



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:22 PM GMT

PDB ID : 3X17
Title : Crystal structure of metagenome-derived glycoside hydrolase family 9 endoglucanase
Authors : Okano, H.; Angkawidjaja, C.; Kanaya, S.
Deposited on : 2014-10-30
Resolution : 2.15 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

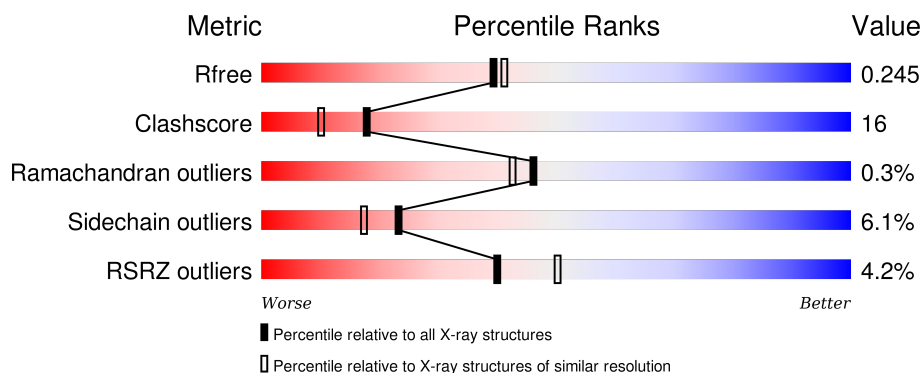
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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 ≥ 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	559	<div> <div>5%</div> <div> <div></div> <div>71%</div> <div>24%</div> <div>• •</div> </div> </div>
1	B	559	<div> <div>4%</div> <div> <div></div> <div>76%</div> <div>20%</div> <div>• •</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CA	B	602	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8881 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 Endoglucanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	548	Total	C	N	O	S	0	0	0
			4239	2706	748	776	9			
1	A	548	Total	C	N	O	S	0	0	0
			4239	2706	748	776	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	19	MET	-	EXPRESSION TAG	UNP W8PF21
A	19	MET	-	EXPRESSION TAG	UNP W8PF21

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Ca	0	0
			2	2		
3	A	2	Total	Ca	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	229	Total	O	0	0
			229	229		

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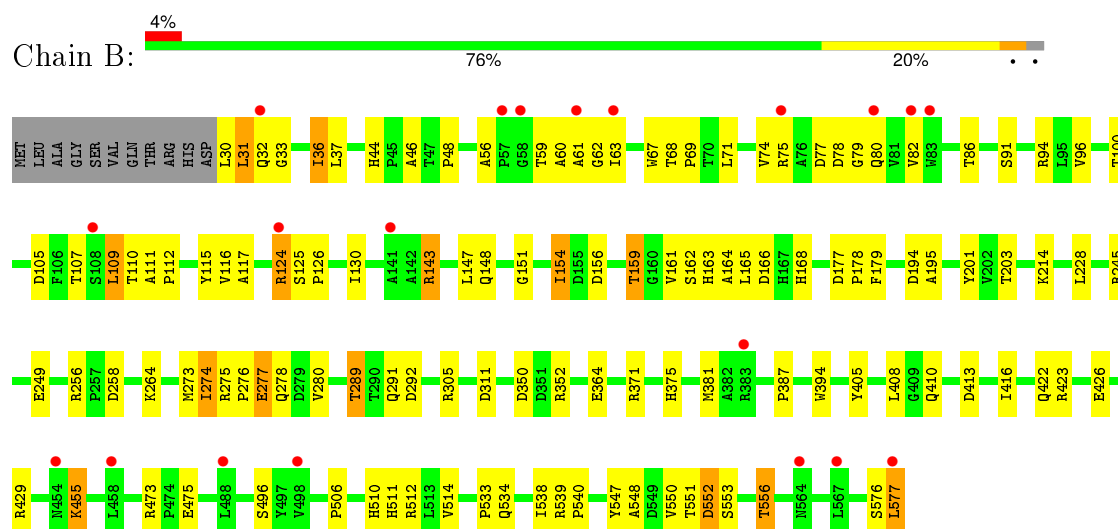
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	168	Total 168	O 168	0	0

