B:2368:VAL:CG1	1:B:2368:VAL:O	2.52	0.57
1:B:2410:ASP:OD1	1:B:2486:HIS:HD2	1.88	0.57
1:A:1287:VAL:HG22	1:A:1295:LEU:HD22	1.85	0.57
1:A:1134:HIS:HD2	1:A:1140:LYS:NZ	2.03	0.57
1:A:1368:VAL:O	1:A:1368:VAL:CG1	2.52	0.56
1:A:1045:ARG:HG2	2:A:3302:HOH:O	2.05	0.56
1:A:1286:LYS:HD2	1:A:1309:THR:OG1	2.06	0.55
1:A:1385:VAL:CG2	1:A:1502:VAL:HG21	2.21	0.55
1:B:2009:ILE:HD13	1:B:2050:TRP:NE1	2.21	0.55
1:A:1009:ILE:HD13	1:A:1050:TRP:NE1	2.22	0.55
1:B:2286:LYS:HD2	1:B:2309:THR:OG1	2.06	0.55
1:A:1422:LYS:HZ1	1:A:1442:SER:HB3	1.71	0.54
1:A:1410:ASP:OD1	1:A:1486:HIS:HD2	1.90	0.53
1:B:2287:VAL:CG2	1:B:2295:LEU:HB3	2.38	0.53
1:A:1422:LYS:NZ	1:A:1442:SER:HB3	2.24	0.53
1:B:2385:VAL:HG21	1:B:2502:VAL:CG2	2.22	0.52
1:B:2146:ILE:HD13	1:B:2160:ILE:CD1	2.35	0.52
1:A:1287:VAL:CG2	1:A:1295:LEU:HB3	2.39	0.52
1:B:2422:LYS:NZ	1:B:2442:SER:HB3	2.25	0.52
1:A:1040:ARG:HH22	1:A:1335:GLN:HE22	1.57	0.52
1:B:2172:VAL:HG12	1:B:2173:GLY:N	2.25	0.52
1:B:2211:GLU:HA	1:B:2238:THR:HG22	1.91	0.51
1:A:1004:ARG:O	1:A:1048:LYS:HE2	2.10	0.51
1:A:1211:GLU:HA	1:A:1238:THR:HG22	1.91	0.51
1:A:1089:ILE:HD13	1:A:1107:LEU:HD13	1.92	0.51
1:A:1172:VAL:HG12	1:A:1173:GLY:N	2.26	0.51
1:A:1146:ILE:HD11	1:A:1177:ASN:ND2	2.26	0.51
1:A:1484:VAL:HG13	1:A:1487:MET:HE2	1.93	0.51
1:B:2385:VAL:CG2	1:B:2502:VAL:HG21	2.21	0.51
1:A:1399:MET:HB2	1:A:1507:GLN:NE2	2.14	0.51
1:B:2146:ILE:HD11	1:B:2177:ASN:ND2	2.25	0.51
1:B:2040:ARG:HH22	1:B:2335:GLN:HE22	1.58	0.51
1:A:1040:ARG:NH2	1:A:1335:GLN:NE2	2.58	0.51
1:B:2156:PHE:CG	1:B:2186:LEU:HA	2.46	0.51
1:A:1156:PHE:CG	1:A:1186:LEU:HA	2.47	0.51
1:B:2333:HIS:CD2	1:B:2335:GLN:H	2.30	0.50
1:A:1146:ILE:HD13	1:A:1160:ILE:CD1	2.37	0.50
1:B:2484:VAL:O	1:B:2484:VAL:CG1	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2040:ARG:NH2	1:B:2335:GLN:NE2	2.59	0.50
1:B:2089:ILE:HD13	1:B:2107:LEU:HD13	1.93	0.50
1:B:2234:LEU:HG	1:B:2235:VAL:HG23	1.94	0.50
1:B:2004:ARG:HB3	1:B:2310:ALA:HB2	1.94	0.50
1:A:1324:LEU:HD13	1:A:1325:ASP:N	2.27	0.50
1:A:1333:HIS:CD2	1:A:1335:GLN:H	2.30	0.49
1:A:1385:VAL:HG11	1:A:1402:LEU:HD11	1.95	0.49
1:B:2385:VAL:HG11	1:B:2402:LEU:HD11	1.93	0.49
1:A:1127:GLY:HA3	1:A:1145:MET:O	2.13	0.49
1:B:2356:HIS:HD2	1:B:2519:ASP:OD1	1.96	0.49
1:A:1134:HIS:HD2	1:A:1140:LYS:HZ3	1.61	0.48
1:B:2324:LEU:HD13	1:B:2324:LEU:C	2.34	0.48
1:B:2324:LEU:HD13	1:B:2325:ASP:N	2.28	0.48
1:A:1044:SER:HB2	1:A:1050:TRP:CD2	2.48	0.48
1:A:1484:VAL:O	1:A:1484:VAL:CG1	2.61	0.48