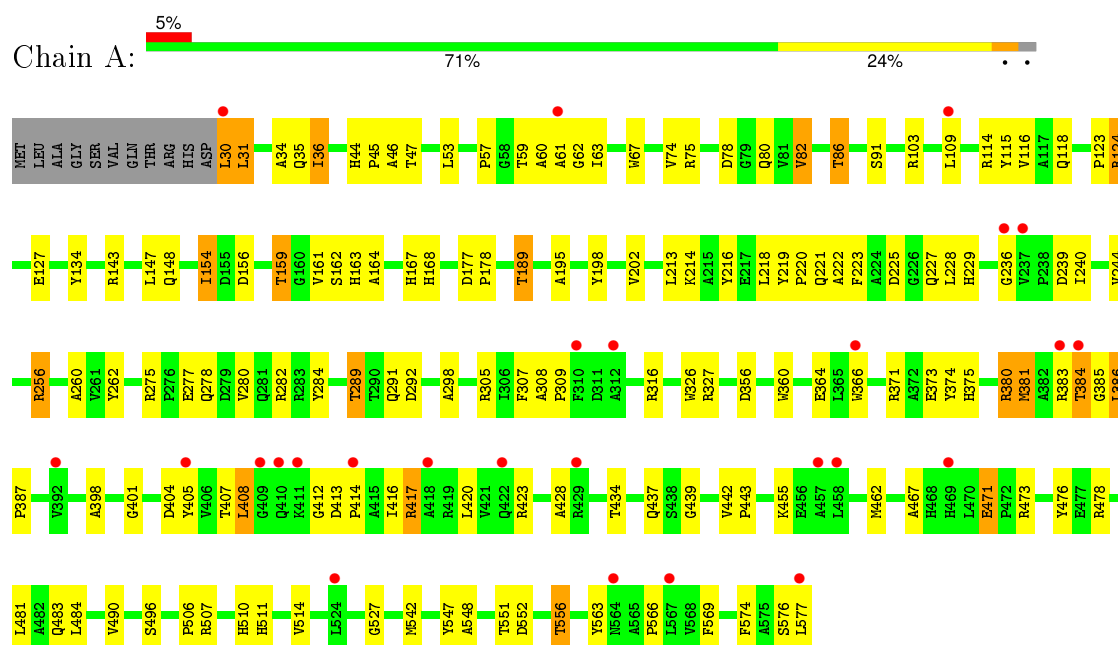
3 Residue-property plots

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: Endoglucanase



• Molecule 1: Endoglucanase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.63Å 89.91Å 151.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.96 – 2.15 43.95 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.7 (43.96-2.15) 99.7 (43.95-2.15)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.187 , 0.246 0.188 , 0.245	Depositor DCC
R_{free} test set	3207 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	39.3	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 63283 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8881	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

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

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	0.53	0/4365	0.59	0/5968
1	B	0.63	0/4365	0.65	1/5968 (0.0%)
All	All	0.58	0/8730	0.62	1/11936 (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	143	ARG	NE-CZ-NH2	-5.52	117.54	120.30

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	4239	0	4098	138	0
1	B	4239	0	4098	126	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	168	0	0	13	0
4	B	229	0	0	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8881	0	8196	263	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 16.

All (263) 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:59:THR:CG2	1:B:60:ALA:H	1.46	1.22
1:B:59:THR:HG22	1:B:60:ALA:N	1.48	1.21
1:A:60:ALA:CB	1:A:61:ALA:HA	1.70	1.21
1:A:60:ALA:HB1	1:A:61:ALA:CA	1.79	1.12
1:B:533:PRO:HB3	1:B:538:ILE:CD1	1.84	1.06
1:B:143:ARG:HD2	1:B:228:LEU:O	1.54	1.06
1:A:124:ARG:HH11	1:A:124:ARG:HG3	1.17	1.05
1:A:60:ALA:HB1	1:A:61:ALA:HA	1.04	1.03
1:A:30:LEU:O	1:A:30:LEU:HD12	1.60	1.01
1:B:533:PRO:HB3	1:B:538:ILE:HD12	1.43	0.99
1:B:159:THR:HG22	1:B:161:VAL:H	1.27	0.98
1:B:156:ASP:OD2	1:B:159:THR:HB	1.63	0.96
1:A:156:ASP:OD2	1:A:159:THR:HB	1.63	0.96
1:A:289:THR:HG22	1:A:292:ASP:H	1.35	0.89
1:B:289:THR:HG22	1:B:292:ASP:H	1.36	0.89
1:B:60:ALA:CB	1:B:63:ILE:HG13	2.03	0.89
1:B:60:ALA:HB1	1:B:63:ILE:N	1.87	0.87
1:B:159:THR:HG23	1:B:161:VAL:HG23	1.57	0.87
1:A:159:THR:HG22	1:A:161:VAL:H	1.40	0.87
1:B:550:VAL:HG23	4:B:752:HOH:O	1.76	0.85
1:A:289:THR:CG2	1:A:291:GLN:HG3	2.08	0.84
1:A:542:MET:HG3	4:A:750:HOH:O	1.78	0.83
1:A:168:HIS:HB2	4:A:826:HOH:O	1.79	0.82
1:B:539:ARG:HB2	1:B:540:PRO:HD2	1.61	0.82
1:B:533:PRO:HB3	1:B:538:ILE:HD11	1.60	0.82
1:A:417:ARG:HG3	1:A:417:ARG:O	1.80	0.81
1:A:44:HIS:HD2	1:A:46:ALA:H	1.24	0.81
1:B:33:GLY:HA2	4:B:799:HOH:O	1.81	0.81
1:B:116:VAL:HG11	1:B:124:ARG:HD3	1.64	0.80
1:B:143:ARG:CD	1:B:228:LEU:O	2.32	0.78
1:B:60:ALA:HA	1:B:61:ALA:HB3	1.65	0.78
1:A:124:ARG:NH1	1:A:124:ARG:HG3	1.96	0.76
1:B:548:ALA:H	1:B:556:THR:HG21	1.50	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:THR:HG22	1:B:60:ALA:H	0.64	0.76
1:B:289:THR:CG2	1:B:291:GLN:HG3	2.16	0.76
1:B:60:ALA:HB3	1:B:63:ILE:HG13	1.67	0.75
1:A:159:THR:HG23	1:A:161:VAL:HG23	1.69	0.75
1:A:86:THR:CG2	4:A:851:HOH:O	2.34	0.74
1:B:32:GLN:HA	4:B:799:HOH:O	1.85	0.74
1:B:159:THR:CG2	1:B:161:VAL:H	1.99	0.73
1:A:36:ILE:HG13	1:A:123:PRO:HG2	1.70	0.73
1:A:548:ALA:H	1:A:556:THR:HG21	1.52	0.73
1:A:289:THR:HG23	1:A:291:GLN:HG3	1.70	0.72
1:A:381:MET:O	1:A:385:GLY:N	2.22	0.72
1:B:44:HIS:HD2	1:B:46:ALA:H	1.37	0.72
1:A:148:GLN:OE1	1:A:511:HIS:HE1	1.72	0.72
1:B:60:ALA:HB1	1:B:63:ILE:HG13	1.72	0.72
1:A:316:ARG:NH2	4:A:865:HOH:O	2.22	0.72
1:A:177:ASP:HB2	1:A:178:PRO:HD2	1.71	0.71
1:A:159:THR:CG2	1:A:161:VAL:HG23	2.21	0.71
1:A:60:ALA:CB	1:A:61:ALA:CA	2.50	0.70
1:A:225:ASP:OD2	1:A:236:GLY:N	2.26	0.69
1:A:86:THR:HG21	4:A:851:HOH:O	1.91	0.68
1:A:256:ARG:HD2	1:A:260:ALA:HB3	1.74	0.68
1:A:143:ARG:NH1	1:A:228:LEU:O	2.26	0.68
1:A:327:ARG:HD3	4:A:808:HOH:O	1.93	0.67
1:B:547:TYR:CD1	1:B:556:THR:HG23	2.30	0.67
1:A:366:TRP:HH2	1:A:412:GLY:HA2	1.58	0.67
1:A:222:ALA:HB2	1:A:576:SER:HB3	1.76	0.67
1:B:94:ARG:HD3	4:B:871:HOH:O	1.95	0.66
1:B:56:ALA:HB3	1:B:59:THR:OG1	1.96	0.65
1:B:67:TRP:CH2	1:B:69:PRO:HG3	2.30	0.65
1:B:473:ARG:NH1	1:B:475:GLU:OE2	2.29	0.65
1:B:74:VAL:CG1	1:B:79:GLY:HA2	2.26	0.65
1:B:256:ARG:HD2	1:B:258:ASP:OD1	1.96	0.65
1:A:34:ALA:HB1	1:A:53:LEU:HD11	1.79	0.65
1:B:148:GLN:OE1	1:B:511:HIS:HE1	1.81	0.64