1:B:2519:ASP:HB3	2:B:3272:HOH:O	2.12	0.48
1:B:2127:GLY:HA3	1:B:2145:MET:O	2.14	0.48
1:A:1146:ILE:HG21	1:A:1160:ILE:HD13	1.94	0.48
1:A:1234:LEU:HG	1:A:1235:VAL:HG23	1.96	0.48
1:B:2287:VAL:HG23	1:B:2296:ARG:O	2.14	0.48
1:A:1306:ARG:HG2	1:A:1306:ARG:NH1	2.28	0.48
1:B:2352:GLU:CD	1:B:2360:ARG:HH12	2.17	0.48
1:B:2044:SER:HB2	1:B:2050:TRP:CD2	2.48	0.48
1:A:1340:ARG:NE	1:A:1368:VAL:HG13	2.29	0.48
1:A:1352:GLU:CD	1:A:1360:ARG:HH12	2.16	0.48
1:A:1080:SER:OG	1:A:1134:HIS:HE1	1.97	0.47
1:B:2146:ILE:HG21	1:B:2160:ILE:HD13	1.96	0.47
1:B:2068:ASN:O	1:B:2368:VAL:HG13	2.14	0.47
1:A:1484:VAL:HG12	2:A:3017:HOH:O	2.14	0.47
1:B:2306:ARG:NH1	1:B:2306:ARG:HG2	2.29	0.47
1:A:1356:HIS:HD2	1:A:1519:ASP:OD1	1.96	0.47
1:B:2484:VAL:HG12	2:B:3032:HOH:O	2.14	0.47
1:A:1068:ASN:O	1:A:1368:VAL:HG13	2.15	0.47
1:B:2432:LYS:HE3	1:B:2486:HIS:HB3	1.96	0.47
1:B:2514:LYS:HD2	2:B:3362:HOH:O	2.14	0.47
1:A:1432:LYS:HE3	1:A:1486:HIS:HB3	1.97	0.47
1:B:2080:SER:OG	1:B:2134:HIS:HE1	1.98	0.47
1:A:1427:GLN:NE2	1:A:1440:LEU:HB2	2.30	0.47
1:A:1272:LYS:CG	1:A:1461:GLU:HG2	2.45	0.46
1:B:2272:LYS:CG	1:B:2461:GLU:HG2	2.45	0.46
1:A:1324:LEU:C	1:A:1324:LEU:HD13	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1272:LYS:HG3	1:A:1461:GLU:HG2	1.97	0.46
1:A:1081:TYR:OH	1:A:1084:GLY:HA2	2.16	0.46
1:B:2427:GLN:NE2	1:B:2440:LEU:HB2	2.31	0.46
1:B:2340:ARG:NE	1:B:2368:VAL:HG13	2.30	0.46
1:B:2413:TYR:CE1	1:B:2507:GLN:NE2	2.84	0.46
1:A:1321:GLU:CD	1:A:1321:GLU:H	2.19	0.46
1:B:2081:TYR:OH	1:B:2084:GLY:HA2	2.15	0.46
1:A:1235:VAL:HG21	1:A:1263:LEU:HD23	1.98	0.46
1:A:1042:HIS:HD2	2:A:3291:HOH:O	1.99	0.46
1:A:1043:HIS:HB3	1:A:1053:VAL:CG1	2.47	0.45
1:A:1013:PHE:CE1	1:A:1498:THR:HA	2.52	0.45
1:B:2272:LYS:HG3	1:B:2461:GLU:HG2	1.98	0.45
1:B:2013:PHE:CE1	1:B:2498:THR:HA	2.50	0.45
1:B:2009:ILE:HD12	1:B:2284:ILE:CG2	2.46	0.45
1:A:1233:PRO:O	1:A:1302:ASN:ND2	2.50	0.45
1:A:1287:VAL:HG23	1:A:1296:ARG:O	2.16	0.45
1:A:1514:LYS:HD2	2:A:3107:HOH:O	2.17	0.45
1:B:2484:VAL:HG13	1:B:2487:MET:HE2	1.97	0.44
1:A:1009:ILE:HD12	1:A:1284:ILE:CG2	2.47	0.44
1:B:2134:HIS:HD2	1:B:2140:LYS:HZ3	1.65	0.44
1:A:1112:ASN:HB3	1:A:1114:GLU:OE1	2.17	0.44
1:A:1040:ARG:NH2	1:A:1335:GLN:HE22	2.13	0.44
1:B:2315:GLU:HG2	1:B:2317:PRO:HD3	1.99	0.44
1:A:1315:GLU:HG2	1:A:1317:PRO:HD3	1.99	0.44
1:B:2043:HIS:HB3	1:B:2053:VAL:CG1	2.47	0.44
1:A:1009:ILE:HG22	1:A:1010:LEU:HG	2.00	0.44
1:A:1089:ILE:CD1	1:A:1107:LEU:HD13	2.47	0.44