1:B:163:HIS:HD2	1:B:164:ALA:O	1.80	0.64
1:B:44:HIS:CD2	1:B:46:ALA:H	2.16	0.64
1:A:412:GLY:O	1:A:414:PRO:HD3	1.98	0.64
1:B:31:LEU:HD11	1:B:67:TRP:CH2	2.33	0.64
1:A:405:TYR:CD2	1:A:420:LEU:HD12	2.33	0.64
1:A:386:LEU:HB3	1:A:387:PRO:HD2	1.78	0.64
1:A:118:GLN:NE2	1:A:124:ARG:HG3	2.13	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:371:ARG:NH2	4:B:804:HOH:O	2.31	0.63
1:A:289:THR:CG2	1:A:292:ASP:H	2.09	0.62
1:A:163:HIS:HD2	1:A:164:ALA:O	1.81	0.62
1:A:62:GLY:HA3	4:A:745:HOH:O	1.99	0.62
1:A:116:VAL:HG11	1:A:124:ARG:HD3	1.80	0.62
1:B:289:THR:CG2	1:B:292:ASP:H	2.09	0.62
1:B:30:LEU:HD23	1:B:30:LEU:O	2.00	0.62
1:A:159:THR:HG22	1:A:161:VAL:N	2.13	0.62
1:B:289:THR:HG23	1:B:291:GLN:HG3	1.80	0.61
1:B:36:ILE:HD13	1:B:125:SER:N	2.15	0.61
1:A:366:TRP:CH2	1:A:412:GLY:HA2	2.34	0.61
1:B:168:HIS:HE1	1:A:552:ASP:OD2	1.84	0.61
1:B:275:ARG:HB3	1:B:277:GLU:OE1	2.00	0.61
1:B:59:THR:CG2	1:B:60:ALA:N	2.20	0.60
1:A:44:HIS:CD2	1:A:46:ALA:H	2.13	0.60
1:B:60:ALA:HA	1:B:62:GLY:N	2.17	0.60
1:A:308:ALA:HB3	1:A:309:PRO:HD3	1.84	0.60
1:B:576:SER:O	1:B:577:LEU:HB2	2.01	0.60
1:A:159:THR:CG2	1:A:161:VAL:CG2	2.79	0.60
1:A:471:GLU:OE1	1:A:471:GLU:O	2.20	0.59
1:B:159:THR:CG2	1:B:161:VAL:HG23	2.30	0.59
1:A:124:ARG:HH11	1:A:124:ARG:CG	2.03	0.59
1:B:36:ILE:HD11	1:B:124:ARG:C	2.23	0.59
1:B:36:ILE:CD1	1:B:125:SER:N	2.65	0.59
1:B:553:SER:OG	1:B:556:THR:HB	2.02	0.59
1:B:177:ASP:HB2	1:B:178:PRO:CD	2.32	0.59
1:A:159:THR:CG2	1:A:161:VAL:HB	2.33	0.58
1:B:179:PHE:CD2	1:B:256:ARG:HD3	2.38	0.58
1:A:60:ALA:HB1	1:A:61:ALA:C	2.23	0.58
1:B:36:ILE:CD1	1:B:124:ARG:C	2.72	0.58
1:B:375:HIS:HE1	1:B:405:TYR:OH	1.85	0.58
1:B:126:PRO:HD3	4:B:880:HOH:O	2.04	0.58
1:A:360:TRP:O	1:A:364:GLU:HG2	2.03	0.58
1:A:548:ALA:H	1:A:556:THR:CG2	2.16	0.58
1:A:289:THR:HG21	1:A:291:GLN:HG3	1.85	0.57
1:A:164:ALA:HB3	1:A:277:GLU:HG2	1.86	0.57
1:B:36:ILE:HD11	1:B:124:ARG:CA	2.35	0.57
1:A:371:ARG:HD2	1:A:373:GLU:OE2	2.04	0.56
1:A:356:ASP:HB2	1:A:398:ALA:HB2	1.88	0.56
1:A:510:HIS:HD2	1:A:551:THR:O	1.89	0.56
1:A:563:TYR:O	1:A:566:PRO:HD2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:TYR:N	1:A:220:PRO:HD3	2.22	0.55
1:B:32:GLN:CB	4:B:799:HOH:O	2.53	0.55
1:B:115:TYR:CE2	1:B:130:ILE:HD12	2.42	0.55
1:A:78:ASP:HB3	1:A:80:GLN:H	1.70	0.55
1:B:177:ASP:HB2	1:B:178:PRO:HD2	1.88	0.55
1:B:68:THR:HG21	1:B:86:THR:OG1	2.06	0.55
1:A:60:ALA:HB2	1:A:63:ILE:HD12	1.87	0.54
1:A:496:SER:O	1:A:506:PRO:HD3	2.08	0.54
1:B:59:THR:O	1:B:61:ALA:CB	2.55	0.54
1:B:60:ALA:CA	1:B:61:ALA:HB3	2.35	0.54
1:B:548:ALA:H	1:B:556:THR:CG2	2.19	0.54
1:A:30:LEU:C	1:A:30:LEU:HD12	2.28	0.53
1:B:533:PRO:CB	1:B:538:ILE:HD11	2.33	0.53
1:B:82:VAL:HG21	4:B:920:HOH:O	2.09	0.53
1:A:213:LEU:HD21	1:A:244:VAL:HG11	1.91	0.53
1:A:462:MET:HG3	1:A:569:PHE:CE1	2.44	0.53
1:B:115:TYR:CD2	1:B:130:ILE:HD12	2.44	0.52
1:A:434:THR:HA	1:A:437:GLN:HE21	1.73	0.52
1:A:202:VAL:HG21	1:A:262:TYR:O	2.09	0.52
1:B:249:GLU:HG2	4:B:922:HOH:O	2.09	0.52
1:B:539:ARG:HB2	1:B:540:PRO:CD	2.37	0.52
1:B:289:THR:HG21	1:B:291:GLN:HG3	1.90	0.52
1:B:60:ALA:HB1	1:B:63:ILE:H	1.72	0.52
1:A:383:ARG:HD2	4:A:807:HOH:O	2.09	0.52
1:A:547:TYR:CD1	1:A:556:THR:HG23	2.45	0.52
1:A:511:HIS:HD2	1:A:514:VAL:H	1.58	0.52
1:B:63:ILE:HD11	1:B:100:THR:HG21	1.91	0.51
1:B:68:THR:CG2	1:B:86:THR:OG1	2.58	0.51
1:A:134:TYR:CE1	1:A:484:LEU:HD13	2.45	0.51
1:A:366:TRP:CD1	1:A:375:HIS:HB2	2.46	0.51
1:A:481:LEU:HB2	1:A:574:PHE:CZ	2.45	0.51
1:B:426:GLU:OE1	1:B:429:ARG:NH1	2.43	0.51
1:A:159:THR:HG21	1:A:161:VAL:HB	1.92	0.51
1:B:381:MET:SD	1:B:387:PRO:HD3	2.51	0.51
1:A:298:ALA:HB1	1:A:360:TRP:CE2	2.46	0.51
1:B:60:ALA:CB	1:B:63:ILE:N	2.69	0.51
1:B:264:LYS:HE2	4:B:884:HOH:O	2.12	0.50
1:A:386:LEU:CD2	1:A:420:LEU:HD21	2.41	0.50
1:B:77:ASP:OD1	1:B:78:ASP:N	2.43	0.50
1:A:82:VAL:HG13	1:A:109:LEU:HD13	1.93	0.50
1:B:31:LEU:HD11	1:B:67:TRP:HH2	1.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:ARG:NH2	1:B:311:ASP:OD2	2.41	0.50
1:A:275:ARG:HD2	1:A:278:GLN:NE2	2.27	0.50
1:A:177:ASP:HB2	1:A:178:PRO:CD	2.39	0.50
1:A:159:THR:CG2	1:A:161:VAL:CB	2.90	0.49
1:B:510:HIS:HD2	1:B:551:THR:O	1.95	0.49
1:B:375:HIS:HD2	4:B:793:HOH:O	1.95	0.49
1:A:44:HIS:HB3	1:A:47:THR:HG23	1.94	0.49
1:A:227:GLN:HG2	1:A:228:LEU:HD23	1.94	0.49
1:B:154:ILE:O	1:B:162:SER:HA	2.13	0.49
1:A:434:THR:HA	1:A:437:GLN:NE2	2.27	0.48
1:A:576:SER:O	1:A:577:LEU:CB	2.60	0.48
1:A:60:ALA:HB3	1:A:61:ALA:HA	1.82	0.48
1:A:386:LEU:HD12	1:A:386:LEU:H	1.78	0.48
1:B:163:HIS:HE1	4:B:723:HOH:O	1.97	0.48
1:A:163:HIS:HB2	1:A:277:GLU:CD	2.34	0.47
1:B:59:THR:C	1:B:61:ALA:HB3	2.35	0.47
1:A:405:TYR:HD2	1:A:420:LEU:HD12	1.75	0.47
1:B:59:THR:O	1:B:61:ALA:HB3	2.15	0.47
1:A:473:ARG:HD2	1:A:476:TYR:CD2	2.50	0.47
1:A:103:ARG:NH2	1:A:439:GLY:O	2.47	0.47
1:A:63:ILE:O	1:A:63:ILE:HG22	2.14	0.47
1:A:223:PHE:HA	1:A:227:GLN:OE1	2.14	0.47
1:A:326:TRP:CD1	1:A:374:TYR:HE1	2.32	0.47
1:B:179:PHE:CE2	1:B:256:ARG:HD3	2.49	0.47
1:B:105:ASP:OD1	1:B:107:THR:OG1	2.23	0.47
1:B:110:THR:O	1:B:112:PRO:HD3	2.14	0.47
1:B:60:ALA:HA	1:B:61:ALA:C	2.34	0.47
1:A:289:THR:HG22	1:A:292:ASP:N	2.17	0.47
1:A:44:HIS:CD2	1:A:45:PRO:HD2	2.50	0.46
1:A:86:THR:HG23	4:A:838:HOH:O	2.15	0.46
1:B:510:HIS:CD2	1:B:551:THR:O	2.68	0.46
1:B:60:ALA:HA	1:B:61:ALA:CB	2.30	0.46
1:A:35:GLN:O	1:A:53:LEU:HD12	2.15	0.46
1:B:109:LEU:C	1:B:109:LEU:CD2	2.83	0.46
1:A:380:ARG:O	1:A:384:THR:CG2	2.64	0.46
1:B:32:GLN:CA	4:B:799:HOH:O	2.54	0.46
1:A:442:VAL:HA	1:A:443:PRO:HD3	1.83	0.46
1:A:59:THR:HG22	4:A:745:HOH:O	2.16	0.45
1:A:163:HIS:HB2	1:A:277:GLU:OE1	2.17	0.45
1:B:203:THR:HG22	1:B:394:TRP:HB2	1.98	0.45
1:A:404:ASP:O	1:A:408:LEU:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:305:ARG:NH2	1:B:364:GLU:OE1	2.50	0.45
1:A:375:HIS:HB3	4:A:829:HOH:O	2.17	0.45
1:B:75:ARG:NH2	1:B:78:ASP:OD2	2.49	0.45
1:A:473:ARG:HD2	1:A:476:TYR:CE2	2.51	0.45
1:A:576:SER:C	1:A:577:LEU:HG	2.37	0.45