1:B:2187:THR:CG2	1:B:2203:VAL:HG21	2.48	0.44
1:A:1187:THR:CG2	1:A:1203:VAL:HG21	2.48	0.44
1:B:2089:ILE:CD1	1:B:2107:LEU:HD13	2.48	0.44
1:A:1272:LYS:HE2	1:A:1485:THR:HG21	1.99	0.44
1:B:2021:ARG:HD3	1:B:2026:TYR:CZ	2.52	0.44
1:B:2321:GLU:H	1:B:2321:GLU:CD	2.18	0.44
1:A:1413:TYR:CE1	1:A:1507:GLN:NE2	2.84	0.44
1:B:2020:VAL:CG2	1:B:2079:LEU:O	2.66	0.43
1:B:2235:VAL:HG21	1:B:2263:LEU:HD23	1.99	0.43
1:B:2188:GLU:O	1:B:2203:VAL:CG2	2.64	0.43
1:A:1418:TRP:CH2	1:A:1420:GLU:HA	2.53	0.43
1:A:1021:ARG:HD3	1:A:1026:TYR:CZ	2.53	0.43
1:A:1385:VAL:HG21	1:A:1502:VAL:CG2	2.22	0.43
1:A:1235:VAL:HG21	1:A:1263:LEU:CD2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2410:ASP:HA	1:B:2431:THR:O	2.19	0.43
1:A:1410:ASP:HA	1:A:1431:THR:O	2.19	0.43
1:B:2418:TRP:CH2	1:B:2420:GLU:HA	2.53	0.43
1:B:2062:GLN:HA	1:B:2120:PRO:HD3	2.01	0.43
1:B:2112:ASN:HB3	1:B:2114:GLU:OE1	2.18	0.43
1:B:2209:GLU:OE2	1:B:2495:VAL:CG2	2.67	0.43
1:B:2009:ILE:HG22	1:B:2010:LEU:HG	2.00	0.42
1:B:2195:LYS:HD3	1:B:2289:TRP:CZ2	2.54	0.42
1:A:1195:LYS:HD3	1:A:1289:TRP:CZ2	2.53	0.42
1:B:2427:GLN:HG3	1:B:2428:ILE:N	2.33	0.42
1:B:2004:ARG:HB2	1:B:2308:VAL:O	2.19	0.42
1:A:1385:VAL:HG11	1:A:1502:VAL:CG2	2.50	0.42
1:B:2419:HIS:HD2	1:B:2422:LYS:H	1.68	0.41
1:A:1062:GLN:HA	1:A:1120:PRO:HD3	2.01	0.41
1:B:2085:THR:HG23	1:B:2087:TYR:CE1	2.55	0.41
1:A:1085:THR:HG23	1:A:1087:TYR:CE1	2.55	0.41
1:B:2235:VAL:HG21	1:B:2263:LEU:CD2	2.50	0.41
1:B:2403:VAL:HG12	1:B:2413:TYR:HD2	1.78	0.41
1:A:1419:HIS:HD2	1:A:1422:LYS:H	1.67	0.41
1:A:1209:GLU:OE2	1:A:1495:VAL:CG2	2.69	0.41
1:A:1427:GLN:HG3	1:A:1428:ILE:N	2.35	0.41
1:B:2005:ILE:CG2	1:B:2009:ILE:HD11	2.51	0.41
1:B:2266:LEU:C	1:B:2266:LEU:HD12	2.40	0.41
1:B:2043:HIS:HB3	1:B:2053:VAL:HG13	2.03	0.41
1:A:1046:ASP:O	1:A:1047:LEU:HB2	2.21	0.41
1:B:2385:VAL:HG11	1:B:2502:VAL:CG2	2.51	0.41
1:A:1020:VAL:CG2	1:A:1079:LEU:O	2.68	0.41
1:B:2385:VAL:HG12	1:B:2402:LEU:HD11	2.03	0.41
1:B:2287:VAL:CG2	1:B:2295:LEU:HD22	2.50	0.41
1:A:1215:THR:HG22	1:A:1233:PRO:HB3	2.03	0.41
1:B:2040:ARG:NH2	1:B:2335:GLN:HE22	2.14	0.40
1:B:2272:LYS:HE2	1:B:2485:THR:HG21	2.03	0.40
1:A:1043:HIS:HB3	1:A:1053:VAL:HG13	2.04	0.40
1:B:2021:ARG:HD3	1:B:2026:TYR:CE1	2.56	0.40
1:B:2046:ASP:O	1:B:2047:LEU:HB2	2.21	0.40
1:A:1005:ILE:CG2	1:A:1009:ILE:HD11	2.51	0.40
1:B:2432:LYS:HG3	1:B:2486:HIS:CD2	2.56	0.40
1:B:2215:THR:HG22	1:B:2233:PRO:HB3	2.03	0.40
1:A:1266:LEU:C	1:A:1266:LEU:HD12	2.42	0.40