1:A:305:ARG:NH2	1:A:364:GLU:OE1	2.49	0.45
1:B:151:GLY:HA2	1:B:166:ASP:O	2.16	0.45
1:B:124:ARG:NE	4:B:802:HOH:O	2.50	0.45
1:A:307:PHE:O	1:A:308:ALA:C	2.55	0.45
1:B:159:THR:CG2	1:B:161:VAL:CG2	2.94	0.45
1:B:148:GLN:OE1	1:B:511:HIS:CE1	2.67	0.45
1:B:511:HIS:HD2	1:B:514:VAL:H	1.64	0.45
1:A:398:ALA:O	1:A:401:GLY:N	2.50	0.45
1:B:276:PRO:HD2	1:B:277:GLU:OE1	2.17	0.44
1:A:115:TYR:O	1:A:127:GLU:HA	2.18	0.44
1:B:159:THR:CG2	1:B:161:VAL:HB	2.47	0.44
1:B:274:ILE:HB	1:B:278:GLN:HE21	1.82	0.44
1:B:59:THR:O	1:B:61:ALA:HB2	2.17	0.44
1:A:576:SER:O	1:A:577:LEU:HB2	2.17	0.44
1:A:218:LEU:C	1:A:220:PRO:HD3	2.38	0.44
1:B:163:HIS:HB2	1:B:277:GLU:CD	2.38	0.44
1:A:275:ARG:HD2	1:A:278:GLN:HE21	1.81	0.44
1:B:78:ASP:HB2	1:B:80:GLN:H	1.83	0.43
1:A:118:GLN:NE2	1:A:124:ARG:HH11	2.16	0.43
1:A:60:ALA:HB2	1:A:63:ILE:CD1	2.49	0.43
1:B:159:THR:HG21	1:B:161:VAL:HB	2.01	0.43
1:A:78:ASP:CB	1:A:80:GLN:H	2.32	0.43
1:A:239:ASP:O	1:A:240:ILE:C	2.57	0.43
1:B:273:MET:HA	1:B:512:ARG:HG2	2.01	0.43
1:B:214:LYS:HD2	1:B:214:LYS:HA	1.87	0.43
1:A:510:HIS:CD2	1:A:551:THR:O	2.69	0.42
1:A:74:VAL:HG12	1:A:75:ARG:O	2.19	0.42
1:B:413:ASP:HB3	1:B:416:ILE:HD12	2.01	0.42
1:B:350:ASP:O	1:B:352:ARG:HG3	2.20	0.42
1:A:221:GLN:HG2	1:A:576:SER:HB2	2.00	0.42
1:B:71:LEU:HD11	1:B:117:ALA:HB1	2.01	0.42
1:A:218:LEU:HD23	1:A:218:LEU:HA	1.80	0.42
1:A:82:VAL:HG13	1:A:109:LEU:CD1	2.49	0.42
1:A:148:GLN:OE1	1:A:511:HIS:CE1	2.61	0.42
1:A:143:ARG:NH1	1:A:229:HIS:HB2	2.34	0.42
1:A:527:GLY:HA2	1:A:563:TYR:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:TYR:C	1:A:216:TYR:CD2	2.93	0.42
1:A:413:ASP:OD2	1:A:416:ILE:HG13	2.20	0.42
1:B:74:VAL:HG13	1:B:79:GLY:C	2.40	0.41
1:A:189:THR:HB	4:A:737:HOH:O	2.19	0.41
1:A:57:PRO:C	1:A:59:THR:H	2.23	0.41
1:B:177:ASP:CB	1:B:178:PRO:CD	2.95	0.41
1:A:490:VAL:HG12	1:A:490:VAL:O	2.19	0.41
1:B:455:LYS:HD2	1:B:455:LYS:C	2.40	0.41
1:B:194:ASP:HB2	1:B:201:TYR:CD1	2.55	0.41
1:B:48:PRO:HA	1:B:107:THR:OG1	2.21	0.41
1:B:63:ILE:HA	4:B:924:HOH:O	2.20	0.41
1:A:31:LEU:HD21	1:A:67:TRP:HZ2	1.84	0.41
1:B:68:THR:HA	1:B:69:PRO:HD3	1.89	0.41
1:A:443:PRO:HD3	1:A:483:GLN:OE1	2.21	0.41
1:B:56:ALA:O	1:B:59:THR:HB	2.21	0.41
1:B:550:VAL:HG22	1:B:552:ASP:OD1	2.21	0.41
1:A:154:ILE:O	1:A:162:SER:HB2	2.21	0.41
1:B:496:SER:O	1:B:506:PRO:HD3	2.21	0.40
1:A:167:HIS:CE1	1:A:198:TYR:HB3	2.56	0.40
1:B:111:ALA:HA	1:B:112:PRO:HD2	1.90	0.40
1:B:74:VAL:HG11	1:B:79:GLY:HA2	2.02	0.40
1:A:386:LEU:HD22	1:A:420:LEU:CD2	2.51	0.40
1:A:507:ARG:HD2	4:A:702:HOH:O	2.21	0.40
1:A:428:ALA:HB2	1:A:467:ALA:HB2	2.03	0.40
1:A:282:ARG:HG2	1:A:284:TYR:CZ	2.57	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	546/559 (98%)	510 (93%)	35 (6%)	1 (0%)	52 51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	546/559 (98%)	521 (95%)	23 (4%)	2 (0%)	39	34
All	All	1092/1118 (98%)	1031 (94%)	58 (5%)	3 (0%)	46	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	195	ALA
1	A	195	ALA
1	B	96	VAL

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	419/428 (98%)	391 (93%)	28 (7%)	20	13
1	B	419/428 (98%)	396 (94%)	23 (6%)	27	21
All	All	838/856 (98%)	787 (94%)	51 (6%)	23	17

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	31	LEU
1	B	36	ILE
1	B	37	LEU
1	B	91	SER
1	B	109	LEU
1	B	124	ARG
1	B	147	LEU
1	B	154	ILE
1	B	159	THR
1	B	165	LEU
1	B	274	ILE
1	B	277	GLU
1	B	280	VAL

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Mol	Chain	Res	Type
1	B	289	THR
1	B	408	LEU
1	B	410	GLN
1	B	422	GLN
1	B	423	ARG
1	B	455	LYS
1	B	534	GLN
1	B	552	ASP
1	B	556	THR
1	B	577	LEU
1	A	30	LEU
1	A	31	LEU
1	A	36	ILE
1	A	82	VAL
1	A	86	THR
1	A	91	SER
1	A	114	ARG
1	A	124	ARG
1	A	147	LEU
1	A	154	ILE
1	A	159	THR
1	A	189	THR
1	A	214	LYS
1	A	256	ARG
1	A	280	VAL
1	A	289	THR
1	A	380	ARG
1	A	381	MET
1	A	384	THR
1	A	386	LEU
1	A	407	THR
1	A	408	LEU
1	A	417	ARG
1	A	423	ARG
1	A	455	LYS
1	A	471	GLU
1	A	478	ARG
1	A	556	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	44	HIS
1	B	118	GLN
1	B	163	HIS
1	B	168	HIS
1	B	278	GLN
1	B	343	ASN
1	B	375	HIS
1	B	422	GLN
1	B	433	GLN
1	B	437	GLN
1	B	510	HIS
1	B	511	HIS
1	B	534	GLN
1	A	44	HIS
1	A	118	GLN
1	A	163	HIS
1	A	278	GLN
1	A	433	GLN
1	A	510	HIS
1	A	511	HIS
1	A	534	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 ⓘ