1:A:1287:VAL:CG2	1:A:1295:LEU:HD22	2.49	0.40
1:A:1068:ASN:O	1:A:1368:VAL:CG1	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1302:ASN:O	1:A:1302:ASN:ND2	2.55	0.40
1:B:2053:VAL:O	1:B:2054:SER:HB3	2.21	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	520/528 (98%)	494 (95%)	21 (4%)	5 (1%)	19	11
1	B	520/528 (98%)	496 (95%)	19 (4%)	5 (1%)	19	11
All	All	1040/1056 (98%)	990 (95%)	40 (4%)	10 (1%)	19	11

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1238	THR
1	B	2238	THR
1	A	1013	PHE
1	B	2013	PHE
1	A	1470	GLU
1	B	2470	GLU
1	A	1039	VAL
1	B	2039	VAL
1	A	1115	GLY
1	B	2115	GLY

### 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	453/459 (99%)	439 (97%)	14 (3%)	47	46
1	B	453/459 (99%)	439 (97%)	14 (3%)	47	46
All	All	906/918 (99%)	878 (97%)	28 (3%)	47	46

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1085	THR
1	A	1114	GLU
1	A	1160	ILE
1	A	1192	LEU
1	A	1203	VAL
1	A	1216	LEU
1	A	1242	GLU
1	A	1257	GLN
1	A	1302	ASN
1	A	1331	GLN
1	A	1376	ARG
1	A	1449	GLU
1	A	1474	GLU
1	A	1490	ASP
1	B	2085	THR
1	B	2114	GLU
1	B	2160	ILE
1	B	2192	LEU
1	B	2203	VAL
1	B	2216	LEU
1	B	2242	GLU
1	B	2257	GLN
1	B	2302	ASN
1	B	2331	GLN
1	B	2376	ARG
1	B	2449	GLU
1	B	2474	GLU
1	B	2490	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1042	HIS
1	A	1134	HIS
1	A	1240	GLN
1	A	1257	GLN
1	A	1302	ASN
1	A	1333	HIS
1	A	1337	ASN
1	A	1379	GLN
1	A	1382	HIS
1	A	1411	HIS
1	A	1419	HIS
1	A	1427	GLN
1	A	1459	HIS
1	A	1486	HIS
1	A	1507	GLN
1	B	2082	HIS
1	B	2134	HIS
1	B	2257	GLN
1	B	2302	ASN
1	B	2333	HIS
1	B	2337	ASN
1	B	2379	GLN
1	B	2382	HIS
1	B	2411	HIS
1	B	2419	HIS
1	B	2427	GLN
1	B	2459	HIS
1	B	2486	HIS
1	B	2507	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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	522/528 (98%)	-0.11	11 (2%) 67 67	11, 20, 35, 52	0
1	B	522/528 (98%)	-0.03	11 (2%) 67 67	13, 21, 36, 49	0
All	All	1044/1056 (98%)	-0.07	22 (2%) 67 67	11, 21, 36, 52	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2238	THR	4.6
1	B	2115	GLY	4.4
1	A	1115	GLY	3.9
1	B	2449	GLU	3.8
1	B	2493	LYS	3.8
1	A	1238	THR	3.7
1	A	1421	GLU	3.4
1	B	2296	ARG	2.9
1	A	1152	GLY	2.6
1	B	2421	GLU	2.5
1	B	2319	GLU	2.5
1	B	2320	LYS	2.4
1	A	1320	LYS	2.4
1	A	1493	LYS	2.4
1	A	1006	GLN	2.4
1	B	2473	ALA	2.4
1	B	2006	GLN	2.4
1	A	1449	GLU	2.4
1	A	1470	GLU	2.3
1	A	1321	GLU	2.2
1	A	1331	GLN	2.2
1	B	2321	GLU	2.2

## 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.