Of 6 ligands modelled in this entry, 6 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, 95th 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 ²)	Q<0.9
1	A	548/559 (98%)	0.23	26 (4%) 35 46	30, 45, 69, 93	0
1	B	548/559 (98%)	-0.09	20 (3%) 46 57	28, 37, 56, 85	0
All	All	1096/1118 (98%)	0.07	46 (4%) 40 50	28, 41, 66, 93	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	577	LEU	8.2
1	B	61	ALA	6.7
1	A	418	ALA	4.3
1	A	405	TYR	3.9
1	A	411	LYS	3.5
1	A	312	ALA	3.4
1	A	410	GLN	3.1
1	B	75	ARG	3.0
1	A	310	PHE	3.0
1	B	488	LEU	2.8
1	A	383	ARG	2.8
1	B	63	ILE	2.8
1	A	237	VAL	2.8
1	B	141	ALA	2.6
1	A	366	TRP	2.6
1	B	57	PRO	2.6
1	B	458	LEU	2.6
1	B	58	GLY	2.5
1	B	80	GLN	2.5
1	A	236	GLY	2.5
1	A	409	GLY	2.5
1	A	422	GLN	2.4
1	B	124	ARG	2.4
1	A	30	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	61	ALA	2.3
1	B	498	VAL	2.3
1	A	458	LEU	2.3
1	A	429	ARG	2.3
1	A	524	LEU	2.3
1	A	457	ALA	2.3
1	B	32	GLN	2.3
1	B	82	VAL	2.2
1	A	392	VAL	2.2
1	A	109	LEU	2.2
1	A	577	LEU	2.2
1	A	414	PRO	2.1
1	A	384	THR	2.1
1	B	383	ARG	2.1
1	B	108	SER	2.1
1	B	454	ASN	2.1
1	B	83	TRP	2.1
1	A	567	LEU	2.1
1	A	564	ASN	2.1
1	A	469	HIS	2.0
1	B	564	ASN	2.0
1	B	567	LEU	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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(\AA^2)	Q<0.9
3	CA	B	602	1/1	0.99	0.21	3.14	56,56,56,56	0
3	CA	A	602	1/1	0.97	0.24	1.36	79,79,79,79	0
2	ZN	A	601	1/1	1.00	0.10	0.86	40,40,40,40	0
3	CA	B	603	1/1	0.99	0.07	-1.03	33,33,33,33	0
2	ZN	B	601	1/1	1.00	0.06	-1.61	34,34,34,34	0
3	CA	A	603	1/1	0.98	0.05	-4.15	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.